```
5, 2006, 22:08:53 ; Search time 91.1379 Seconds (without alignments) 60.201 Million cell updates/sec
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                          2589679
                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       2589679 segs, 457216429 residues
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geneseqp2000s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genesedp2005s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   geneseqp1980s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           geneseqp1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              geneseqp2001s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             geneseqp2002s:*
                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
                                                                                                                                                                                                              1 FQGVLQQVRFVF 12
                                                                                                                                                                         US-10-030-735-20
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A_Geneseq_8:*
                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                           Minimum DB E
Maximum DB E
                                                                       OM protein
                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                         Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesegp2006s:

10:

Human myo Human myo Angiotens Human can Angiotens TSF polyp Angiotens Alpha3bet Alpha3bet Alpha3bet Alpha3bet Thrombosp Human thr Angiotens Human thr Human thr Human thr Human thr Human thr Human COP Aab35379 Alpha3bet Human var Description Aau02913 / Aab00042 F Aau74771 F Abb82285 F Aab74450 F Aab90800 F Aae25030 F Aau75315 F Abp96780 F Aab35378 Aab35376 Abb32336 Abb72834 Ad170641 Ad439359 Ad439359 Ad439359 Aab43602 Aab43602 Aab43602 Aab43602 Aab43602 Aab43602 SUMMARIES AAB35379 AAB35352 AAB35378 ADL70641 ADQ39359 ADQ39357 AAU02916 AAB43602 AAU02915 ADN02474 AAU02913 AAB00042 AAU74771 ABB82285 AAB90800 AAE25030 AAU75315 ABP96780 AAB35380 ABG72834 AAB35376 В Query Match Length 91.7 91.7 91.7 91.7 91.7 91.7 Score Result Ņ.

Abu03474 Angiogene Abg74673 Human THB		Abr62059 Human thr	Adn39852 Cancer/an	Adj76124 Marker ge	Adj75296 Marker ge	Adl70639 Human thr	Adl35874 Human thr	Adq26070 Thrombosp	Adp54179 Human PRO	Adq39358 Human myo	Adq39356 Human myo	Adq39355 Human myo	Thromb	Aeb87781 Human thr	Aeb46751 Human thr	Aab35361 Alpha3bet	Aab35373 Alpha3bet	Aab35381 Alpha3bet	Aab35364 Alpha3bet	Aab35374 Alpha3bet	
ABU03474 ABG74673	AAE36228	ABR62059	ADN39852	ADJ76124	ADJ75296	ADL70639	ADL35874	ADQ26070	ADP54179	ADQ39358	ADQ39356	ADQ39355	AD221688	AEB87781	AEB46751	AAB35361	AAB35373	AAB35381	AAB35364	AAB35374	
1170 6	1170 6	1170 7			-		1170 8		1170 8	1170 8	1170 8	1170 8	170 9	1170 9	170 9	12 4	12 4	12 4	12 4	12 4	
	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7			2 86.7	98	85.	œ	
	26 55			ហ		ß										Ú					

ALIGNMENTS

RESULT 1 AAB35379

Alpha3betal integrin binding peptide #44. AAB35379 standard; peptide; 12 AA. (first entry) 08-MAY-2001 AAB35379;

Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.

Synthetic.

WO200105812-A2.

25-JAN-2001.

12-JUL-2000; 2000WO-US018986

99US-0144549P 15-JUL-1999; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Krutzsch HC; Roberts DD,

WPI; 2001-182656/18.

New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and cancer

Claim 4; Page 34; 84pp; English.

The present invention provides a number of peptides which bind to alphalbetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psorlasis and restenosis. The present sequence is an example of one of the peptides of the invention

Sequence 12 AA;

~

,

```
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha3betal integrin binding peptide #41.
                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                             Example 2; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB35376 standard; peptide; 12
                                                                                                            12-JUL-2000; 2000WO-US018986.
                                                                                                                                99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0144549P.
                                                                                                                                                                                                                                                                                                                                                                      91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                 FQGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roberts DD, Krutzsch HC;
                                                                                                                                                                                         WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  of the invention
                                                                                                                                                                                                                                                                                                                                                    Sequence 12 AA;
                                                                    WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200105812-A2
                                                                                                                                15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999;
                                                                                        25-JAN-2001.
                                                                                                                                                                     Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001.
                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB35376;
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                             New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB35376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention
                                                                                                                                                                                       Alphaßbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                          New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
100.0%; Score 60; DB 4; Length 12; 100.0%; Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55; DB 4; Length 1., Pred, No. 0.0013;
                 0; Indels
                   0; Mismatches
                                                                                                                                                                     Alpha3betal integrin binding peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha3betal integrin binding peptide #43.
                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                          AAB35352 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB35378 standard; peptide; 12
                                                                                                                                                                                                                                                                                          12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                              99US-0144549P
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                    Krutzsch HC;
                   Conservative
                                      1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOGVLONVRFVF 12
                                                        FOGVĽÓQVŘFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOGVLOOVRFVF
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-182656/18.
          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 AA;
                                                                                                                                                                                                                                                   WO200105812-A2.
                                                                                                                                                                                                                                                                                                                                                    Roberts DD,
                  12;
                                                                                                                                                 08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2001
                                                                                                                                                                                                                                                                       25-JAN-2001
                                                                                                                                                                                                                                 Synthetic
                                                                                                                              AAB35352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB35378;
Query Match
           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                   Matches
                                                                                                 AAB35352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB3537
                                                         셤
                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXEXEXE,
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides that bind to or are recognized by alpha3-betal integrins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 4;
Pred. No. 0.0013;
```

WPI; 2001-182656/18.

```
The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of peptides which bind to alpha3beta1 integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                            New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                            Score 55; DB 4; Length 12;
Pred. No. 0.0013;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            integrin binding peptide #45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB35380 standard; peptide; 12 AA
                                                                                                                               Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                            91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                            1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                  1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                             of the invention
                                                                                                                                                                                                                                                                             Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200105812-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha3beta1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB35380;
                                                                                                cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer
                                                                                                                                                                                                                                                                                                                                              Matches
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to diagnosing cancer other than prostate cancer in a male mammal, comprising assaying a test sample for increased level of semenogalin, or cancer in a female by assaying for the presence of semenogalin. Administering a semenogalin protein or polypeptide fragment or a semenogalin. Protein or antibody or active fragment, or a recombinant vector expressing the protein or antibody, is useful for inducing an immune response to a cancer in a mammal, where the cancer is not prostate cancer and semenogalin is a marker. The invention is used to diagnose cancer, particularly of epithelial origin such as lung cancer, papillary renal cell carcinoma, colon cancer, especially small-cell lung cancer (SCLC), or a melanoma. The present sequence represents the amino acid sequence of the thrombospondin-1 sequence containing synthetic peptide which binds to alpha-3-beta-1 integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A new diagnosis for cancer other than prostate cancer in a mammal useful to detect cancer including lung cancer, particularly small cell lung cancer and melanoma comprises detecting semenogelin in a sample.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                    Human, thrombospondin-1; cytostatic; immunostimulant; cancer; epithelial cancer; lung cancer; papillary renal cell carcinoma; colon cancer; small-cell lung cancer; SCLC; melanoma.
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Score 55, DB 4, Length 12;
Pred. No. 0.0013;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%; Score 55; DB 6; Length 12; 91.7%; Pred. No. 0.0013; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                   Thrombospondin-1 sequence containing synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                               ABG72834 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 14; 32pp; English.
   91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-2002; 2002WO-US010535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2001; 2001US-0281994P
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krutzsch HC;
                                      11; Conservative
                                                                       1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                       1 FOGVLODVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-103329/09.
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200281630-A2
                                                                                                                                                                                                                                                                  24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
   Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                          RESULT 6
                                                                        à
                                                                                                       g
                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

ö

Gaps ö RESULT 7 ADL70641

Sequence 12 AA;

```
The present sequence is that of the N-terminal domain of human thrombospondin-1 (TSP) ADL70639. The invention relates to TSP fragments thrombospondin-1 (TSP) ADL70639. The invention relates to TSP fragment conclinical assays for cancer and for generation of antibodies and other colinical assays for cancer and for generation of antibodies and other binding agents. A method that distinguishes TSP from a TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion of TSP plus not in the fragment or portion; (2) using an epitope present in TSP but not in the fragment or portion to obtain a quantitation of TSP plus TSP fragment or portion of the TSP fragment or portion of TSP only; and (3) using the difference between (1) and quantitation of TSP put not in the fragment or portion. Suitable epitope present in TSP but not in the fragment or portion of the TSP fragment or portion is performed in order to obtain a quantitation of the TSP fragment or portion is performed in order to detect the presence, or monitor the course, of a disease or condition selected from cancer, renal failure, renal disease, atopic dermatitis, vasculitis, polyarteritis of infarction, liver disease, splenactomy, dermatchowistis, polyarteritis ondosa, systemic lupus erythematosus, lupus erythematosus Kawasaki theometrion, an opecific vasculitis juvenile rheumatoid arthritis, resulting, accompanied with placelet cut activation, a condition associated with intravascular coagulation, a condition associated with placelet activation, a condition associated with intravascular coagulation, a condition associated with machorial coagulation, a condition associated with endothelial activation, a condition and coagulation, a condition and proper properation and properation and properation and properation and prop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fragment, urticaria, hives, angioedema, a drug reaction, an antibiotic reaction, an aspartame reaction, atopic dermatitis, ecsema, hypersensitivity, scleroderma, conditions associated with plugging of vessels, a condition associated with a cryotibrinogen, a condition
                                                                                                                                                                                 Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Fibrinogen binding region"
                                                                                                                                                                                                                                                                                                         23. .32
/note= "Heparin binding region"
77. .82
                                                                                                                                                                                                                                                                                                                                                                        /note= "Heparin binding region"
                                                                                                                                      !uman thrombospondin-1 N-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 40; 76pp; English.
                                                                                                                                                                                                                                                                               Location/Qualifiers
ADL70641 standard; protein; 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2002; 2002US-0405494P.
21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2003; 2003WO-US026023.
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                .164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WILL/) WILLIAMS K J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-226901/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004018995-A2
                                                                                                                                                                                                                                    Homo sapiens
                                                                                        20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams
                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                  Region
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino
              cardiolipin antibody. The cancer is selected from adenoma, adenocarcinoma, carcinoma, lymphoma, leukaemia, solid cancer, liquid cancer, pre-metastatic cancer, pre-metastatic cancer, pre-metastatic cancer, pre-metastatic cancer, a cancer with vascular invasion, internal cancer, skin cancer, cancer of the respiratory system, circulatory system, musculoskeletal system, muscle, bone, a joint, tendon or ligament, digestive system, liver or biliary system, pancreas, head, neck, endocrine system, reproductive system (male or female), genitourinary system, kidney, urinary tract, sensory system, nervous system, lymphoid organ, blood, a gland, mammary gland, prostate gland, endometrial tissue, mesodermal tissue, ectodermal tissue, andodermal tissue, a teratoma, a poorly-differentiated cancer, a well-differentiated cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human myocardial infarction-associated gene derived protein, SEQ ID 1022.
associated with a cryoglobulin, and a condition associated with an anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                   Score 55; DB 8; Length 240;
Pred. No. 0.033;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; SEQ ID NO 1022; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iakoubova 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ39359 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiant; gene therapy; human
                                                                                                                                                                                                                                                                                                                       91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           190 FOGVLONVRFVF 201
                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cargill M, Devlin JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-533949/51.
N-PSDB; ADQ38531.
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                  Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004058052-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ39359;
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ39359
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
```

```
acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The caches is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction.

sescuence represents the protein of a human myocardial infarction. Note: This sequence was not shown in the specification. The sequence has come from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an electronic sequence listing downloaded from the WIPO website.
          $$$$$$$$$$$$$$$$$$$$$$$$$
```

Sequence 432 AA;

```
Gaps
                     ö
  Length 432;
                     1; Indels
 Score 55; DB 8;
Pred. No. 0.063;
); Mismatches
                     ö
91.7%;
91.7%;
                                                            208 FOGVLONVRFVF 219
                     11; Conservative
                                        1 FOGVLOOVREVE 12
           Local Similarity
 Query Match
                     Matches
                                                          셤
                                         ઠે
```

ö

RESULT 9

ADQ39357 standard; protein; 432 AA (first entry) 18-NOV-2004 ADQ39357;

Human myocardial infarction-associated gene derived protein, SEQ ID 1020. Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human

Homo sapiens.

WO2004058052-A2.

15-JUL-2004

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P. 10-MAR-2003; 2003US-0453135P. 30-APR-2003; 2003US-0466412P. 23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP

Iakoubova 0;

Devlin JJ,

Σ

Cargill

WPI; 2004-533949/51.

N-PSDB; ADQ38529.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 10; SEQ ID NO 1020; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's The invention has an altered

altered risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention further comprising at least a contiguous nucleotides where one of the mucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequence given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specification and main acid sequence given in the specification; an antibody comprising an smplified polypucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and comprising in SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and containing an SNP in a nucleic acid sof the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction method has an increased or decreased risk for developing myocardial infarction may be used in gene therapy. The method is useful in identifying an myocardial infarction may be used in gene therapy. The method is useful in identifying an myocardial infarction method has an increased or decreased risk for developing myocardial infarction may be used in gene therapy. The method is useful in identifying an myocardial infarction method has an increased or decreased risk for developing myocardial infarction method is useful in identifying an myocardial infarction method is not not reasting the model of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or method is useful in identifying an individual who myocardial infarction method is useful in identifying an individual who myocardial infarction method is useful in myocardial in ö Angiotensin converting enzyme splice variant; ACBV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; arcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidosic pulmonary granulomattous disease; endothelial abnormality; associated gene containing one or more SNP's of the invention. Note: Thi sequence was not shown in the specification. The sequence has come from Gaps This composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-Angiotensin converting enzyme (ACEV) splice variant protein #16. an electronic sequence listing downloaded from the WIPO website .. 0 91.7%; Score 55; DB 8; Length 432; 91.7%; Pred. No. 0.063; ive 0; Mismatches 1; Indels Bernstein J; Khosravi R, AAU02916 standard; protein; 459 AA. vascular disorder; asbestosis. Azar I, 17-NOV-2000; 2000WO-IL000766. 99IL-00132978. 99IL-00133455. (first entry) 1|||| ||||| 208 FQGVLQNVRFVF 219 11; Conservative 1 FOGVLOOVRFVF 12 (COMP-) COMPUGEN LTD. Levine Z, David A, WPI; 2001-336004/35. N-PSDB; AAS06016. Best Local Similarity Sequence 432 AA; WO200136632-A2 17-NOV-1999; 10-DEC-1999; Homo sapiens. 12-SEP-2001 25-MAY-2001. AAU02916; Query Match RESULT 10 AAU02916 Matches ò 셤

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy,
                                                                                                                                                                                                                                                                                                                                                                                              cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                  Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological, neuroprotective, thrombolytic, coaquiant, nootropic, vasotropic, antipsoriatic, antiangiogenic, gene therapy, inflammation, immune disorder, haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                  Immune disorders such as immune complex nephritis, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, cancer associated gene, cancer antigen, detection, cancer, diagnosis, cytostatic, proliferative, vulnerary, immunomodulator, antidiabetic, antiasthmatic, antirheumatic, antiarthritic, antiviral, antinflammatory, antithyroid, antiallergic, antibacterial, cardiant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haemostatic; thrombolytic; cardiovascular disorder; infection;
neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 4; Length 459;
Pred. No. 0.067;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer associated protein sequence SEQ ID NO:1047.
                                                                                                                                                                                                                                                                                                                                                                                                                                            abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB43602 standard; protein; 466 AA.
                                                                                                 Claim 4; Fig 16; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2000; 2000WO-US005882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0124270P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||||| |||||
208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 91.7
nes 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-587533/55.
N-PSDB; AAC77811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VO200055350-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB43602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
AAB43602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
AAC77607 to AAC78448 encode the human cancer associated proteins given in tissues and cells the genes are expressed in. Example of activities tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antithreumatic; antiarthritic; antidiabetic; antisyload; antialthritic; antidiabetic; antisyload; antialthritic; antidiabetic; antisyload; antialticyload; are antiantial antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The nootropic; vasotropic; antipsoriatic and antiangiogenic. The coagulant; ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides can be used for preventing, treating or ameliorating the proliferation, differentiation or mobilisation of immune cells to treat disorders of haematopoietic cells, autoimmune cills to treat disorders of haematopoietic cells, autoimmune rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disease; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angiotensin converting enzyme (ACEV) splice variant protein #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%; Score 55; DB 3; Length 466; 91.7%; Pred. No. 0.068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levine Z, David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                            Claim 11; Page 1636-1638; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU02915 standard; protein; 546 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99IL-00132978.
99IL-00133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 FÓGVLÓNVRFVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MO200136632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU02915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02915
   \texttt{FFXXX}\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PART OF THE STATE OF THE STATE
```

ö

Gaps

ö

Score 55; DB 7; Length 548; Pred. No. 0.081; 0; Mismatches 1; Indels

91.78;

The present invention relates to a novel recombinant adenovirus vector mediated anti-neoplastic composition is prepared through cloning the cDNA Tumor suppressing polypeptide TSF and gene therapy vector composition adenovirus vector; anti-neoplastic; TSF polypeptide; cancer. (TAID-) TAIDA LIFE SCI TECH RES CENT HEMATOLOGY. abnormality such as deep vein thrombosis Claim 2; SEQ ID NO 1; 13pp; Chinese ADN02474 standard; protein; 548 AA. Claim 4; Fig 15; 519pp; English 91.7%; 91.7%; 21-AUG-2002; 2002CN-00129408. 21-AUG-2002; 2002CN-00129408 17-JUN-2004 (first entry) 208 FOGVLONVREVE 219 Query Match
Best Local Similarity 91.7
Matches 11; Conservative 1 FQGVLQQVRFVF 12 WPI; 2003-469302/45. N-PSDB; ADN02475. WPI; 2001-336004/35 N-PSDB; AAS06015 Sequence 546 AA; TSF polypeptide Liu P; Homo sapiens CN1401387-A. 12-MAR-2003 ADN02474; Han Z, g 8

```
sequence from the human peripheral blood cell by specific primer and reverse transcription-polymerase chain reaction (RT-PCR) method for coding TSF polypeptide, construction in human embryonic kidney cell 293 by AdEasy system, and packaging and expressing the recombinant adenovirus vector of TSF. It can suppress the growth and transfer of cancer. The present sequence represents the TSF polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin converting enzyme (ACEV) splice variant protein #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU02914 standard; protein; 555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                             208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                            Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02914
          8888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disoarders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                            The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
                                                                                                                                       Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 4; Length 546;
Pred. No. 0.08;
); Mismatches 1; Indels
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis,
                                                                                                                                 Angiotensin converting enzyme splice variant; ACBV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; glatelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidoric pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bernstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      David A, Azar I, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Fig 14; 519pp; English
                                                                                                                                                                                                                                                                                                                              vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99IL-00132978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS06014
                                                                                                                                                                                                                                                                                                                                                                                                            WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levine Z,
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis,
myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nultiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiotensin converting enzyme (ACEV) splice variant protein #13
                                                                                                                                                                                                                          ö
                                                                                                                                                                               Score 55; DB 4; Length 555;
Pred. No. 0.082;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Khosravi R,
                                                                                                      abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                          AAU02913 standard; protein; 731 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 13; 519pp; English.
                                                                                                                                                                               91.7%;
ilarity 91.7%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Levine Z, David A, Azar I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99IL-00132978.
99IL-00133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                        208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                  1 FOGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-336004/35
                                                                                                                                                                                               Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS06013.
                                                                                                                                             Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200136632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02913;
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                     888888838
                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                  ò
```

```
ö
myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidocic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                               Gaps
                                                                                                                                                                                               ö
                                                                                                                                                           Score 55; DB 4; Length 731;
Pred. No. 0.11;
                                                                                                                                                                                               1; Indels
                                                                                                                                                                                               0; Mismatches
                                                                                         abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                        5, 2006, 22:24:58
                                                                                                                                                             91.7%;
91.7%;
                                                                                                                                                                                                                                                                     208 FOGVLONVRFVF 219
                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                  1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                    completed: June
ne : 91.1379 secs
                                                                                                                                                                               Local Similarity
                                                                                                                          Sequence 731 AA;
                                                                                                                                                              Query Match
                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                          Job time
                                                                                                                                                                                                                                                                                                                        Search
     88888888888
                                                                                                                                                                                                                                                                   q
```

5.1.9	Siocceleration Ltd.
version	- 2006
GenCore	(c) 1993
	Copyright

- protein search, using sw model OM protein

Run on:

June

5, 2006, 22:25:22 ; Search time 13.9655 Seconds (without alignments) 82.675 Million cell updates/sec

US-10-030-735-20 60 1 FQGVLQQVRFVF 12 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

pirl: pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	thrombospondin 1 -	thrombospondin 1 p	Н	probable imidazole	hypothetical prote	tRNA-pseudouridine	thrombospondin 2 p	thrombospondin 2 p	ğ	hypothetical prote	protein F15D4.3 [i	two-component hybr		NSP3 protein - hum	53K glycoprotein -	methylmalonyl-CoA	hypothetical prote	probable penicilli	M polyprotein prec	M polyprotein prec	thrombospondin pre	xanthine dehydroge	hypothetical prote	hypothetical prote	35K GTP-binding pr	ribose/galactose A	hypothetical prote	Ø	amino acid permeas
)				
SUMMARIES	ID		TSHUP1	A40558	D81929	T33595	C57253	TSHUP2	A42587	D81910	T20985	B88349	AH2090	G81105	S51728	845068	E84019	T49212	T36795	GNVUPH	JQ1604	A39804	хонирн	C83862	75	B54575	F70184	T24890	24	D86669
	DB	~		~	7	~	~	Н	~	~	~	~	N	~	~	~	ď	~	7	-	Н	Н							~	7
	Query Match Length	229	1170	1170	212	469	151	1172	1172	102	145	162	1299	102	313	471	516	527	893	1142	1148	1178	1333	165	175	295	311	400	0	459
d	Query Match	91.7	91.7	91.7	63.3	63.3	61.7	61.7	61.7	0.09	0.09	0.09	0.09	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	56.7	56.7	56.7	56.7	56.7	56.7	
	Score	55	52	55	38	38	37	37	37	36	36	36	36	35	35	35	35	35	35	35	35	35	35	34	34	34	34		34	34
	Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

L2 protein - Europ	probable integral-	probable ptrBa pro	hypothetical prote	oligopeptidase B (oligopeptidase B (proteinase II (imp		proteinase II (imp	two component resp	probable transcrip	neurofilament prot	probable negative		DNA-directed DNA p	hypothetical prote
P2WLEP	E87021	A70709	T23843	AC0741	E64946	C90948	G85796	F87187	AE2929	A98353	T52485	T39103	868593	S71551	F96625
н	~	~	~	7	٦	~	~	~	~	~	~	~	~	~	7
477	505	552	565	683	686	989	989	724	747	783	913	1142	1312	1670	82
56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	55.0
34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	33
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
Cipate: Dellerin, S. Keramidas, M.; Chambaz, E.M.; Feige, J.J.
Sulate: Sipate: Sipate: regulation of thrombospondin-1 and CISP/thrombospondin-2 expressing A; Reference number: Sipates
A; Reference number: Sipates
A; Reference number: Sipates
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Coss-references: UNIPROT: Q28194; UNIPARC: UPI000008740A; EMBL: X89511; NID: G899228; PIDA
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 2; Length 229
Pred. No. 0.0017;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Guest Local Similarity 91...
Best Local Similarity 91...
```

190 FQGVLQNVRFVF 201 1 FOGULOQURFUF 12 g ઠે

RESULT 2

thrombospondin 1 precursor - human C.Species: Homo sapiens (man) C.Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004 C.Accesion: A25, A34274; A30140; A25812; A05172; A42927 R.Lawler, J.; Hynes, R.O.

R,Lawler, J.; Hynes, R.O. J. Cell Biol. 103, 1635-1648, 1986 A,Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple ca A,Reference number: A26155; MUID:87057617; PMID:2430973 A; Accession: A26155

A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1170 «LAW>
A; Rosidues: 1-1170 «LAW>
A; Cross-references: UNIPROT: P07996; UNIPARC: UPI0000046821; GB: X04665; NID: g37137; PIDN: C;
A; Note: parts of this sequence, including the amino end of the mature protein, were deter
B; Laherty, C.D.; Gierman, T.M.; Dixit, V.M.
J; Biol: Chem. 264, 11222-11227, 1989
A; Title: Chem. 264, 1122-11227, MUID: 89291870; PMID: 2544587

A;Molecule type: DNA A;Residues: 1-166 <LAH> A;Cross-references: UNIPARC:UP100001742BF; GB:J04835 F;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, I T;Hennessy, S.W.; Frazier, B.A.; Kim, Bequence includes potential regulatory sites in the A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the

us-10-030-735-20.rpr

```
probable imidazole-glycerol phosphate synthase amidotransferase component (EC 2.4.2.-) NN C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C; Accession: D81929
F; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
F; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
F; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A, Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A, Reference number: A81775; MuID:20222556; PMID:10761919
                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT: P35441; UNIPARC: UPI0000028012; GB:M62469; GB:M62469; GB:M62463; R;Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
A;Title: Characterization of the mouse thrombospondin gene and evaluation of the role of A;Reference number: A37905; MUID:90375546; PMID:2398070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1152, P', 1154-1170 <LAH>
A;Cross-references: UNIPARC:UP10000177496; GB:M87276
A;Cross-references: UNIPARC:UP10000177496; GB:M87276
A;Note: sequence extracted from NCBI backbone (NCBIP:81501)
R;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FRBS Lett. 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar
A;Reference number: S68787; MUID:96234006; PMID:8654563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 19-26, XY, 28-37 < CHE>
A;Residues: 19-26, XY, 28-37 < CHE>
A;Residues: 19-26, XY, 28-37 < CHE>
A;Cross-references: UNIPARC:UPIO000177A97
C;Complex: homotrimer, disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
C;Keywords: calcium binding; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <AMAT>
F;37-37/Domain: thrombospondin 1 #status predicted <AMAT>
F;37-429/Domain: thrombospondin type 1 repeat homology <THR2>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;431-547/Domain: EGF homology <EGF>
F;551-586/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary
A,Molecule type: DPA
A,Residues: 1-212 <PAR>
A,Cross-references: UNIPROT:Q9JVH3; UNIPARC:UPI000012C805; GB:AL162754; GB:AL157959; NID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI000016D076; GB:J05605; GB:J05606; NID:g201991; PIDN:AAA404; R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M. J. Biol. Chem. 267, 2274-3221, 1992
A;Title: Chem. 267, 2274-3221, 1992
A;Title: Chemracterization of mouse thrombospondin 2 sequence and expression during cell § A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: B42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 91.7%; Score 55; DB 2; Length 1170; Local Similarity 91.7%; Pred. No. 0.0095; nes 11; Conservative 0; Mismatches 1; Indels
                                 A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FQGVLQNVŘFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-490 < BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary A; Molecule type: DNA
                                                                                                                                A; Accession: A40558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A37905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.)Description: participates in cell migration and adhesion, and in platelet aggregation C, Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc C, Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer F;19-1170/Product: thrombospondin 1 #status.predicted <MAT> F;18-1170/Product: thrombospondin 1 #status predicted <MAT> F;317-375/Domain: thrombospondin type 1 repeat homology <THR1> F;314-490/Domain: thrombospondin type 1 repeat homology <THR2> F;491-547/Domain: thrombospondin type 1 repeat homology <THR3> F;50-689/Domain: EGF homology <EGF1> F;50-689/Domain: EGF homology <EGF2> F;26-9288/Region: cell attachment (R-G-D) motif F;11-232/Disulfide bonds: #status predicted F;171-232/Disulfide bonds: #status predicted F;270,274/Disulfide bonds: interchain #status predicted F;20/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted F;1051/Binding site: carbohydrate (Asn) (covalent) #status predicted F;1051/Binding site: erythro-beta-hydroxyasparagine (Asn) #status absent
                                                                            A; Molecule type: mRNA
A; Residues: 1-83,'A', 85-522,'A', 524-1170 A; Residues: 1-83,'A', 85-522,'A', 524-1170 A; Residues: 1-83,'A', 85-522,'A', 524-1170 A; Cross-references: UNIPARC: UPI0000038AB1; EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PIL A; Note: parts of this sequence, including the amino end of the mature protein, were determined: S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P. Bornstein, P. Bochemiarty 25, 8418-8425, 1986
A; Title: Partial amino acid sequence of human thrombospondin as determined by analysis of A; Reference number: A25812; MUID:87157592; PMID:3030396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-83.74', 85-397 <KOB>
A;Cross-references: UNIPARC:UPI000016B0CA; GB:M25631; NID:g538353; PIDN:AAA36741.1; PID:
R;Dixit, V.M.; Hennessy, S. W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A;Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-83, A', 85-374, RC' < DIX>
A; Residues: 1-83, A', 85-374, RC' < DIX>
A; Cross-references: UNIPARC: UPI000016B140; GB:M14326; NID:g340005; PIDN:AAA61237,1; PII
A; Nove: parts of this sequence, including the amino end of the mature protein, were det
R; Sun, X.; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A; Title: Disulfides modulate RQD-inhibitable cell adhesive activity of thrombospondin.
A; Reference number: A42927; MUID:92348511; PMID:1379247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787
A;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 1; Length 117
Pred. No. 0.0095;
0; Mismatches 1; Indels
number: A30140; MUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Rosidues: 987-1003 <SUN.
A;Cross-references: UNIPARC:UPI00001742C0
A;Note: Cys-992 is shown to have a free sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: the list of introns may be incomplete C; Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Gene: GDB:THB81; TSP1; TSP
A;Cross-references: GDB:120438; OMIM:188060
A;Map position: 15q15-15q15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 POGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: A42927
                                          A; Accession: A30140
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A25812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: A05172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Introns: 23/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
Chromoospondin 2 precursor - human
C;Species: Homo sapiens (man)
C;Daccession: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A47379; A42173
R;LaBell, T.L.; Byers, P.H.
Genomics 17, 225-259, 1993
A;Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: poter A;Reference number: A47379; MUID:94010892; PMID:8406456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1172 <LAB>
A; Cross-references: UNIPROF. P35442; UNIPARC: UPI0000046680; GB:L12350; NID:g307505; PIDN:;
R; Labell, T.L.; Milewicz, D.J.; Disteche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992
A; Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression of
A; Reference number: A42173; MUID:92217961; PMID:1559694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A'pescription: participates in cell migration and adhesion, and in platelet aggregation c'Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor C'Seywords: beta-hydroxyasparagine; calculum binding; cell adhesion; glycoprotein; trimer E7:1-18/Domain: signal sequence #status predicted <SIG> F:1-18/Domain: von Willabrand factor type C repeat homology <VWC> F:319-317/Domain: thrombospondin type 1 repeat homology <THR1> F:380-431/Domain: thrombospondin type 1 repeat homology <THR2> F:523-589/Domain: EGF homology <EGF!> F:552-691/Domain: EGF homology <EGF!> F:552-691/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombospondin 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42587; A39851
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A;Fitle: Characterization of mouse thrombospondin 2 sequence and expression during cell &
A;Reference number: A42587; MUID:92147683; PMID:1371115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Status: 1172 < LAH
A;Cross-references: UNIPROT:Q03350; UNIPARC:UPI0000029847; GB:L07803; GB:M87275; NID:g34(
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
R;Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.7%; Score 37; DB 1; Length 1172; 58.3%; Pred. No. 46; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPARC: UPI00001742C1; GB: M81339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:128789; OMIM:188061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 58.3
nes 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGULOQURFUF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 560-1172 <LA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: THBS2; TSP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A47379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999
B;Maggi, L.; Goela, D.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid C40All.
A;Reference number: Z21374
A;Accession: T33595
A;Accession: T33595
A;Accession: T33595
A;Accession: T33595
A;Accession: T33595
A;Accession: T33595
A;Accession: T3469
A;Accession: T3469
A;Accession: T3469
A;Accessive T469
A;Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: C57253

K;Kok, R. G; van Thor, J.J.; Nugteren-Roodzant, I.M.; Vosman, B.; Hellingwerf, K.J.
J; Bacteriol. 177, 3295-3307, 1995

A;Title: Characterization of lipase-deficient mutants of Acinetobacter calcoaceticus BD4

A;Reference number: A57253; MUID:95286514; PMID:7768830

A;Accession: C57253

A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tRNA-pseudouridine synthase (BC 5.4.99.-) - Acinetobacter calcoaceticus (fragment) NiAlternate names: hypothetical protein lipB 5'-region (5.8pecies: Acinetobacter calcoaceticus (5.8pecies: Acinetobacter calcoaceticus (5.8pecies: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. CTOSS-TEFETENCES: UNIVERS.UPI000017879A; GB:X80800
C;Superfamily: tRNA pseudouridine synthase B
C;Keywords: intramolecular transferase; isomerase; tRNA modification
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                 Score 38, DB 2; Length 212;
Pred. No. 4.6;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C40A11.9 - Caenorhabditis elegans
                                                                                   A;Gene: hisH; NMAO840
C;Superfamily: amidotransferase hisH; trpG homology
C;Keywords: glycosyltransferase; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 2;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.7%; Score 37; DB 2; 70.0%; Pred. No. 5.1;
A; Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                 63.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 2
A;Introns: 199/2; 315/2; 424/2
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 FQGIPQDTRFYF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58..
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 FNGVVTQIYFVF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||:||:|
GVLQKVRWLF 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-151 < KOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Genetics:
A, Gene: CESP: C40A11.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

ö

Gaps

ö

```
protein FISD4.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: B88349
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Title: Dublished errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: B88349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: UNIPROT: Q93511; UNIPARC: UP10000179EEB; GB: chr_II; PIDN: CAB02486.1; P1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gispecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2080
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 201
A;Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          two-component hybrid sensor and regulator alr2279 [imported] - Nostoc sp. (strain PCC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q8YUQ6; UNIPARC:UPI00000CE3A6; GB:BA000019; PIDN:BAB73978.1; A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 2; Length 1299;
Pred. No. 82;
3; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 2
Pred. No. 8.8;
3; Mismatches
                                                                                 Score 36; DB:
Pred. No. 7.9;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%;
50.0%;
                                                                                    60.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | || | :|::|
FMGVAQGLRYIF 101
                                                                                 Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGULOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|: || | :|
71 FEGICQQTRSLF 82
                                                                                                                                                                                                      1 FOGULQOVRFVF 12
                                                                                                                                                                                                                                                            73 FMĠVAQGLRYIF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1299 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-162 <STO>
A; Map position: 2
A; Introns: 21/3; 82/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: AH2090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: alr2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                            8
                                                                                                                                                                                             %;Cross-references: UNIPARC:UPI000016D077; GB:M64866; NID:g201994; PIDN:AAA40432.1; PID: C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vG C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 2;319-3377/Domain: von Willebrand factor type C repeat homology <VWC> F;310-337/Domain: thrombospondin type 1 repeat homology <THR1> F;436-492/Domain: thrombospondin type 1 repeat homology <THR2> F;436-492/Domain: thrombospondin type 1 repeat homology <THR3> F;553-588/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 <PAR>
A;Cross-references: UNIPROT:Q9JUB1; UNIPARC:UPI0000C4BB6; GB:AL162755; GB:AL157959; NID
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein NMA1411 [imported] - Neisseria meningitidis (strain 22491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cjaccession: D81910

K. Actheman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

Nature 404, 502-506, 2000

AjTille: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-145 <WIL>
A;Cross-references: UNIPROT:Q93511; UNIPARC:UP100007BE33; EMBL:Z80344; PIDN:CAB02486.2;
A;Experimental source: clone F15D4
   J. Biol. Chem. 266, 12821-12824, 1991
A;Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
A;Reference number: A39851; MUID:91302287; PMID:1712771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Accession: T20985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: Neisseria meningitidis hypothetical protein NMB1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 1172;
46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F15D4.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 2;
Pred. No. 5.4;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, September 1996 A;Reference number: Z19354 A;Accession: T20985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.7%; Score 37; 58.3%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 FRGLLONVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGVLQQVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAVMQQVRF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
7, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 7; Conserv
                                                                                                                  A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-873 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: CESP:F15D4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: NMA1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

ö

Gaps

ö

Length 162; 3; Indels ö

Gaps

```
ઠે
                                                                                                                                                                                                                                        g
                                                    C; Species: Neisseria meningitidis
C; Date: 31. Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Date: 31. Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Accession: G31105
R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.R Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A; Machana, G., Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A; Ascession: G81105
                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: CTET>
A,Crossi-teferences: UNIPROT: Q9JZ87; UNIPARC:UPI00000C4675; GB:AE002472; GB:AE002098; NID
A,Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53K glycoprotein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 545068
R;Boyd, K.L.; Kutchai, H.; Takeyasu, K.
submitted to the EMBL Data Library, January 1993
A;Description: Molecular cloning of the 53kDa glycoprotein from chicken sarcoplasmic ret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: mRNA
A,Residues: 1-313 <RAO>
A,Cross-references: UNIPROT:Q82051; UNIPARC:UPI00000F1AE7; EMBL:X81425; NID:g607091; PIU
C,Superfamily: rotavirus nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:Q90577; UNIPARC:UPI00000FE0AA; EMBL:Z21720; NID:g496324; PID
G81105
hypochetical protein NMB1242 [imported] - Neisseria meningitidis (strain MC58 serogroup C;Species: Neisseria meningitidis
C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alvariety: strain 69M
C;Date: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: S51728
R;Rao, C.D.; Das, M.; Rao, B.S.; Gowda, K.
Babmitted to the EMBL Data Library, September 1994
A;Reference number: S51709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: Neisseria meningitidis hypothetical protein NMB1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 2;
Pred. No. 8.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 2
Pred. No. 29;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSP3 protein - human rotavirus (strain 69M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: NS34 protein
C;Species: human rotavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|:||| :::
299 FKGLLQQSNYIY 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGULQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | |:||:||
54 QAVMQQIRF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 QGVLQQVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S45068
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-471 <BOY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: NMB1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
C,Superfamily: sarcoplasmic reticulum 53K glycoprotein C;Keywords: glycoprotein
```

```
Gaps
                            ö
 Length 471;
                         2; Indels
Score 35; DB 2
Pred. No. 44;
4; Mismatches
Query Match 58.3%;
Best Local Similarity 50.0%;
Matches 6; Conservative
```

ö

1 FQGVLQQVRFVF 12

52 FSGVLORLRKIY 63

Search completed: June 5, 2006, 22:45:00 Job time : 14.9655 secs

THIS PAGE BLANK (USPTO)

```
SO THE PERSON OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homo sapien
brachydanio
tetraodon n
sus scrofa
tetraodon n
tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q28194 bos taurus
Q7sy84 xenopus lae
Q28178 bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mus musculu
xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trypanosoma
sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterococcu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xenopus lae
xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            geobacillus
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yarrowia li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nitrosococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neisseria n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmodium
                                                                                                                                                         5, 2006, 22:09:41; Search time 108.931 Seconds (without alignments) 101.901 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00191984
0028118
0028118
001583
001583
001583
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
00159
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
001593
00159
00159
00159
00159
00159
0015
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2849598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2849598 seqs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q28194_BOVIN
Q7SY84_XENLA
TSP1_BOVIN
TSP1_HUMAN
TSP1_MOUSE
Q3TR40_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0715A3_RAT
080CR2 MOUSE
080CR2 MOUSE
080CR2 MOUSE
178P1 XENIA
055PG5_BRARE
055PG5_BRARE
055PG6_BRARE
054PG3 PIG
04RLRS_TETING
04RLRS_TETING
06CKQ2 KLULA
04CV08 TRYCR
04DZY6 TRYCR
04DZY6 TRYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q5L310 GEOKA
Q9TZA3 CAEEL
Q3JDG4 NITOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6CH81_YARLI
Q4XGT3_PLACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4SHB8_TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q5FAZ1 NEIG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q4DZY6_T
Q976Q1_5
                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q82ZE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6IR63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                      US-10-030-735-20
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         June
                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \u03b4 \u
                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
No.
```

```
ö
                                                                                                         verbena x h
aspergillus
dictyosteli
 aspergillus
                intes
                           pseudomonas
                                           pseudomonas
                                                       pseudomonas
                                                                    caldicellul
acinetobact
                                                                                          burkholderi
                                                                                                                                                 homo sapien
                                                                                                                                                                mus musculu
                                                                                                                                                                              homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Opposite regulation of thrombospondin-1 and corticotropin-induced secreted protein/thrombospondin-2 expression by adrenocorticotropic hormone in adrenocortical cells ". J. Cell. Physiol. 167:164-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE-56331130; Pubmed-8698834;
DOI=10.1002/(SIC11097-4652(199604)167:1<164::AID-JCP19>3.3.CO;2-0;
Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chambaz E.M.,
                ciona
                                                                                                                                                                                                                                                                             94 EDVIN

928 1947.

028194;

01-NOV-1996, integrated into UniProtKB/TrEMBL.

01-NOV-1996, sequence version 1.

07-FEB-2006, entry version 24.

Thrombospondin-1 (Fragment).

Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
05avq8 c
05vh52 c
04arb8 E
04arb8 E
087av0 E
022gj9 c
022gj9 c
02ff18 c
03ff19 v
04wl82 a
04wl82 a
04wl82 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 2; Length 229;
Pred. No. 0.016;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25015 MW; 90D9EBCE4E6B669C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X89511; CAA61682.1; -; mRNA.
PIR; S57957; S57957
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR013129; ConA like_subgrp.
InterPro; IPR031129; Laminin_G_TSP_N.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTSY84 XENLA

ID Q7SY84_XENLA PRELIMINARY; PRT; 496 AA.

AC 07SY84.

OTSY84.

DT 01-0CT-2003, integrated into UniProtKB/TrEMBL.

DT 01-0CT-2003, sequence version 1.

DT 07-FEB-2006, entry version 12.
OSAVQB_EMENI

OSVAHS2_CIDIN

OSVENSE

O4ZRP4_PSEU2

O8ZRAQ PSESM

O2ZGJ9_CALSA

TRUB_ACIAD

O3F18B_9BURK

C3PF19_9LAMI

O4MLS2_ASPU

O5SP13_DICDI

TSP2_MOUSE
                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                          QSRI52 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLOOVRFVF 12
 494
210
210
210
210
220
226
334
341
494
494
689
11172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
 NCBI TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feige J.J.;
  3333777883377888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                      BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
  028194
```

214 FQGVLQNVRFVF 225

```
RESULT
엄
                                                                                                                                                                                                                                                              TISSUB-Whole;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altsuberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

D. Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gaurarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Menner A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, BC054970; AAH54970.1; -; mRNA.
GO, GO:0005198; F:structural molecule activity; IEA.
GO, GO:0007155; P:cell adhesion; IEA.
InterPro; IPR013320; ConA like_subgrp.
InterPro; IPR03329; Laminin_G_TSP_N.
InterPro; IPR00884; TSP1.
InterPro; IPR008088; TSP 1.
InterPro; IPR001007; VWF_C.
Pfam; PP00090; TSP 1, 2.
Pfam; PP00099; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50092; TSP1; 2.
PROSITE; PS01208; VWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_2; 1.
SEQUENCE 496 AA; 54843 MW; E4FDZF07CB7EF51B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ind mouse cDNA sequences.";
>roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11arity 91.7%; Score 55; DB 2; Onservative 0; Mismatches
                                   Kenopus laevis (African clawed frog)
                                                                                                                                    Kenopodinae; Xenopus; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1705; TSPIREPEAT.
SMART; SM00209; TSP1; 2.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
SO DER RESERVA DE RESE
```

```
CC --- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type V collagen and integrins alpha-V/beta-1, alpha-CC V/beta-1, alpha-III/beta-3 and alpha-lib/beta-3. May play a role in dentinogenesis and/or maintenance of dentin and dental pulp.

C --- SUBUNIT: Homotrimer; disulfide-linked.

C --- SIMILARITY: Contains 3 EGF-like domains.

C --- SIMILARITY: Contains 1 TSP C-terminal (TSPC) domain.

C --- SIMILARITY: Contains 3 TSP type-1 domains.

C --- SIMILARITY: Contains 7 TSP type-1 domains.

C --- SIMILARITY: Contains 7 TSP type-3 domains.

C --- SIMILARITY: Contains 1 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Aortic endothelium;
Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin stimulatory effect of TGF-beta.";
                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [MRNA].
STRAIN=HOLStein; TISSUE=Tooth;
MEDLINE=9813713; PubMed=9507054; DOI=10.1016/S0167-4838(97)00188-X;
MEDLINE=9813773; PubMed=9507054; DOI=10.1016/S0167-4838(97)00188-X;
Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
                                                                                                                Thrombospondin-1 predursor.
Name=THBS1; Synonyms=TSP-1, TSP1;
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                   Inoue H.; cDNA cloning of bovine thrombospondin 1 and its expression in conducolasts and predentin."; Biochim. Biophys. Acta 1382:17-22(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
TSPI BOVIN

ID TSPI BOVIN

AC 028179;
DJ 01-00V-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2000, sequence version 2.
DT 07-MAR-2006, entry version 56.
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA] OF 1-18 AND 710-1170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, ABO05287; BAA21115.1; -; mRNA.
EMBL, X87618; CAA60950.1; -; mRNA.
EMBL, X87619; CAA60951.1; -; mRNA.
FIR, SS5501; S55501.
HSSP, P07996; 1LSL.
SMR; Q28178; 549-1169.
GlycosultedBy Q28178; -
GlycosultedBy Q28178; -
InterPro; IPR013320; ConA_like_subgrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; 19800042; EGF 3.
Interpro; IPR001881; EGF Ca bd.
Interpro; IPR001881; EGF Ca bd.
Interpro; IPR013032; EGF like reg.
Interpro; IPR01312; EGF like reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001881; EGF_Ca_LinterPro; IPR006209; EGF_like InterPro; IPR013129; EGF_like InterPro; IPR00884; TSP1.
InterPro; IPR00884; TSP1.
InterPro; IPR00885; TSP1.
InterPro; IPR008859; TSP2.
InterPro; IPR008859; TSP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00008; EGF; 1.
Pfam; PF00090; TSP 1; 3.
Pfam; PF02412; TSP 3; 13.
                                                                                                                                                                                                                              NCBI_TaxID=9913;
```

ö

Gaps

ö

1; Indels

1 FOGVLOOVREVE 12

ð

11;

Best Loc Matches

```
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins.
                                                                                                                                                                                                                        T 4
HUMAN
                                                    Matches
                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSP type-3 1.
TSP type-3 2.
TSP type-3 3.
TSP type-3 3.
TSP type-3 4.
TSP type-3 4.
TSP type-3 6.
TSP type-3 6.
TSP type-3 6.
TSP type-3 7.
TSP C-terminal.
Heparin-binding (Potential).
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
Interchain (Probable).
Interchain (Probable).
Interchain (Probable).
Interchain (Probable).
By similarity.
By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y similarity.
; > G (in Ref. 2).
; obb6ADF3E5FA031A CRC64;
                                                                 SWART; SW00181; EGF; 3.

SWART; SW00209; TSP1; 3.

SWART; SW00210; TSP1; 3.

SWART; SW00210; TSP1; 3.

SWART; SW00210; TSP1; 1.

PROSITE; PS00022; EGF 1; PALSE_NEG.

PROSITE; PS00026; EGF 2; 1.

PROSITE; PS00209; TSP1; 3.

PROSITE; PS01208; VWFC 1; 1.

PROSITE; PS01208; VWFC 2; 1.

Reparin-binding; Repeat; Signal.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                           By similarity.
Thrombospondin-1.
/FTId=PRO_0000035841.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2; ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129534 MW;
                                Ptam; PF00093; VWC; 1.
PRINTS; PR01705; TSP1REPEAT.
TSP_C, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               708
1067
1085
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             813
836
874
874
890
910
946
116
805
1170 AA;
                                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
  ODARAN ODBRAN OBRAN OB
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Endothelial cell;
MEDLINE=87057677; PubMed=2430973; DOI=10.1083/jcb.103.5.1635;
Lawler J., Hymes R.O.,
"The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 1-374.
MEDLINE=86287276; PubMed=3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
UCharacterization of a CDNA encoding the heparin and collagen binding domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 1-397.
MEDILINES#87157592; PubMed=3030396;
MEDILINES#87157592; PubMed=3030396;
Kobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.;
"Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite proteins.";
Biochemistry 25:8418-8425(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 1-166.
MEDLINE-89291870; PubMed=2544587;
Laherty C.D., Gierman T.M., Dixit V.M.;
"Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.";
J. Biol. Chem. 264:11222-11227(1989).
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89139590; PubMed=2918029; DOI=10.1083/jcb.108.2.729; Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L., Baumgartel D.M., Rotwein P., Frazier W.A.; "Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region."; J. Cell Biol. 108:729-736(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE OF 1028-1170.

Ta Fleur M., Jobin C., Gauthier J., Kreis C.G.;

"Expression of thrombospondin in chronic inflammation: neutrophils from synovial fluids synthesize a novel 3.9 kD TSP mRNA.";

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441; THR-460; TRP-498 AND THR-507. TRP-450; TRP-498 AND THR-507. TRSUE=Platelet; TRP-488 AND THR-507. TRP-488 AND THR-500; MEDLINE=21125860; Pubmed=11067851; DOI=10.1074/jbc.M008073200;
Length 1170;
                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                          TSP1 HUMAN STANDARD; PRT; 1170 AA. P07956; Q15667; Q15667; Q10404-1988, integrated into UniProtKB/Swiss-Prot. O1-AUG-1988, sequence version 1. O7-MAR-2006, entry version 78. Thrombospondin-1 precursor. Name-THS1; Stonyma=TSP, TSP1; Homo sapiens (Human).
   DB 1;
                                0.088;
                                                                        Mismatches
   Score 55;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell Biol. 103:1635-1648(1986)
                                                                        ..
0
   91.7%;
91.7%;
                                                                                                                                                                                     208 FQGVLQNVRFVF 219
                                                                        Conservative
                                                                                                                                      1 FOGULQOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                        HID DIT OF THE SERVICE SERVICE
```

```
708
1067
270
274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
316
316
4435
5492
588
577
7723
7723
818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3391
3395
4447
7462
504
508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOTIF
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
NODER NOTE TO THE STATE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYDRATE-LINKAGE SITES ASN-248 AND ASN-1067.

PubMed=16335952; DOI=10.1021/pr0502065;

Liu T., Qian W.-J., Gartsenko M.A., Camp D.G. II, Monroe M.E.,

Liu T., Qian W.-J., Gartsenko M.A., Camp D.G. II, Monroe M.E.,

Moore R.J., Smith R.D.; Gartsenko M.A., Camp D.G. II, Monroe M.E.,

T. "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,

T. "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,

T. "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,

J. Proteome Res. 4:2070-2080(2005).

J. Proteome Res. 4:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                 THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES.
MEDLINE=22338361; PubMed=12450399; DOI=10.1021/bi026463u;
Huwller K.G., Veetling M.M., Annis D.S., Mosher D.F.;
"Biophysical characterization, including disulfide bond assignments, of the anti-anglogenic type 1 domains of human thrombospondin-1.";
Biochemistry 41:14329-14339(2002).
Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J.,
Mosher D.F., Peter-Katalinic J.;
"C-mannosylation and O-fucosylation of the thrombospondin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 188060; gene.

Reactome; P07996; ---

Red; G0:0004866; F:endopeptidase inhibitor activity; TAS.

G0; G0:0004871; F:signal transducer activity; TAS.

RO; G0:0004871; F:signal transducer activity; TAS.

RINTERPO; IPR006210; EGF.

RINTERPO; IPR001801; EGF.

RINTERPO; IPR001801; EGF.

RINTERPO; IPR001801; EGF.

RINTERPO; IPR001302; EGF.

RINTERPO; IPR001302; EGF.

RINTERPO; IPR001303; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M25631; AAA36741.1; -; mRNA.
EMBL; X14787; CAA28370.1; -; mRNA.
EMBL; X14787; CAA28370.1; -; mRNA.
EMBL; M14326; AAA61237.1; ALT SEQ; mRNA.
EMBL; M99425; AAA61178.1; -; Genomic_DNA.
EMBL; A26152; TSHUP1. ; Genomic_DNA.
PDB; 1LSL; X-ray; A=434-546.
PDB; 1LX1; X-ray; A=19-233.
PDB; 1Z78; X-ray; A=19-257.
PDB; 2RR; X-ray; A=19-257.
PDB; 2RR; X-ray; A=10-257.
PDB; 2RR; X-ray; A=25-233.
GGP; PO7996; 549-1169.
GGP; PO7996; -.
CGP; PO7996; -.
Ensembl; ENSG00000137801; Homo sapiens.
                                                                                                                              Biol. Chem. 276:6485-6498(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPN000884; TSP1.
Interpro; IPN000885; TSP1.
Interpro; IPN003367; tsp_3.
Interpro; IPN008859; TSP_C.
Interpro; IPN001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00008; EGF; 2.
Pfam; PF00090; TSP 1; 3.
```

```
ö
R Pfam; PF02412; TSP 3; 12.

R Pfam; PF05735; TSP_C; 1.

R PRIMTS; PR01093; VWC; 1.

R PRIMTS; PR01016; TSPLC; 1.

R SMART; SM00181; EGF; 3.

R SMART; SM00210; TSPL; 3.

R SMART; SM00210; TSPL; 3.

R PROSITE; PS00225; EGF 1; PALSE_NEG.

R PROSITE; PS0026; EGF 2; 1.

R PROSITE; PS01086; EGF 2; 1.

R PROSITE; PS01089; VWC 2; 1.

R PROSITE; PS01089; VWFC 2; 1.

R PROSITE; PS01094; VWC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                             TSP type-1 1.
TSP type-1 2.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2.
TSP type-3 1.
TSP type-3 1.
TSP type-3 4.
TSP type-3 4.
TSP type-3 7.
TSP type-3 6.
TSP type-1 7.
TSP type-1 7.
TSP type-1 6.
TSP type-1 7.
TSP type-1 7.
TSP type-1 7.
TSP type-1 6.
TSP type-1 7.
TSP type-1 7.
TSP type-1 7.
TSP type-1 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=CAR 000208.
O-linked [Fuc. . .).
/FTId=CAR 000209.
C-linked (Man).
/FTId=CAR 000210.
/FTId=CAR 000211.
/FTId=CAR 000211.
N-linked (GlCNAC. .). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-linked (GlcNAc. .).
N-linked (GlcNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 1; Length 1170;
Pred. No. 0.088;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-linked (GlcNAc. . .
Interchain (Probable)
Interchain (Probable)
                                                                                                                                                                                                                                                                                                          Thrombospondin-1.
/FTId=PRO_000035842.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=CAR 000205.
O-linked (Fuc. .).
/FTId=CAR 000206.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTId=CAR 000207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-linked (Man).
                                                                                                                                                                                                                                                                          Heparin-binding; Repeat; Signal. SIGNAL 1 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 91.7
Les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                 429
429
547
587
645
645
690
781
781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394
```

```
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                      EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type V collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-IIb/beta-3.
                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 1-490.
MEDLINE=90375546; PubMed=2398070;
Bornstein P., Alfi D., Devarayalu S., Framson P., Li P.;
"Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";
J. Biol. Chem. 265:16691-16698(1990).
                                                                                                                                                                                                                                                                                                              "Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development.", J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE OF 19-37.

PubMed=8654563; DOI=10.1016/0014-5793(96)00460-7;

Chen H., Aeschlimann D., Nowlen J., Mosher D.F.;

"Expression and initial characterization of recombinant mouse thrombospondin 1 and thrombospondin 3.";

FEBS Lett. 387:36-41(1996).
                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
MEDLINE=92128941; PubMed=1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.
Jenkins N.A.;
                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=92147683; PubMed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of the murine thrombospondin gene."; Genomics 11:587-600(1991).
                                                               01-UNN-1994, integrated into UniProtKB/Swiss-Prot. 01-UUN-1994, sequence version 1. 07-MAR-2006, entry version 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, M62470; AAA50611.1; -; Genomic DNA.
EMBL, M62451; AAA50611.1; JOINED; GENOMIC DNA.
EMBL, M62451; AAA50611.1; JOINED; GENOMIC DNA.
EMBL, M62451; AAA50611.1; JOINED; GENOMIC DNA.
EMBL, M62454; AAA50611.1; JOINED; GENOMIC DNA.
EMBL, M62454; AAA50611.1; JOINED; GENOMIC DNA.
EMBL, M62455; AAA50611.1; JOINED; GENOMIC DNA.
EMBL, M62455; AAA50611.1; JOINED; GENOMIC DNA.
EMBL, M62457; AAA50611.1; JOINED; GENOMIC DNA.
EMBL, M62459; AAA50611.1; JOINED; GENOMIC DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic_DNA
                                           PRT; 1170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M62458; AAA50611.1; JOINED;
M62459; AAA50611.1; JOINED;
M62460; AAA50611.1; JOINED;
                                                                                               Thrombospondin-1 precursor.
Name=Thbs1; Synonyms=Tsp1;
Mus musculus (Mouse).
                                           STANDARD;
                                                                                                                                                                 NCBI TaxID=10090;
                                        TSP1 MOUSE
P35441;
```

```
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6J; TISSUE-Aorta and vein;
PubMed-16141072; DOI=10.1126/science.113014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V. B., Brenner S. Batalov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Aorta and vein; MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530055N06 product:thrombospondin 1, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                              Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                         0443E493615E7F06 CRC64;
N-linked (GlcNAc. ..)
Interchain (Probable).
By similarity.
                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Score 55;
                                                                                                                                                                                                                                                                                                        910 930 By E
946 1167 By E
1025 1025 F ->
1170 AA; 129647 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
Q3TR40 MOUSE
ID Q3TR40 MOUSE PRELIMINARY;
AC Q3TR40;
                                                                                                                                                                                                                                                                                                                                                            91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                             208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Thbs1
                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                       DISULFID
                                   DISULFID
                                               DISULFID
                                                        DISULFID
                                                                    SULFID
                                                                             DISULFID
                                                                                        DISULFID
                                                                                                  DISULPID
                                                                                                              DISULFID
                                                                                                                        DISULFID
                                                                                                                                  DISULFID
                                                                                                                                             DISULFID
                                                                                                                                                                  DISULPID
                                                                                                                                                                             DISULFID
                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
```

```
Daniel M., Baxger L., Beinel K.W., Bergano T., Bench H., Chalk A.M., Chora M.W., Daniel W., Baxer L., Beinel K.W., Barger Chora M.W., Daniel B., Stringhes B. B. Bench H., Chalk C. Crose M.W., Daniel B., Stringhes B. B., Bell B., Boll B., Bell B.,
```

Laminin G_TSP_N

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                               NEULECTIDE SEQUENCE.

OX STRAING-STEAL SEQUENCE.

OX STRAING-SUBL/G1. TISSUE-AORTEA and vein;

NAMANI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Rang R., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Marchionni K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Marchions K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Aorta and vein; MEDLINE=20499374; Dubmed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shibata K., Itoh M., Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUCLEOTIDE SEQUENCE.

STRAIN-C57BL/6J; TISSUE-Aorta and vein;

Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,

Hori F., Iida J., Imamura K., Imotani K., Itch M., Kanagawa S.,

Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,

Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,

Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,

Muramatsu M., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARTAIN=CSTBL/61; TISSUE=Aorta and vein;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO: 0005615; C: extracellular space; IDA.
GO; GO: 0005615; C: extracellular space; RCA.
GO; GO: 0005615; C: extracellular space; RCA.
GO; GO: 0016525; E: extracellular space; RCA.
InterPro; IPR006210; EGF.
InterPro; IPR001742; EGF.
InterPro; IPR001881; EGF.
InterPro; IPR00180209; EGF.
InterPro; IPR013032; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AK163092; BAE37190.1; -; mRNA.
MGI; MGI:98737; Thbs1.
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
   HERE BERKER B
BERKER BE
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-Noperivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                              ö
                  R InterPro; IPR008085; TSP 1.

R InterPro; IPR008085; TSP 1.

R InterPro; IPR0080859; TSP 2.

R InterPro; IPR0080859; TSP 2.

R Pfam; PF00008; EGF; 2.

R Pfam; PF000095; TSP 1; 3.

R Pfam; PF000095; TSP 1; 3.

R Pfam; PF000095; WWC; 1.

R PRINTS; PR01705; TSP1REPEAT.

R SMART; SM00210; TSPN; 1.

R SMART; SM00210; TSPN; 1.

R SMART; SM00210; TSPN; 1.

R PR0SITE; PS01086; EGF 2; UNKNOWN 1.

R PROSITE; PS01208; WWC 1.

R PROSITE; PS01208; WWC 2; 1.

R PROSITE; PS01208; WWC 2; 1.

R PROSITE; PS01208; WWC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley;
Iwabu A., Hirohata S., Kusachi S., Nakamura K., Murakami T.,
Ninomiya Y., Tguji T.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                          Score 55, DB 2; Length 1170;
Pred. No. 0.088;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMR; QTISA3; 834-1169.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005198; F:calcium ion binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR013210; Cond_like_subgrp.
InterPro; IPR013210; GGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY; PRT; 1170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF 3.
EGF Ca bd.
EGF like.
EGF like reg.
Laminin G ISP N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF309630; AAQ14549.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 9.
Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                               91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSP1.
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FOGVLONVRFVF 219
InterPro; IPR000884; TSP1
InterPro; IPR008085; TSP
                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000742;
InterPro; IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006209;
InterPro; IPR013032;
InterPro; IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR003367;
IPR008859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q71SA3_RAT
Q71SA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Tsp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q71SA3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
```

œ

```
01-MAR-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBCGB2_MOUSE PRELIMINARY; PRT; 1171 AA.
Q8CGB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                InterProj irrovallo described irrova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50022, TSPI; 3.
PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003, sequence version 1. 07-FEB-2006, entry version 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGULOQURFUF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTRAINE-CSTEL/G. TISSUE-Brain;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.E., Zeeberg B.B., Bencow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.E., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Brownstein M.J., Warusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahawal M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                   Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                             129671 MW; 6F38D3DCE733060F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CSTBL/6; TISSUE=Brain;
Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                     91.7%; Score 55; DB 2; 91.7%; Pred. No. 0.088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003, integrated into UniProtKB/TrEMBL. 01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBOYQ1_MOUSE PRELIMINARY; PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                            PRINTS; PRO1705; TSPHREPEAT.
SWART; SMO0181; EGF; 3.
SWART; SM00210; TSP1; 3.
SWART; SM00210; TSPN; 1.
SWART; SM00214; VWC; 1.
SWART; SM00214; VWC; 1.
PROSITE; PS01086; EGF; 2; 1.
PROSITE; PS50026; TSP1; 3.
PROSITE; PS50186; EGF; 3; 2.
PROSITE; PS50184; VWFC; 1.
PROSITE; PS50184; VWFC; 1.
SEQUENCE 1170 AA; 129671 MW; 6F30D3
                 Pfam, PF00008; EGF; 2.
Pfam, PF00090; TSP 1; 3.
Pfam, PF02412; TSP 3; 12.
Pfam; PF05735; TSP C; 1.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                        Query Match
ð
```

```
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchoncoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombospondin 1 (Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library, clone:G930018021 product:thrombospondin 1, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE_22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Morre T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
EMBL; BCO50917; AAH50917.1; -; mRNA.
HSSP; D07996; 1LSL.
SMR; Q80YQ1; 835-1170.
EMSembl; ENSMUSG00000040152; Mus musculus.
MG1; MG1:98737; Thbs1.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0016525; P:negative regulation of angiogenesis; IDA.
InterPro; IPR013210; ConA_like_subgrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1171 AA; 129690 MW; 12E077B50C64E2D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 2;
Pred. No. 0.088;
```

σ

[5] NUCLEOTIDE SEGUENCE,

RC TISSUB-Ammmary gland,

RA Carminci P., Kaaukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,

RA Carminci P., Kaaukawa T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,

RA Garma R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,

Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,

Bajic V.B., Wilmid L.G., Apweller R., Aturaliya R.N., Bailey T.L.,

RA Ambesi-Impionabato A., Apweller R., Aturaliya R.N., Bailey T.L.,

Banaal M., Baxter L., Beisel K.W., Bersand T., Bono H., Chalk A.M.,

RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,

RA Georgii-Hemming P. Gingers T.R., Gojobori T., Green R.E.,

Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,

RHILD., Huminiecki L., Iacono M., Ikeo K., Imama A., Ishikawa T.,

Aitano H., Kallas G., Krishnan S.P., Kruger A., Kumereld S.K.,

Kurochkin I.V., Lareau L.F., Lazarevic D., Libovich L., Liu J.,

Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,

RA Matsuda H., Mateuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

Noteagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,

Liuni S., McWilliam S., Nishikwa S., Nori F., Ohara O.,

RA Okazaki Y., Orlando V., Pang K.P., Sandelin A., Schneider C.,

Schonbach C., Sakiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,

Schonbach C., Sakiguchi K., Semple C.A., Seno S., Sessa L.,

Shinata Y., Shinada H., Shinada K., Silva D., Sinclair B.,

RA Sperling S., Stupka E., Suigura K., Sultana R., Takenaka Y.,

Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,

Ramanishi H., Zabarovsky E., Zhu S., Zhuen S., Walkan K., Matakin K.,

Rawashima T., Kojima M., Schodo S., Konno H., Wakaen J.,

Rawashima T., Kojima M., Rondo S., Konno H., Nakano K., Ninomiya N.,

Rawashima T., Kojima M., Plessy C., Shibate K., Sultai R., Sultai J., Kavashima J.,

Ragami M., Waki K., Holls M., Mataliki A., Sultai R., Sultai J., Sultai J., Sultai J., Sultai J., Sultai J., Sultai J., Sultai Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sthugta A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Gener than 15,000 full-length human TISSUE=Mammary gland; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).

```
REMINITION SUCCEMPLE.

RAY ONG ACTION OF ACTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mawai U., Shinagawa A., Shibata K., Yoshino W., Itoh W., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H., Radota K., Matsuda H., Rikaja D., Lewis S., Matsuo Y., Nikajao I., Ring B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikajao I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Baka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Shoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Mammary gland;
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
Garninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muranatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
TISSUE=Mammary gland;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Mammary gland;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 420:563-573(2002).
                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
```

```
Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heparin-binding; Repeat; Signal.
                                                                                                                                                                                                                              InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP 1.
InterPro; IPR00367; tsp 3.
InterPro; IPR001367; tsp 3.
InterPro; IPR001007; VWF C.
Pfam; PF00009; EGF; 1.
Pfam; PF02412; TSP 1.
Pfam; PF02412; TSP 3; 12.
Pfam; PF02412; TSP 3; 12.
Pfam; PF00033; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01705; TSP1REPEA
SWART; SW00181; EGF; 2.
SWART; SW00210; TSP1, 3.
SWART; SW00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa M., Nishi K., Ratsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunato S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunato H., Sakaguchi S., Ikegami T., Kabhiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Nakzaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                     TISSUE=Mammary gland;
Arakawa T., Carninol P., Fukuda S., Hashizume W., Hayashida K.,
Arakawa T., Carninol P., Fukuda S., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA].
Urry L.A., Ramos J., Duquette M., Desimone D.W., Lawler J.;
"Cloning, characterization and expression of thrombospondin-1 in
Xenopus laevis embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 2; Length 1171;
Pred. No. 0.088;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC042422; AAH42422.1; -; mRNA.
EMBL; AK145202; BAE26293.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994, sequence version 1. 07-MAR-2006, entry version 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombospondin-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Local Similarity
Local 11, Conservative
To 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=thbs1; Synonyms=tsp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P07996; 1LSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISP1 XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P35448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSPI_XENLA
ACC
AMPHOD
TSPIA
DI TSPIA
DI
     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
TSP type-1 3.
EGF-like 1.
EGF-like 2; calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSP type-3 1.
TSP type-3 2.
TSP type-3 3.
TSP type-3 3.
TSP type-3 4.
TSP type-3 5.
TSP type-3 5.
TSP type-3 7.
TSP type-3 7.
TSP type-3 7.
TSP type-6 6.
TSP type-6 6.
TSP type-6 6.
TSP type-7 7.
TSP type-1 7.
TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO1022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS50027; WFC_1; 3.
PROSITE; PS501208; WWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
Calcium; Cell adhesion; EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombospondin-1.
/FTId=PRO 0000035844.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-linked (Glorke...
By similarity.
EMBL, L04278; -; NOT_ANNOTATED_CDS; mRNA.
HSSP, P07996; 1LSL.
SMR; P35448; 552-1172.
InterPro; 1PR013320; ConA_like_subgrp.
InterPro; 1PR001320; CGF.
InterPro; 1PR000742; EGF.
InterPro; 1PR001881; EGF.Ca_bd.
InterPro; 1PR016209; EGFlike.
InterPro; 1PR016209; EGFlike.
InterPro; 1PR013129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
```

ઠ g

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collagen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chorafish) (Danio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-2004, sequence version 1.
21-FBB-2006, entry version 12.
Novel protein similar to vertebrate thrombospondin 1.\n\ (Fragment)
ORFNames=DKEY-11E23.1-001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.7%; Score 55; DB 2; Length 1225; 91.7%; Pred. No. 0.093; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1225 AA; 134849 MW; 9888B16E57157B12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL928866; CAI20599.1; -; Genomic_DNA.
SMR; Q5SPG5; 751-804, 754-1089.
Ensembl; ENSDARG00000107085; Danio rerio.
G0; G0: 0005576; C: extracellular region; IEA.
G0; G0: 0005509; F: calcium ion binding; IEA.
G0; G0: 0005510; F: heparin binding; IEA.
G0; G0: 0005515; F: protein binding; IEA.
G0; G0: 0005515; P: extractural molecule activity; IEA.
G0; G0: 0007155; P: cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSSPGS;
21-DEC-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSSPGS_BRARE PRELIMINARY; PRT; 1090 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF 3.
EGF Ca bd.
EGF like
EGF like reg.
Laminin G TSP N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPR013320; ConA_like_subgrp.
InterPro, IPR002048; EF hand_Ca_bd.
InterPro, IPR006210; EGF.
InterPro; IPR001007; VWF_C.
Pfam; PF00008; BGF; 2.
Pfam; PF000412; TSP_1; 3.
Pfam; PF00412; TSP_2; 12.
Pfam; PF001412; TSP_C; 1.
PRINTS; PF00093; VWC_1.
PRINTS; PR01705; TSPIREPEAT.
SWART; SW00210; TSPI; 3.
SWART; SW00210; TSPI; 3.
SWART; SW00210; TSPI; 3.
SWART; SW00210; TSPI; 3.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01026; EGF_3; 2.
PROSITE; PS01026; EGF_3; 2.
PROSITE; PS01026; EGF_2; 1.
PROSITE; PS01026; EGF_2; 1.
PROSITE; PS0104; VWFC_1; 1.
Cell adhesion; EGF-1ike domain.
NON TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 91.7
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 FOGVLÓNVRFVF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000742;
InterPro; IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006209;
InterPro; IPR013032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barker D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q5SPG5_
       DAR AND DAR BERNARD OF STATES OF STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2005, sequence version 1.
21-FBB-2006, entry version 10.
Thrombospondin 1 variant (Fragment).
Homo sapiens (Human)
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
TISSUE=Aorta endothelial cell;
TISSUE=Aorta endothelial cell;
TISSUE=Aorta endothelial cell;
Takenii, Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 1; Length 1173;
Pred. No. 0.089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                A9F036D6516C0F24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB209912; BAD93149.1; -; mRNA.
SMR; Q59E99; 886-939, 889-1225.
Ensembl; ENSG00000137801; Homo sapiens.
GO; GO: 0005576; C: extracellular region; IEA.
GO; GO: 0005509; F: calcium ion binding; IEA.
GO; GO: 0005101; F: heparin binding; IEA.
GO; GO: 0005101; F: protein binding; IEA.
GO; GO: 0005155; F: structural molecule activity; IEA.
GO; GO: 0007155; P: cell adhesion; IEA.
InterPro; IPRR013320; ConA_like_subgrp.
InterPro; IPR006210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-2005, integrated into UniProtKB/TrEMBL
                                                                                                                          similaritý.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                        similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OS9E99 HUMAN PRELIMINARY; PRT; 1225 AA Q59E99;
                                                                            similarity.
similarity.
                                                                                                                                                                                                                                 similarity.
                                                                                                                                                                                                                                                   similarity.
                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                      similarity
                                                                                                                                                                                                                                                                                                                                                                           similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR0001215; EGF 3.
InterPro; IPR001881; EGF Ca bd.
InterPro; IPR001881; EGF Ca bd.
InterPro; IPR0013032; EGF like reg.
InterPro; IPR0013032; EGF like reg.
InterPro; IPR001884; TSP1.
InterPro; IPR001884; TSP1.
InterPro; IPR001885; TSP1.
InterPro; IPR0018859; TSP2.
     91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1173 AA; 130020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 FQGVLQNVRFVF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
  DISULFID
DISULFID
DISULFID
DISULFID
                                                                                              DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
Q59E99 HUN
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50, DB 2; Length 1193;
Pred. No. 0.96;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang K., Mauco G., Hauet T.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1193 AA; 133256 MW; 6E8781648FCEC7F2 CRC64;
                                                                  SME, 045758, 811-1148.

SME, 045758, 811-1148.

GO; GO:0005505; C:extracellular region; IEA.

GO; GO:0005201; F:beparin binding; IEA.

GO; GO:0005195; F:protein binding; IEA.

InterPro; IPR00142; EGF 3.

InterPro; IPR001801; EGF 2.

InterPro; IPR001801; EGF 1.

InterPro; IPR001804; TSP1.

R InterPro; IPR000884; TSP1.

R InterPro; IPR000885; TSP 1.

R Ffam; PF00009; FSP 1.3

R Ffam; PF00009; TSP 1.3

R Ffam; PF000193; VWF C.

R Ffam; PF000193; VWF C.

R Ffam; PF000193; VWF C.

R Ffam; PF000193; VWC; 1.

R Ffam; PF000193; VWC; 1.
                                                     EMBL; CAAE01014723; CAG03524.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
07-FEB-2006, entry version 7.
Thrombospondin 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY773342; AAV38110.1; -; mRNA.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01186; EGF 2; UNKNOWN_1. PROSITE; PS50026; EGF 3; 2. PROSITE; PS50092; TSP1; 3. PROSITE; PS01208; WFC_1; 1. PROSITE; PS50184; WFC_2; 1. Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 FMGVLQNVRFVF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00181; BGF; 2.
SMART; SM00209; TSP1; 3.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q5U903 PIG
Q5U903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLECTIDE SEQUENCE.
NUCLECTIDE SEQUENCE.
NUCLECTIDE SEQUENCE.
NUCLECTIDE SEQUENCE.
Adailon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutaneau J.-P., Gouzy J.,
Rellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2005, sequence version 1.
21-FEB-2006, entry version 8.
Chromosome 14 SCAF14723, whole genome shotgun sequence. (Fragment)
ORFNames-GSTENG00022976001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%; Score 50; DB 2; Length 1090;
83.3%; Pred. No. 0.87;
.ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                 1090 AA; 120978 MW; 5A9320504A22D836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1193 AA.
                                                                                                                                                                                                                   SWART; SM00214; VWC; 1.
PROSITE; PS000018; EF HAND 1; UNKNOWN_1.
PROSITE; PS010186; SGF_2; 1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS50092; TSP1; 2.
PROSITE; PS50184; VWFC_1; 1.
Cell adhesion; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                  Pfam; PF00008; EGF; 1.
Pfam; PF00009; TSP_1; 2.
Pfam; PF00409; TSP_1; 2.
Pfam; PF05735; TSP_C; 1.
Pfam; PF05735; TSP_C; 1.
PRINTS; PR01705; TSPIREPEAT.
SMART; SM00210; TSP1; 2.
SMART; SM00210; TSP1; 2.
SMART; SM00210; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q4S758_TETNG PRELIMINARY;
Q4S758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 FMGVLONVRFVF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 83.3
nes 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEING
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
```

셤

```
Search completed: June
Job time: 109.931 secs
                OR SET THE SECOND SECON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15496914; DOI=10.1038/nature03025;
A Jaillon O., Aury Ju-M., Brunet F., Petit J.-L., Stange-Thomann N.,
A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
21-FBB-2006, entry version 8.
Chromosome 10 SCAF15019, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENG00032374001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Tetradontoidea; Tetradontoidea; Tetraodontidae; Tetraodont, Tetradontiformes; NCBL TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.7%; Score 49; DB 2; Length 249; 90.9%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                             249 AA; 27560 MW; 465D664BE0329C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QARLRS; 834-887, 837-1171.
GO:0005576; C:extracellular region; IEA.
GO:0008201; F:heparin binding; IEA.
GO:000515; F:protein binding; IEA.
GO:000515; F:protein binding; IEA.
GO:000515; F:protein binding; IEA.
GO:0007155; F:ctuctural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; CAAE01015019; CAG10667.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TETNG PRELIMINARY; PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the early vertebrate proto-karyotype.";
Pfam; PF00090; TSP_1; 2.
Pfam; PF00093; VWC; 1.
SMART; SM02209; TSP1; 1.
SMART; SM02209; TSP1; 1.
SMART; SM02214; VWC; 1.
PROSITE; PS50192; TSP1; 1.
PROSITE; PS50184; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 OGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QGVLQNVRFVF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                          NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NA CARA DE RACE DE RAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           유
```

5, 2006, 22:42:40

```
DR InterPro; IPRO00142; EGF 3.

DR InterPro; IPRO01812; EGF Ca_bd.

DR InterPro; IPRO01812; EGF_Ca_bd.

DR InterPro; IPRO01812; EGF_Ca_bd.

DR InterPro; IPRO01812; EGF_Ca_bd.

DR InterPro; IPRO01805; TSP1.

DR InterPro; IPRO01005; TSP1.

DR Fdam; PFO0009; TSP_1; 3.

DR Pfam; PFO0009; TSP_2; 1.

DR PROSTITE; PS00186; EGF 2; UNKNONN_1.

DR ROSTITE; PS00186; EGF 2; UNKNONN_1.

DR PROSTITE; PS01086; TSP1; 3.

DR PROSTITE; PS01086; EGF 2; UNKNONN_1.

DR PROSTITE; PS01086; EGF 2; UNKNONN_1.

PROSTITE;
```

THIS PAGE BLANK (USPTO)

```
Sequence 97, Application US/09939853A

Sequence 97, Application US/09939853A

Patent No. 6989232

GRNERAL INFORMATION:

APPLICANT: Burgess et al.

TITLE OF INVENTION: No. 6989232e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-099

CURRENT APPLICATION NUMBER: US/09/939,853A

CURRENT PILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 482
LENGTH: 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                             5, 2006, 22:43:07; Search time 23.8966 Seconds (without alignments) 43.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued Patents AA:*
: / EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-002-482
US-09-939-853A-97
US-09-939-853A-98
US-08-313-288B-20
US-09-949-002-350
US-09-949-016-11112
US-09-949-016-11112
US-09-949-016-11112
US-09-949-016-11112
US-09-949-016-6333
US-09-949-016-6333
US-09-949-016-6333
US-09-299-268-15
US-09-724-884-1
US-09-73-222-1
US-09-73-222-1
US-09-73-222-1
US-09-949-016-7739-8
US-09-949-016-7739-8
US-09-949-016-773-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-489-039A-14121
US-09-134-000C-5578
US-08-271-364A-7
US-08-222-715B-26
US-09-698-341-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                650591 segs, 87530628 residues
                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                  1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                 US-10-030-735-20
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11170
11700
11690
11722
111722
111722
11722
11722
11723
11723
11733
11733
11730
11730
11730
11730
11730
11730
11730
                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          991.7
991.7
665.0
661.7
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
660.0
                                                                                                                                                  June
                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                              OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
Š
```

```
Sequence 482, Application US/09949002

Betent No. 690016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLO00790

CURRENT PELING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR PAPLICATION NUMBER: 60/231,401

PRIOR PLING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: FREESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                      6, Appli
5, Appli
5, Appli
                                                                                                6605, Ap
7481, Ap
9668, Ap
11953, A
288379, A
1719, Ap
25258, A
16, Ap
10, App
                                                                                                                                                                                                                                                                                                            Appl
Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                        seduence
sequence
seq
sequence
sequence
sequence
sequence
sequence
sequence
sequence
sequence
seq
seq
seq
seq
s
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55; DB 2; Length 825;
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                    US-09-006-535-6
US-09-28-634-5
US-09-06-535-5
US-09-949-016-6605
US-09-949-016-7481
US-09-949-016-7481
US-09-949-016-968
US-09-949-016-968
US-09-949-018-37
US-09-252-991A-28379
US-09-252-991A-28379
US-09-252-991A-25258
US-09-252-991A-25258
US-09-252-991A-25258
US-09-252-991A-25558
US-09-264-9938-10
US-08-444-596A-10
US-08-444-596A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 FÓGVLÓNVRFVF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FQGVLQQVRFVF 12
```

```
US-09-949-002-350
; Sequence 350, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 91.7%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91...
11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGULOOVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98, Application US/09939853A

Sequence 98, Application US/09939853A

Patent No. 6989222

GENERAL INFORMATION:

APPLICANT: Burgess et al.

TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099

CURRENT APPLICATION NUMBER: US/09/939,853A

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR FILING DATE: 2001-02-08

PRIOR PILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOFTWARE: Patentin Ver. 2.1

FEAST OF TOWN OF 98
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence 20, Application US/08313288B |
| Sequence 20, Application US/08313288B |
| Patent No. 5750502 |
| GENERAL INFORMATION: |
| APPLICANT: Jessell, Thomas M. and Avihu Klar |
| TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A |
| TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN |
| NUMBER OF SEQUENCES: 20 |
| CORRESPONDENCE ADDRESS: | ADDRESSEE Cooper & Dunham LLP |
| STREET: 1185 Avenue of the Americas |
| CITY: New York |
| STATE: New York |
| COUNTRY: USA |
|
                                                                                                                                                                                                                                                                         Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 831;
                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                         Score 55; DB 2;
Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 2;
Pred. No. 0.015;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                         91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
; NUMBER OF SEQ ID NOS: 159; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 97; LENCHR: 831; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                 1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGANISM: Mus musculus US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-313-288B-20
                                                                                                                                                                                                       US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERALI INFORMATION:

APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Lander, James S.
APPLICANT: Eneland, James S.
APPLICANT: Dolk, Stacey
APPLICANT: Dolk, George Q.
APPLICANT: More S. 1027-001
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/123,357
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 1; Length 1170;
Pred. No. 0.021;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 2;
Pred. No. 0.021;
TELERANCE (212) 391-0526

CLASSIFICATION: 435

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEFRONE: (212) 278-0400
TELEFRAX: (212) 391-0526
TELERA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                Score 37; DB 2; Length 1045;
Pred. No. 79;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC Compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NORFR:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET NUMBER: 40028-A-PCT-US
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB:
Pred. No. 89;
2; Mismatches
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-031,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11112
LENGTH: 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-313-288B-19; Sequence 19; Application US/08313288B Patent No. 5750502; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.7%;
58.3%;
                                                                                                                                                                                                                                                                61.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1172 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 391-0526
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                             281 FRGLLONVHLVF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                     1 FOGULOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                  Local Similarity
hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1105 ...
                                                                                                                                                                                                 ; ORGANISM: Human
US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-313-288B-19
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (29)...(70)
LOCATION: Amino acids 29, 30, 59 & 70 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-3511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; sequence 3511, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICATION:
; APPLICATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SEQ ID NO 3511
; SEQ ID NO 3511
  APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLO00790

CURRENT APPLICATION NUMBER: US/09/949,002

CURRENT FILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: FRASES FOR WINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11112, Application US/09949016

Redent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 2; Length 1170;
Pred. No. 0.021;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.0%; Score 39; DB 2; Length 169; Best Local Similarity 77.8%; Pred. No. 4.2; Matches 7; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                     91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLOOVR 9
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                          ; ORGANISM: Human
US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-134-000C-3511
                                                                                                                                                                                                                                           SEQ ID NO 350
                                                                                                                                                                                                                                                                                        TYPE: PRT
```

셤 ð

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-269-268-15
; Sequence 15, Application US/09299268
; Parent No. 621080:
; Parent No. 621080:
; Parent No. 621080:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.0%; Score 36; DB 1; Length 440; Best Local Similarity 41.7%; Pred. No. 48; Matches 5; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: U.S."
                                                                                                                                       2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: UF35.1.FWCC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TITLE OF INVENTION: Live Vaccine Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-UUL-1992
RRIOR APPLICATION NUMBER: US 07/908,630
RILING DATE: 29-UN-1992
CLASSIFICATION: 435
RRIOR APPLICATION DATA:
RPLICATION NUMBER: US 07/342,212
RILING DATE: 21-APR-1992
CLASSIFICATION NUMBER: US 07/342,212
RILING DATE: 21-APR-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                       ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 440 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: ::| |:|:|
272 FKSIVQYVKFIF 283
                                NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Sa
STREET: 2421 N.W. 41st
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-307-499-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                   Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                           STATE: Florida COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18826, Application US/09252991A

Sequence 18826, Application US/09252991A

Sequence 18826, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF 
              Sequence 6333, Application US/09949016

Sequence 6333, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-06

SOUTHARE: FBSESEQ for Windows Version 4.0

SOUTHARE: FBSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08307499

Patent No. 5651972

GREEN ADDITION:
APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 2; Length 1172; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.0%; Score 36; DB 2; Length 175; Best Local Similarity 63.6%; Pred. No. 17; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.5.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 FRGLLONVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 QGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ÓGVLDAVQFLF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-307-499-15
```

셤

ð

us-10-030-735-20.rai

```
5, 2006, 22:48:54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7.
                             :||||||:
29 YQGVLQQIQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||||||::
29 YQGVLQQIQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQGVLQQVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: June
Job time: 24.8966 secs
                                                                                                                             US-09-724-884-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hartman, James J.
APPLICANT: Hartman, James J.
APPLICANT: Hartman, James J.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of Microtubule
ITILE OF INVENTION: Depolymerization Inhibitors
ITILE OF INVENTION: Depolymerization Inhibitors
FILE REFERENCE: 18557B-000510US
CURRENT APPLICATION NUMBER: US/09/291,170A
CURRENT PILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 60/081,734
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 1
LENGTH: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2; Length 440;
Pred. No. 48;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.0%; Score 36; DB 2; Length 516; Best Local Similarity 66.7%; Pred. No. 57; Matches 6; Conservative 3; Mismatches 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                  FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION:
ATTORNEY/ACTION:
ATTORNEY/ACTION:
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Strongylocentrotus purpuratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: katanin p60 subunit
US-09-291-170A-1
                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,268
                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/901,127
FILING DATE:
APPLICATION NUMBER: US 07/908,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09291170A Patent No. 6410687
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 440 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: ::| |:|
272 FKSIVQYVKFIF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGULQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-09-299-268-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-291-170A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                              Sequence 1, Application US/09724884

Sequence No. 6429304

GENERAL INFORMATION:

APPLICANT: Vale.

APPLICANT: The Regents of the University of California

TILLE OF INVENTION: Assays for the Detection of Microtubule

TILLE OF INVENTION: Depolymerization Inhibitors

TILLE OF INVENTION: Depolymerization Inhibitors

FILE REPERENCE: 185578-00051005

CURRENT FILING DATE: 2000-11-28

PRIOR FILING DATE: 1999-04-13

FRIOR FILING DATE: 1999-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%; Score 36; DB 2; Length 516; 66.7%; Pred. No. 57; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Strongylocentrotus purpuratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: katanin p60 subunit
US-09-724-884-1
1 FOGVLOOVR 9
Š
```

THIS PAGE BLANK (USPTO)

```
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-474-213-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-474-213-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Appl
Sequence 40, Appl
Sequence 1020, Ap
Sequence 1022, Ap
Sequence 1047, Ap
Sequence 454, Appl
Sequence 456, Appl
Sequence 461, Appl
Sequence 461, Appl
Sequence 461, Appl
Sequence 451, Appl
Sequence 451, Appl
Sequence 11, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114, App
2, Appli
1170, Ap
38, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA Main:*

: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                               5, 2006, 23:46:43; Search time 78.6207 Seconds (without alignments) 70.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-474-213-28

US-10-419-462-40

US-10-741-600-1020

US-10-741-600-1022

US-11-043-806-462

US-09-925-301-1047

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-10-939-833A-98

US-11-043-806-451

US-10-043-806-451

US-11-043-806-451

US-11-043-806-451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-008-093-2
US-10-295-027-1170
US-10-211-462-38
US-10-231-956A-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-017-721-2
US-10-021-660-114
                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                              2097797 seqs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                      1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                   US-10-030-735-20
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB E
Maximum DB E
                                                                                        OM protein
                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
```

```
Sequence 40, Application US/10419462
Publication No. US20040053392A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
FILE REFERENCE: WI107-2005
CURRENT APPLICATION NUMBER: US/10/419,462
CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOFFWARE: Patentin version 3.2
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Roberts, David D
APPLICANT: Roberts, David D
APPLICANT: RATESCH, Henry C
TITLE OF INVENTION: USE OF SEMENOGELIN IN THE DIAGNOSIS, PROGNOSIS AND TREATMENT OF
TITLE OF INVENTION: USE OF SEMENOGELIN IN THE DIAGNOSIS, PROGNOSIS AND TREATMENT OF
TITLE OF INVENTION: UNDER: 2013-10-06
PRIOR PEPLICATION NUMBER: US/10/474,213
CURRENT FILING DATE: 2003-10-06
PRIOR PILING DATE: 2002-04-03
PRIOR PILING DATE: 2001-04-06
NUMBER: OF SQ ID NOS: 28
SPCTWARE: PATENTIN VERSION 3.2
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                               38, Appl
44, Appl
548, App
1376, Ap
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                         Sequence
Sequence
                                                                                                                  Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.7%; Score 55; DB 4; Length 12; 91.7%; Pred. No. 0.0022; ive 0; Mismatches 1; Indels
                                                US-10-741-600-1019
US-10-741-600-1021
US-10-741-600-1021
US-10-849-989-44
US-10-814-67-548
US-10-831-997-2
US-10-995-561-594
US-10-995-561-595
US-11-037-713-51
US-11-046-456-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 28, Application US/10474213
; Publication No. US20040214248A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
911.7
```

```
WS-11-043-806-462

Sequence 462, Application US/11043806

Sequence 462, Application US/11043806

Publication No. US20060051774A1

GENERAL INFORMATION:

TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods

TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods

TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 462

LENGTH: 459
                                                                                                                                                                                                                     Sequence 1022, Application US/10741600

Sequence 1022, Application US/20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1022
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%; Score 55; DB 6; Length 459; 91.7%; Pred. No. 0.1; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 5;
Pred. No. 0.095;
  Pred. No. 0.095;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(432)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1047, Application US/09925301 Patent No. US20020053308A1 GENERAL INFRWATION: APPLICANT: Rosen et al.
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.78;
                                                                                                             208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FOGVLONVRFVF 219
  Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
                                                                                                                                                                                              RESULT 5
US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-043-806-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            合
                                                                          ð
                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-10-782-968-40

| Sequence 40, Application US/10782968
| Publication No. US20050065324A1
| GENERAL INFORMATION:
| APPLICANT: Kevin J. Williams, Kevin J.
| TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents |
| TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents |
| TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents |
| TITLE OF INVENTION NUMBER: US/10/782,968 |
| CURRENT FILING DATE: 2004-02-20 |
| PRIOR PILING DATE: 2004-02-21 |
| NUMBER OF SEQ ID NOS: 53 |
| SOFTWARE: PatentIn version 3.2 |
| LENGTH: 240 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1020, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE REPERRENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
SURPHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1020
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                           OTHER INFORMATION: Thrombospondin Region plus N-terminal domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Thrombospondin Region plus N-terminal domain
                                                                                                                                                                   Query Match 91.7%; Score 55; DB 4; Length 240; Best Local Similarity 91.7%; Pred. No. 0.051; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 5;
Pred. No. 0.051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%; Score 55; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)...(432)
OTHER INFORMATION: Xaa = Any Amino Acid
                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 91.7%;
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                               ||||||| |||||
190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 FOGVLONVREVE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                      1 FOGULOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-741-600-1020
                                                                                                                         US-10-419-462-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-782-968-40
    LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                     g
```

```
Sequence 452, Application US/11043806

Publication No. US20060051774A1

Publication No. US20060051774A1

Publication No. US20060051774A1

APPLICANT Compugen Ltd

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: UNMER: US/11/043,806

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

LENGTH: 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Compugen Ltd
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
LENGTH: 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-043-806-455

Sequence 455, Application US/11043806

Sequence 455, Application WS/11043806

Sequence 455, Application WS/11043806

Sequence 455, Application World World William World Worl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%; Score 55; DB 6; Length 804; 91.7%; Pred. No. 0.18; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 685;
0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 6
Pred. No. 0.15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 453, Application US/11043806; Publication No. US20060051774A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FQGVLQNVRFVF 219
                                                                              208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 91.7
Matches 11; Conservative
                                          1 FOGVLOOVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLOOVREVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGULQOVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                RESULT 10
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 454, Application US/11043806
Publication No. US20060051774A1
GRNERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REPERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR APPLICATION NUMBER: 60/124,270
; RECOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SEQ ID NOS: 1694
; SEQ ID NO 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.7%; Score 55; DB 6; Length 578; 91.7%; Pred. No. 0.13; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 6,
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 3
Pred. No. 0.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 456, Application US/11043806; Publication No. US20060051774A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 91.7%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 FQGVLQNVRFVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-043-806-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-043-806-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
අු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
```

```
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: June
Job time: 78.6207 secs
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 97, Application US/09939853A

Bublication No. US20040039163A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: No. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same
FILE REPREBENCE: 21402-099
CURRENT FILING DATE: 2001-08-27
FRIOR APPLICATION NUMBER: 60/228,191
FRIOR APPLICATION NUMBER: 60/267,300
FRIOR APPLICATION NUMBER: 60/267,300
FRIOR PILING DATE: 2001-02-08
FRIOR PILING DATE: 2001-02-08
FRIOR FILING DATE: 2001-03-20
FRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-939-853A-98

Sequence 98, Application US/09939853A

Publication No. US20040039163A1

GENERAL INFORMATION:

APPLICANT: Burgess et al.

TILE OF INVENTION: No. US20040039163A1el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099

CURRENT APPLICATION NUMBER: US/09/939,853A

CURRENT FILING DATE: 2001-08-27

PRIOR PILING DATE: 2001-08-27

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

PRIOR PILING DATE: 2001-03-20

PRIOR PILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SEQ ID NO 98

LENTH BATEL BATELL BATEL
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 3; Length 831;
Pred. No. 0.19;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                 Score 55; DB 6; Length 828;
Pred. No. 0.19;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGULQOVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 831
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-853A-97
                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-939-853A-97
     LENGTH: 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: Lhereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 461
                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                     Gaps
                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Score 55; DB 3; Length 831;
Pred. No. 0.19;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%; Score 55; DB 6; Length 855; 91.7%; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6, 2006, 00:00:10
                                                                                                                                                                                                                                           US-11-043-806-461

: Sequence 461, Application US/11043806

: Publication No. US20060051774A1

: GENERAL INFORMATION:
    Query Match 91.7%;
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                    1 FOGVLOOVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLOOVREVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Homo sapiens
US-11-043-806-461
```

26, Appl 24350, A 3555, Ap 3527, Ap 22132, A 21131, A 21131, A 21130, A 28462, A 28462, A

Sequence Seq Sequence

Sequence Sequence

57, Appl 28460, A

Sequence Sequence Sequence

35596,

Sequence Sequence Sequence

Sequence

OM protein

е Е

Run

Sequence:

Minimum DB Maximum DB

Database

Residit

Searched:

```
GENERAL IN WOMMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Pry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US,10/511,937
CURRENT FILING DATE: 2003-04-10-19
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Length 1333;
                                 US-110-953-349-31206
US-110-953-349-21206
US-110-953-349-24350
US-110-953-349-24350
US-110-953-349-2407
US-110-953-349-2207
US-110-953-349-2206
US-110-953-349-28461
US-110-953-349-28461
US-110-953-349-28461
US-110-953-349-3597
US-110-953-349-3597
US-110-953-349-3597
US-110-953-349-3597
US-110-953-349-3597
US-110-953-349-3597
S-10-953-349-985
S-10-953-349-31207
S-10-953-349-31206
S-10-982-908-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 6
Pred. No. 34;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3323, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2992, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
 327 FRGVLEQLRW 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGVLQQVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-511-937-2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-10-511-937-2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-293-697-3323
 TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3323, Ap Sequence 3323, Ap Sequence 1159, Ap Sequence 1159, Ap Sequence 1157, Ap Sequence 9203, Ap Sequence 9203, Ap Sequence 3971, Ap Sequence 3471, Ap Sequence 9462, Ap Sequence 9462, Ap Sequence 9461, Ap Sequence 94195, Ap Sequence 94195, Ap Sequence 95461, Ap Sequence 95461, Ap Sequence 95461, Ap Sequence 95461, Ap Sequence 25518, Ap Sequence 27516, Ap Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA New:*

1. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

4. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                   GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                  58871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-511-937-2992

US-11-293-697-3323

US-10-953-349-1159

US-10-953-349-1159

US-10-953-349-1157

US-10-953-349-1157

US-10-953-349-9204

US-10-953-349-9203

US-10-953-349-9203

US-10-953-349-9203

US-11-293-697-3971

US-11-293-697-3971

US-10-953-349-5461

US-11-317-983-9

US-11-317-983-9
                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                           58871 seqs, 11565156 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                              1 FQGVLQQVRFVF 12
                                                                                                                                                                                                           US-10-030-735-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1504
2900
3290
341
503
186
188
318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length
                                                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555.0
555.0
555.0
555.0
555.0
555.0
557.0
557.0
557.0
557.0
557.0
557.0
557.0
557.0
557.0
557.0
557.0
557.0
557.0
557.0
557.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0
                                                                                                                                  June
                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
```

ö

Gaps

ö

Indels

```
Publication No. US20060107345A1

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROW, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: SIQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: BICOUNED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

NUMBER OF SEQ ID NOS: 40252

SOFTWARE PATENTIN VETSION 3.3
                                                                                                                                                                                                                            Sequence 1158, Application US/10953349
Publication No. US20660107345A1
GRENEAL INFORMATION
TOTAL OF INVENTIONS SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTIONS SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTIONS ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION WHORER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 158
LENGTH: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1067, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.0%; Score 33; DB 6; Length 249; 50.0%; Pred. No. 14; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.0%; Score 33; DB 6; Length 250; 50.0%; Pred. No. 14; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: |: :|| ||
167 FEAVVDRVRLVF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50...
Fire 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: |: :|| ||
168 FEAVVDRVRLVF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 50.0
Matches 6; Conservative
                           1 FOGULOOVRFVF 12
                                                             |: |: :|| ||
82 FEAVVDRVRLVF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLOOVRFVF 12
                                                                                                                                                                           RESULT 5
US-10-953-349-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-10-953-349-1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-953-349-1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-953-349-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-953-349-1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Sequence | 1159, Application US/10953349 |
| Sequence | 1159, Application US/10953349 |
| Sequence | 1159, Application US/10953349 |
| Sequence | 1159, Application No. US20060107345A1 |
| GENERAL INPORMATION: USCOURCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES |
| TITLE OF INVENTION: ENCONDED THERBY |
| TITLE OF INVENTION: ENCONDED THERBY |
| FILE REFERENCE: 2750-1579PUS2 |
| FILE REFERENCE: 2750-1579PUS2 |
| CURRENT FILING DATE: 2004-09-30 |
| NUMBER OF SEQ ID NOS: 40252 |
| SOFTWARE: Patentin version 3.3 |
| SOFTWARE: Patentin version 3.3 |
| SEQ ID NO 1159 |
| CONTROL OF THE CONTRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 6; Length 164;
Pred. No. 8.7;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 7; Length 490;
Pred. No. 18;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                      DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4335, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
FRIOR APPLICATION NUMBER: US/10/108,260
FRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4335
LENGTH: 490
                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB Pred. No. 4.6; 2; Mismatches
                     CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR PILING DATE: 2005-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3323
LENGTH: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Arabidopsis thaliana
US-10-953-349-1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.0%;
                                                                                                                                                                                                                                                                                                                                                                                      56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.7%;
                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 60...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.6
Matches 5; Conservative
FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-293-697-3323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :|||||:
89 GSMQQVRFI 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-11-293-697-4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||:||:
29 YQGVMQQIQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GVLQQVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLOOVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -293-697-4335
                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
Sequence 9203, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin Version 3.3
SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9202, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE REPRENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9202
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.0%; Score 33; DB 6; Length 401; 50.0%; Pred. No. 23; in Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                       55.0%; Score 33; DB 6; Length 400; 50.0%; Pred. No. 23; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3971, Application US/11293697
; Publication No. US2006010537641
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-AD106
CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3971
; LEMGTH: 609
; TYPE: FRT
                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: |: :|| ||
167 FEAVVDRVRLVF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: |: :|| ||
168 FEAVVDRVRLVF 179
                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGULQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLOQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 10
US-10-953-349-9203
                                                                                                                                                                                                                                                                                                                                  US-10-953-349-9203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-953-349-9202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-953-349-9202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-293-697-3971
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING FOLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PALENTIN VERSION 3.3
SEQ ID NO 1066
LENGTH: 340
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                               Gaps
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 6; Length 315;
Pred. No. 18;
3; Mismatches 3; Indels
                                                                                                                                                     Score 33; DB 6; Length 287;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.0%; Score 33; DB 6; Length 340; 54.5%; Pred. No. 19; tive 2; Mismatches 3; Indels
                                                                                                                                                                                               3; Indels
                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-1066; Application US/10953349; Sequence 1066, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                            ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Arabidopsis thaliana
US-10-953-349-1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Arabidopsis thaliana
US-10-953-349-9204
  ; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1067
; LENGTH: 287
                                                                                                                                                     Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FQGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: |: :|| ||
82 FEAVVDRVRLVF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                    1 FQGVLQQVRFV 11
                                                                                                                                                                                                                                                                        11 YÓSSĽSÓIRFV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGVLQQVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 YOSSLSÖIRFV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                       US-10-953-349-9204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                          Gaps
                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.3%; Score 32; DB 6; Length 1504; 54.5%; Pred. No. 1.5e+02; tive 2; Mismatches 3; Indels
                                                  Score 33; DB 7; Length 609;
Pred. No. 36;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.3%; Score 32; DB 7; Length 763; 75.0%; Pred. No. 73; 0; Indels ative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-10-505-928-662
| Sequence 662, Application US/10505928
| Publication No. US20060088332A1
| GENERAL INFORMATION:
| APPLICANT: Ludwig Institute for Cancer Research et al. TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
| FILE REFREENCE: 28967/39178
| CURRENT FILING DATE: 2004-08-27
| PRIOR APPLICATION NUMBER: US/10/505,928
| CURRENT FILING DATE: 2002-03-07
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: Patentin 3.2
| LENGTH: 1504
                                                                                                                                                                                                            RESULT 13
US-11-293-697-3277
Sequence 3277, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length CDNA; FILE REFERENCE: H1-A0106
CURRENT FILING DATE: 2005-12-05
REIOR APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 3277
LENGTH: 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-10-953-349-5462
Sequence 5462, Application US/10953349
                                                   55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.5.
Best Local Similarity 64.5.
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                            1 FOGVLOOVRFVF 12
                                                                                                                                              6 FOGLITOARLPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :| :||||
751 QHILSSLRFVF 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QGVLQQVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|:|||||
389 EGLLQQVR 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-11-293-697-3277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-505-928-662
; ORGANISM: Homo sapiens
US-11-293-697-3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QGVLQQVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                              ð
                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICAMY: ALEXANDRO, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES;

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-15799082

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT PILING DATE: 2004-09-30

NUMBER: OF 10 NOS: 4025-2

SOFTWARE: Patentin version 3.3

SEQ ID NO 546-2

LENGTH: 290

TYPE: PRT

ORGANISM: Arabidopsis thaliana
US-10-953-349-5462

QUETY MATCh

Best Local Similarity 60.0%; Pred. No. 40;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GVLQQVRFVF 12

Db 142 GLIEEVREVF 151

Db 142 GLIEEVREVF 151

Search completed: June 6, 2006, 00:12:56

Job time: 4.82414 secs
```

```
GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
```

protein search, using sw model OM protein - 5, 2006, 22:08:53 ; Search time 91.1379 Seconds (without alignments) 60.201 Million cell updates/sec June Run on:

US-10-030-735-21 59 1 FQGVLQSVRFVF 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2589679 seqs, 457216429 residues Searched:

2589679

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_8:* Database :

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2006s: geneseqp1980s:* geneseqp1990s:* geneseqp2004s:* geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aab35376 Alpha3bet	Aab35352 Alpha3bet	Aab35361 Alpha3bet			Adl70641 Human thr	Adq39359 Human myo	Adq39357 Human myo	Aau02916 Angiotens	Aab43602 Human can	Aau02915 Angiotens	Adn02474 TSF polyp	Aau02914 Angiotens	Aau02913 Angiotens	Aab00042 Human thr	Aau74771 Human thr	Abb82285 Human thr	Aab74450 Human var	Aab90800 Human she	Aae25030 Human thr	Aau75315 Human thr	Abp96780 Human COP	Abu03474 Angiogene
OI OI	AAB35376	AAB35352	AAB35361	AAB35378	ABG72834	ADL70641	ADQ39359	ADQ39357	AAU02916	AAB43602	AAU02915	ADN02474	AAU02914	AAU02913	AAB00042	AAU74771	ABB82285	AAB74450	AAB90800	AAE25030	AAU75315	ABP96780	ABU03474
98	4	4	4	4	9	œ	œ	œ	4	٣	4	7	4	4	m	ഗ	2	4	4	2	S	9	9
% Query Match Length DB	12	12	12	12	12	240	432	432	459	466	546	548	555	731	1152	1152	1152	1170	1170	1170	1170	1170	1170
& Query Match	100.0	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9	94.9
Score	59	26	26	26	26	26	99	26	26	99	99	99	26	99			26					99	26
Result No.		7	m	4	<u>ι</u> Ω	9	7	8	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23

70 6 ABG74673 70 7 ABR62059 70 7 ABR62059 70 8 ADJ76124 70 8 ADJ76129 70 8 ADJ76296 70 8 ADJ76296 70 8 ADG26070 70 8 ADG26070 70 8 ADG39356 70 8 ADG39356 70 9 ABB7781 71 4 AAB35339 12 4 AAB35380 12 4 AAB35381 12 4 AAB35381 12 4 AAB35381 12 4 AAB35381 12 4 AAB35381 12 4 AAB35381	Abg74673 Human THB Abc82059 Human THB Abr62059 Human ThT Adin39822 Cancer/an Adj75259 Marker ge Adj775296 Marker ge Adj775296 Marker ge Adj775296 Human thr Adj35874 Human thr Add58070 Thrombosp Adg58070 Thrombosp Adg39356 Human myo	Aab35380 Alpha3ber Aab35373 Alpha3bet Aab35381 Alpha3bet Aab35384 Alpha3bet Aab35374 Alpha3bet
	ABG74673 AAB36228 AAB36228 ABM52286 ABM76124 ABM76124 ABM76124 ABM76179 ABM78179 ABM33356 ABM33355 ABM3781 ABM6751	AAB35373 AAB35373 AAB35381 AAB35364 AAB35374
	000000000000000000000000000000000000000	
	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	889 889 889 11.
444444444444444444	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 2 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 4 1 5 6 4 5

ALIGNMENTS

AAB35376 standard; peptide; 12 AA. RESULT 1

AAB35376;

(first entry) 08-MAY-2001

Alpha3betal integrin binding peptide #41.

Alpha3beta1 integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.

Synthetic.

WO200105812-A2

25-JAN-2001.

12-JUL-2000; 2000WO-US018986.

99US-0144549P. 15-JUL-1999; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Krutzsch HC; Roberts DD,

WPI; 2001-182656/18.

New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and cancer

Claim 4; Page 34; 84pp; English.

The present invention provides a number of peptides which bind to alphalbetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention

Sequence 12 AA;

```
Roberts DD, Krutzsch HC;
                                                                                                                                                                             WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 11; Conser
                                                                                                                                                                                                                                                                                                                 the invention
                                                                                                                                                                                                                                                                                                                                    Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200105812-A2.
                                                                 WO200105812-A2
                                                                                                                        15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999;
                                                                                   25-JAN-2001.
                                                                                                                                                              Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB35378;
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                              cancer.
                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB35378
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of peptides which bind to alphaibetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention
                                                                                                                                                                             Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                       New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 4; hears.
100.0%; Score 59; DB 4; Length 12; 100.0%; Pred. No. 0.00011;
                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 4
Pred. No. 0.000
1; Mismatches
                   Mismatches
                                                                                                                                                              Alpha3betal integrin binding peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha3betal integrin binding peptide #26.
                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ż
                                                                                                      AAB35352 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 34; 84pp; English.
                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB35361 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.9%;
91.7%;
                                                                                                                                                                                                                                                                           12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                               99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2001 (first entry)
                                                                                                                                           (first entry
                                                                                                                                                                                                                                                                                                                                     Roberts DD, Krutzsch HC;
                   12; Conservative
                                                 1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FQGVLQNVRFVF 12
                                     1 FOGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 11; Conserv
          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 AA;
                                                                                                                                                                                                                                        WO200105812-A2.
                                                                                                                                                                                                                                                                                               15-JUL-1999;
                                                                                                                                           08-MAY-2001
                                                                                                                                                                                                                                                          25-JAN-2001
                                                                                                                                                                                                                      Synthetic.
                                                                                                                         AAB35352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB35361;
Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                       cancer
                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB35361
ID AAB3
XX AAC AAB3
                                                                                    RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
                                                                                              AAB35352
                                                                                                               g
                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                       8
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of peptides which bind to alpha3beral integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 4; I
Pred. No. 0.00044;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha3beta1 integrin binding peptide #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB35378 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.98;
                                                                                                                                                                                                                                                                                                                                  12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0144549P.
                                                                                                                                                                                                                                                                                                                                                                                                   99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLOSVRFVF 12
```

m

WPI; 2001-182656/18.

```
The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to diagnosing cancer other than prostate cancer in a male mammal, comprising assaying a test sample for increased level of semenogelin, or cancer in a female by assaying for the presence of semenogelin. Administering a semenogelin protein or polypeptide fragment or a semenogelin-specific antibody or active fragment, or a recombinant ovector expressing the protein or antibody, is useful for inducing an immune response to a cancer in a mammal, where the cancer is not prostate cancer and semenogelin is a marker. The invention is used to diagnose cancer, particularly of epithelial origin such as lung cancer, papillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new diagnosis for cancer other than prostate cancer in a mammal useful to detect cancer including lung cancer, particularly small cell lung cancer and melanoma comprises detecting semenogelin in a sample.
                                                   New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; thrombospondin-1; cytostatic; immunostimulant; cancer;
epithelial cancer; lung cancer; papillary renal cell carcinoma;
colon cancer; small-cell lung cancer; SCLC; melanoma.
                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 4; Length 12;
Pred. No. 0.00044;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombospondin-1 sequence containing synthetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                  Example 2; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG72834 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 14; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-2002; 2002WO-US010535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2001; 2001US-0281994P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-103329/09.
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
Les 11; Conserv
                                                                                                                                                                                                                                                                               of the invention
                                                                                                                                                                                                                                                                                                                 Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200281630-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG72834;
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                               cancer.
                                                                                                                                                                                                                                                                                                                                                                                        Matches
```

ö

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of the N-terminal domain of human thrombospondin-1 (TSP) ADL70639. The invention relates to TSP fragments (80-100, 40-55 or 20-35 kDa mol.v.) found in plasma, and their use in clinical assays for cancer and for generation of antibodies and other binding agents. A method that distinguishes TSP from a TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion as a target for a binding molecule, e.g. an antibody, to obtain a quantitation of TSP plus TSP fragment or portion; (2) using an equantitation of TSP plus TSP fragment or portion to obtain a quantitation of TSP only; and (3) using the difference between (1) and (2) as a quantitation of the amount of TSP fragment or portion. Suitable epitopes are provided ADL7063-ADL70639. Detection or quantification of the TSP fragment or portion is performed in order to detect the presence, or monitor the course, of a disease or condition selected from cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes.
renal cell carcinoma, colon cancer, especially small-cell lung cancer (SCLC), or a melanoma. The present sequence represents the amino acid sequence of the thrombospondin-1 sequence containing synthetic peptide which binds to alpha-3-beta-1 integrin
                                                                                                                                                            Gaps
                                                                                                                                                            ö
                                                                                                                         Score 56; DB 6; Length 12;
Pred. No. 0.00044;
.; Mismatches 0; Indels
                                                                                                                           Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151. .164 /
/note= "Fibrinogen binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Heparin binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23. .32
/note= "Heparin binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                        Human thrombospondin-1 N-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 40; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  ADL70641 standard; protein; 240 AA.
                                                                                                                         94.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2002; 2002US-0405494P.
21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2003; 2003WO-US026023
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                          11; Conservative
                                                                                                                                                                                              1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                             1 FOGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77. .82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WILL/) WILLIAMS K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-226901/21.
                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004018995-A2.
                                                                                        Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                     ADL70641;
                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                  RESULT 6
   8 X G G G G
                                                                                                                                                                                              ò
                                                                                                                                                                                                                             g
```

WPI; 2004-533949/51

```
remal failure, remal disease, atopic dermatitis, vasculitis, acute vasculitis, renal allograft, asthma, diabetes mellitus, myocardial inferction, liver disease, splenectomy, dermatcomyositis, polyaretritis nodosa, systemic lupus erythematosus, lupus erythematosus, Kawasaki syndrome, non-specific vasculitis, juvenile rheumatoid arthritis, rhematosus, lupus erythematosus, Kawasaki chrom-Schoenlein purpura, an inflammatory condition, a condition associated with platelet activation, a condition associated with intravascular platelet activation, a condition associated with intravascular coagulation, a condition associated with mand/or a thrombosypopania disseminated intravascular acondition associated with intravascular coagulation, activation, a condition associated with activation, a condition associated with a coagulation, an appartame reaction, and/or a thrombospondin notic reaction, an aspartame reaction, at activation, a condition associated with a cryofibrinosen, activity, sclaroderma, conditions associated with an antiocarcinoma, carcinoma, lumphona, launa condition associated with a cryofibrinosen, accordinoma, launa anchor ancer, is encer, incer, cancer, metastatic cancer, is encer, incer, solid cancer, acancer is elected from adenoma, accer with vascular invasion, internal cancer, incer, especend, procer, or joint, tendon or ligament, digestive system, removous system, parchaed, a gland, manmary system (male or female), genituurinary system, resourcer, a cancer system, parchae, andocianal tissue, endocarmal tissue, endocarmal tissue, endocarmal tissue, endocarmal tissue, a terstoma, a poorty-differentiated cancer, a mederately differentiated cancer or a moderately differentiated cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human myocardial infarction-associated gene derived protein, SEQ ID 1022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.9%; Score 56; DB 8; 91.7%; Pred. No. 0.012; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ39359 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 91.7 ses 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 FOGVLONVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402004058052-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ39359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ39359
             $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

Devlin JJ, Iakoubova O;

Cargill M,

(APPL-) APPLERA CORP.

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's cucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino the specification or its complement and encoding any one of the amino comprising an amino acid sequence given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting and a variant polypeptide; and a method for identifying an agent useful in treating or preventing method for identifying an agent useful in treating or preventing acid molecule; a method of detecting method has cardiant activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human myocardial infarction-associated gene derived protein, SEQ ID 1020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        decreased risk for developing myocardial infarction and for preparing a
                                                         Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition for treating or preventing myocardial infarction. sequence represents the protein of a human myocardial infarct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.9%; Score 56; DB 8; Length 432; 91.7%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                Claim 10; SEQ ID NO 1022; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ39357 standard; protein; 432 AA
                                                                                                        the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiant; gene therapy; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 91.7
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 432 AA;
                   N-PSDB; ADQ38531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MO2004058052-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L8-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2004.
                                                                                    myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ39357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ3935'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
Claim 10; SEQ ID NO 1020; 145pp; English.
        Devlin JJ,
  (APPL-) APPLERA CORP
             WPI; 2004-533949/51.
N-PSDB; ADQ38529.
                                                                                                                     Sequence 432 AA;
        Cargill M,
```

208 FOGVLONVRFVF 219 Best Local Similarity 91.7 Matches 11; Conservative 1 FOGVLOSVRFVF 12 Query Match ઠ 원

ö

Gaps

ö

AAU02916 standard; protein; 459 AA. 12-SEP-2001 (first entry)

granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis. Angiotensin converting enzyme splice variant; ACEV; interleukin 6; Angiotensin converting enzyme (ACEV) splice variant protein #16.

(ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic caids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies. The sequence represents an angiotensin converting enzyme splice variant 94.9%; Score 56; DB 4; Length 459; 91.7%; Pred. No. 0.024; ive 1; Mismatches 0; Indels Levine Z, David A, Azar I, Khosravi R, Bernstein J; Claim 4; Fig 16; 519pp; English. 17-NOV-2000; 2000WO-IL000766 99IL-00132978. 208 FÓGVLÓNVRFVF 219 Query Match Best Local Similarity 91.7 Matches 11; Conservative 1 FQGVLQSVRFVF 12 (COMP-) COMPUGEN LTD. WPI; 2001-336004/35. N-PSDB; AAS06016. Sequence 459 AA; WO200136632-A2 Homo sapiens. 17-NOV-1999; 10-DEC-1999; 25-MAY-2001. AAB43602; RESULT 10 AAB43602 ઠે The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's content action where the presence of the SNP is correlated with an action further comprises an isolated nucleotides where of the snucleotides with an isolated nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino the specification or its complement and encoding any one of the amino card sequences given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in captain; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting an symiant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has an increased or decreased risk for developing myocardial infarction and encoding infarction and for preparing a composition for treating or preventing an encoding infarction and for preparing a sequence and an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a sequence represents the protein of a human moreard and infarction. This ö sequence represents the protein of a human myocardial infarction-sasociated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website. Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids. Gaps o; Length 432; 0; Indels 94.9%; Score 56; DB 8; 91.7%; Pred. No. 0.022; iive 1; Mismatches Iakoubova 0;

Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiarchritic; antivirul; antirhencial antidiabetic; antiarchritic; antiviral; antilnflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermacological; neuroprotective; thrombolytic; coagulant; noctropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening. Human cancer associated protein sequence SEQ ID NO:1047. AAB43602 standard; protein; 466 AA. (first entry) 08-FEB-2001

ω

```
12-MAR-2003
                                                                                                                                                                                                                               evine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN02474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN02474
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BXBXSXXXXXXX
                                                                                                                                                                                                                                                                                                      AAC77607 to AAC7848 encode the human cancer associated proteins given in AAB43398 to AAB4429. The proteins can have activities based on the itssues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiathmatic; antiathritic; antinathmatic; antibacterial; antivital; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; coortropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides can be used for preventing, treating or the present invention may be used to treat immune disorders by activating or the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of isorders, allergic reactions, gifferentiation or mobilisation of cincorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate configuration configuration or an antagonists and antagonists may be also be used in dry screens. AAC78499 to AAC78457 and AAB44440 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                          Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiotensin converting enzyme (ACEV) splice variant protein #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 3; Length 466; Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                 Claim 11; Page 1636-1638; 2352pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU02915 standard; protein; 546 AA.
                                                                                             38-MAR-2000; 2000WO-US005882.
                                                                                                                       99US-0124270P.
                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.98;
91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 FQGVLQNVRFVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention
                                                                                                                                                                           Rosen CA, Ruben SM;
                                                                                                                                                                                                   WPI; 2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                  N-PSDB; AAC77811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 466 AA;
                                        WO200055350-A1.
                                                                                                                       12-MAR-1999;
               Homo sapiens.
                                                                  21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
AAU02915
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic cidentification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various cidisorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases cuch as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenovirus vector; anti-neoplastic; TSF polypeptide; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.9%; Score 56; DB 4; Length 546; 91.7%; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN02474 standard; protein; 548 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 15; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99IL-00132978.
99IL-00133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-336004/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS06015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rsf polypeptide.
                                                                                                                                                                                                                                    WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CN1401387-A.
                                                                                                                                                                                                                                                                                                             25-MAY-2001
```

```
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                      mediated anti-neoplastic composition is prepared through cloning the cDNA agequence from the human peripheral blood cell by specific primer and reverse transcription-polymerase chain reaction (RT-PCR) method for coding TSF polypeptide, construction in human embryonic kidney cell 293 by AdEasy system, and packaging and expressing the recombinant adenovirus vector of TSF. It can suppress the growth and transfer of cancer. The present sequence represents the TSF polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                              The present invention relates to a novel recombinant adenovirus vector
                                                                                                                                 Tumor suppressing polypeptide TSF and gene therapy vector composition.
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiotensin converting enzyme (ACEV) splice variant protein #14.
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                      Length 548;
                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Levine Z, David A, Azar I, Khosravi R, Bernstein J;
                                                     (TAID-) TAIDA LIFE SCI TECH RES CENT HEMATOLOGY.
                                                                                                                                                                                                                                                                                                     Score 56; DB 7;
Pred. No. 0.029;
1; Mismatches
                                                                                                                                                        Claim 2; SEQ ID NO 1; 13pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAU02914 standard; protein; 555 AA.
                                                                                                                                                                                                                                                                                                     94.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000; 2000WO-IL000766.
          21-AUG-2002; 2002CN-00129408
                                21-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99IL-00132978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99IL-00133455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                               208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                  1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COMP-) COMPUGEN LTD
                                                                                                 WPI; 2003-469302/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-336004/35
                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 11; Conser
                                                                                                            N-PSDB; ADN02475
                                                                                                                                                                                                                                                                                Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU02914;
                                                                                                                                                                                                                                                                                                      Query Match
                                                                          Han Z,
X#X#X#X#X#X#X#X#X#X
                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                   ద
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEN) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor; glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases when as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as as asbestosis and vascular phthologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                       Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiotensin converting enzyme (ACEV) splice variant protein #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Levine Z, David A, Azar I, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU02913 standard; protein; 731 AA.
                                                                                                                                                                                                                              Claim 4; Fig 14; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99IL-00133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99IL-00132978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FOGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGULOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-336004/35
N-PSDB; AAS06014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU02913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU02913
```

```
01-FEB-2000; 2000WO-US002482
                                               Homo sapiens
                                                                            03-AUG-2000
                                                                                                Lawler JW;
                     AAB00042;
                                                      Region
                                                           Region
                                                                Region
            RESULT 15
              AAB00042
                 8
   g
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulcoyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated mucleic candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic mephropathy, muscular diseases such as hypertrosis, imminity and construction and coronary arterial thrombosis, renal diseases such as diabetic mephropathy, muscular diseases such as hypertrosis, imminity and construction and coronary arterial thrombosis, renal diseases such as diabetic mephropathy, muscular diseases and as dispatch as diabetic methropathy, muscular diseases and as dispatch as diabetic methropathy, muscular diseases and as diabetic methropathy, muscular diseases and as diabetic methropathy, muscular diseases and as diabetic methropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis
                                                                 Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                      Claim 4; Fig 13; 519pp; English
N-PSDB; AAS06013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 731 AA;
```

```
DB 4; Length 731;
                                0; Indels
Score 56; DB 4;
Pred. No. 0.04;
1; Mismatches
Ouery Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                            208 FOGVLONVRFVF 219
                                                                 1 FOGVLOSVRFVF 12
```

Gaps

ö

TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection; glaucoma. AAB00042 standard; protein; 1152 AA Human thrombospondon-1 (TSP-1). 08-NOV-2000 (first entry)

```
/label= Type 1 repeat region /label= Type 1 repeat region /label= Type 1 repeat region
                 361. .416
/label= Type 1 repeat region
Location/Qualifiers
```

WO200044908-A2

99US-0118053P 01-FEB-1999;

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

WPI; 2000-514823/46.

```
New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin) -1, but not second and third type 1 repeats of human TSP (thrombospondin) -1 containing the second and 1. The nucleic acid of TSP (thrombospondin) -1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerse chain caction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful to reating angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. Anti-

Configuration human immunodeficiency virus (HIV) infection. Anti-
Configuration human immunodeficiency virus (HIV) infection. Anti-
Configuration human immunodeficiency virus (HIV) infection. Anti-
Configuration human immunodeficiency virus (HIV) infection. Anti-
Configuration human immunodeficiency virus (HIV) infection. Anti-
Configuration human immunodeficiency virus (HIV) infection. Anti-
Configuration human independently of growth of tumour cell heterogeneity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
              Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 3; Length 1152; Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: June 5, 2006, 22:24:58 Job time: 91.1379 secs
                                                                                                                                  Disclosure; Fig 1; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    does not induce drug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.98;
91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

5, 2006, 22:25:22 ; Search time 13.9655 Seconds (without alignments) 82.675 Million cell updates/sec Run on:

US-10-030-735-21 59 1 FQGVLQSVRFVF 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
1: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
		94.9	229	7	S57957	thrombospondin 1 -
7		94.9	1170	ч	TSHUP1	thrombospondin 1 p
m		94.9		~	A40558	Н
4	38	4		7	T20985	ㅎ
S		64.4		7	B88349	protein F15D4.3 (i
9		64.4		7	D81929	probable imidazole
7	38	64.4	747	~	AE2929	two component resp
80		64.4	783	N	A98353	probable transcrip
6	38	64.4	1172	٦	TSHUP2	thrombospondin 2 p
10		64.4		7	A42587	N
11	37	62.7	715	N	S70397	zona pellucida gly
12	36	61.0	111	~	S52596	probable membrane
13	36	61.0	151	~	C57253	tRNA-pseudouridine
14	. 36	61.0	993	~	T17230	hypothetical prote
15	36	61.0	1142	7	T39103	probable negative
16		61.0	1178	-	A39804	thrombospondin pre
17		61.0	1312	7	868593	DNA-directed DNA p
18	36	61.0	1670	~	871551	DNA-directed DNA p
19		59.3	82	7	F96625	cal
20		59.3	465	7	AC0347	probable membrane
21		59.3	681	7	T16353	
22	35	59.3	819	~	T07319	hypothetical prote
23	34	57.6	212	~	AE2158	
24	34	57.6	265	7	F69742	hypothetical prote
25	34	57.6	348	7	F70398	p-aminobenzoate sy
56	34	57.6	355	7	T50479	G protein alpha ch
	34	57.6	363	~	AE1712	system
28	34	57.6	364	7	AG1341	44
29	34	57.6	417	7	H83708	hypothetical prote

SIP1 protein - yea probable penicilli	DNA-directed DNA p	hypothetical prote	hypothetical prote	beta lactamase pre	ribose/galactose A	hypothetical prote	type IIS restricti	probable type II r	amino acid permeas	H+-transporting tw	hypothetical prote	53K glycoprotein -	probable integral-
S41984 T36795	S42459	A95877	C30261 AI1167	D70384	F70184	T51082	G64703	G71816	D86669	D84938	T33595	S45068	E87021
00	(7)	0 0	N	7	~	N	N	N	N	~	N	~	7
863	1702	827	167	307	311	372	397	406	459	467	469	471	505
ωv	9	a c	ש ע	σ	σ	σ	σ	σ	σ	σ	σ	σ	6
57.	57.	56.	55.9	55.	55.	55.	55.	55.	55.	55.	55.	55.	55.
34		33.5	າ ຕ	33	33	33	33	33	33	33	33	33	33
30	32	33	3 5	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1
857957
thrombospondin 1 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S57957
R; Lafeuillade, B.; Pellerin, S.; Keramidas, M.; Chambaz, E.M.; Feige, J.J.
submitted to the EMBL Data Library, July 1995
A; Description: Opposite regulation of thrombospondin-1 and CISP/thrombospondin-2 expressi
A;Reference number: S57955
A; Accession: S57957
A;Status: preliminary
A; Molecule type: mRNA
A;Residues: 1-229 <laf></laf>
A.Cross-references: UNIPROT: 028194; UNIPARC: UPI000008740A; EMBL: X89511; NID: 9899228; PIDN
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
Query Match 94.9%; Score 56; DB 2; Length 229;
Best Local Similarity 91.7%; Pred. No. 0.0014. Marches 11: Conservative 1: Mismatches 0: Indels 0: Gans 0:
ii; constructive i; intermetance o, inders o, dape
Qy 1 FQGVLQSVRFVF 12
UD ISO FOGULONVERVE ZOI

thrombospondin 1 precursor - human

C;Species: Homo sapiens (man)
C;Date: 23-Aug-1997 #sequence revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A26155; A34274; Ā30140; A25812; A05172; A42927
R;Lawler, J; Hymes, R.O.
J. Cell Biol: 103, 1635-1648, 1986
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple C6
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple C6
A;Accession: A26155
A;Accession: A26155
A;Accession: A26155
A;Accession: Disparce number: A26155
A;Accession: Disparce number: A26155
A;Accession: Disparce number: A26155
A;Accession: Disparce number: A26155
A;Accession: A34274; MUID: 89291870; PMID: 2544587
A;Accession: A34274; MUID: 89291870; PMID: 2544587
A;Accession: A34274; MUID: 89291870; PMID: 2544587

A;Molecule type: DNA
A;Residues: 1-166 <LAH>
A;Residues: 1-166 <LAH>
A;Cross-references: UNIPARC:UPI00001742BF; GB:J04835
A;Cross-references: UNIPARC:UF D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, F
B;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, F
J. Cell Biol. 108, 729-736, 1989
A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the

us-10-030-735-21.rpr

```
A,Molecule type: DNA
A,Residues: 1-1170 cLAW>
A,Cross-references: UnIPROT: P35441; UNIPARC: UPI0000028012; GB:M62449; GB:M62450; GB:M6245
A; Cross-references: UNIPROT: P35441; UNIPARC: UPI0000028012; GB:M62467; GB:M62468; GB:M62465;
A; GB:M62462; GB:M62463; GB:M62464; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62465;
R; Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
J. Biol. Chem. 265, 16691-16698, USB the mouse thrombospondin gene and evaluation of the role of A; Reference number: A37905; MUID: 90375546; PMID: 2398070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UPI000016D076; GB:J05605; GB:J05606; NID:g201991; PIDN:AAA409; R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M. J. Biol. Chem. 267, 2374-2381, 1992
A;Title: Chem. 267, 2374-2381, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell § A;Reference number: A42587; MUID:92147683; PMID:1371115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1152,'P',1154-1170 <LAH>
A;Residues: 1-1152,'P',1154-1170 <LAH>
A;Cross-references: UNIPARC: UNIPONO177A96; GB:M87276
A;Cross-references: UNIPARC: UNIPONO177A96; GB:M87276
B;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FRBS Lett. 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar
A;Reference number: S68787; MUID:96234006; PMID:8654563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCOMPLEATERINGS: UNITABLE AND ACCOMPLEASE TO ACCOMPLEASE TO ACCOMPLEASE TO ACCOMPLEASE TO ACCOMPLEASE AND ACCOMPLANCE AND ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:033511; UNIPARC:UPI000007BE33; EMBL:Z80344; PIDN:CAB02486.2; A;Experimental source: clone F15D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F1SD4.3 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Taenorhabditis elegans C.Species: Taenorhabditis elegans C.Specession: Taenore Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 2; Length 1170;
Pred. No. 0.0079;
1; Mismatches 0; Indels
                                                              gene.
                                           A,Title: Characterization of the murine thrombospondin ;
A,Reference number: A40558; MUID:92128941; PMID:1774063
A,Accession: A40558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 19-26,'X',28-37 <CHE>
A;Cross-references: UNIPARC:UP10000177A97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 FOGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-490 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A37905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <BOR
                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: B42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Muchaels 181 of introns may be incomplete
C, Complex: homotrimer, disulfide linked
C, Function:
A, Description: participates in cell migration and adhesion, and in platelet aggregation
C, Superfamily: thrombospondin 1; EGF homology; thrombospondin type I repeat homology; vc
C, Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F, 19-1170/Product: thrombospondin 1 #status predicted <MAT>
F, 317-375/Domain: signal sequence #status predicted <MAT>
F, 317-375/Domain: thrombospondin type I repeat homology <WG>
F, 344-490/Domain: thrombospondin type I repeat homology <THR2>
F, 491-447/Domain: thrombospondin type I repeat homology <THR2>
F, 551-586/Domain: EGF homology <EGF1>
F, 551-586/Domain: EGF homology <EGF1>
F, 552-528/Region: cell attachment (R-G-D) motif
F, 171-232/Disulfide bonds: #status predicted
F, 270, 274/Disulfide bonds: interchain #status predicted
F, 260/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F, 1051/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                              A; Molecule type: mRNA
A; Residues: 1-83, 'A', 85-22, 'A', 524-1170 < HEN>
A; Residues: 1-83, 'A', '85-522, 'A', 524-1170 < HEN>
A; Residues: 1-83, 'A', '85-522, 'A', 524-1170 < HEN>
A; Cross-references: UNIPARC:UP10000038AB1; EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
R; Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
B; Cobayashi, S.; B418-8425, 1986
A; Title: Partial amino acid sequence of human thrombospondin as determined by analysis of
A; Reference number: A25812; MUID:87157592; PMID:303036
A; Reference number: A25812
A; Molecule type: mRNA
A; Residues: 1-83, 'A', 85-397 < KOB>
A; Molecule type: mRNA
A; Residues: 1-83, 'A', 85-397 < KOB>
A; Cross-references: UNIPARC:UP1000016B0CA; GB: M25631; NID:g538353; PIDN:AAA36741.1; PID:
B; Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
B; Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: A05172
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Cross-references: 1-83, A', 485-374, 'RC' < DIX>
A, Cross-references: UNIPARC: UPI000016B140; GB:M14326; NID: 9340005; PIDN: AAA61237.1; PID:
A, Note: parts of this sequence, including the amino end of the mature protein, were dete
A; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A, Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A, Reference number: A42927; MUID: 92348511; PMID: 1379247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787
R;Lawler, J.; Duquette, M.; Perro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 1; Length 117
Pred. No. 0.0079;
1; Mismatches 0; Indels
A; Reference number: A30140; MUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 987-1003 <SUNA
A,Cross-references: UNIPARC:UPI00001742C0
A,Note: Cys-992 is shown to have a free sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Genetics:
A,Gene: GDB:THBS1; TSP1; TSP
A,Cross-references: GDB:120438; OMIM:188060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91...
11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Map position: 15q15-15q15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: A42927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 23/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
```

ઠ

```
two component response regulator Atu3035 [imported] - Agrobacterium tumefaciens (strain (
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                 C,Accession: AE2929
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellɛ ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disobable transcription regulator PA1760 [imported] - Agrobacterium tumefaciens (strain C: Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens Species: Agrobacterium tumefaciens Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens) (Spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Specieë: Homo sapiens (man)
C;Dacceseion: AMA-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Dacceseion: A47379; A42173
R;LaBell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A;Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: poter A;Reference number: A47379; MUID:94010892; PMID:8406456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q8UBI1; UNIPARC:UPI0000164787; GB:AE008689; PIDN:AAL43851.1; A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q8UBI1; UNIPARC:UPI00000D2059; GB:AE007870; PIDN:AAK90347.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AE2929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.4%; Score 38; DB 2; 77.8%; Pred. No. 21; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 2
Pred. No. 20;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombospondin 2 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: AGR L 3540
A,Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.4
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GVLQSVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|:|||||
42 GILESVRFV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GILESVRFV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GVLQSVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-747 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-783 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A98353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: Atu3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
TSHUP2
                                                                                AE2929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein F15D4.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B88349
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 < PAR>
A;Cross-references: UNIPROT:Q9JVH3; UNIPARC:UPI000012C805; GB:AL162754; GB:AL157959; NIE
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable imidazole-glycerol phosphate synthase amidotransferase component (EC 2.4.2.-) N C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Species: Os-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C; Accession: D81929
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPROT: Q93511; UNIPARC: UPI0000179EEB; GB: chr_II; PIDN: CAB02486.1;
                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.4%; Score 38; DB 2; Length 212; 58.3%; Pred. No. 5.4; tive 1; Mismatches 4; Indels
                                                                                                                                            Score 38; DB 2; Length 145;
Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: amidotransferase hisH; trpG homology C;Keywords: glycosyltransferase; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
4.1;
                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38;
Pred. No.
                                                                                                                                                    64.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.v.
France 6; Conservative
                                                                                                                                         Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 FMGVAQGLRYIF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 FOGIPODTRFYF 155
                                                                                                                                                                                                                                                                                             1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                       | || | :|::|
73 FMGVAQGLRYIF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
'...a 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-162 <STO>
                                  A; Map position: 2
A; Introns: 21/3; 82/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: hish; NMA0840
A; Gene: CESP:F15D4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: B88349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: D81929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: F15D4.3
A,Map position: 2
                                                                                                                                                                                                                                                                                                                                                              g
```

ò 셤 엄

```
type C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   query Match 62.7%;
Best Local Similarity 80.0%;
Matches 8; Conservative C
von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|:||:|
202 FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||: |::||
4 FQGLYSSIMYVF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 FPGKLOSVRF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLOSVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-715 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-111 < DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Gene: MIPS:YHR063w-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: $52596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S70397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CySuperfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc (Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc (Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc (Signal sequence #status predicted <SIG.)

F;19-1172/Pomain: signal sequence #status predicted <AIA.)

F;39-37/Domain: von Willebrand factor type C repeat homology <VWC.>

F;39-37/Domain: thrombospondin type 1 repeat homology <THR1>
F;493-549/Domain: thrombospondin type 1 repeat homology <THR2>
F;493-549/Domain: EGF homology <EGF1>
F;553-588/Domain: EGF homology <EGF2>
F;553-589/Domain: EGF homology <EGF2>
F;553-589/Domain: EGF homology <EGF2>
F;553-580/Domain: EGF homology <EGF2>
F;554-580/Domain: EGF homology <EGF2>
F;555-580/Domain: EGF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references. UNIPARC:UPI000016D077; GB:M64866; NID:g201994; PIDN:AAA40432.1; PID:
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vd
Ç;Keywords: calcium binding; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A42587
A; Status: preliminary; not compared with conceptual translation
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Molecule type: nucleic acid
A; Molecule type: nucleic acid
A; Residues: 1-1172 < LAH;
A; Cross-references: UNIPROT: Q03350; UNIPARC: UPI0000029847; GB:L07803; GB:M87275; NID:g34
A; Note: sequence extracted from NCBI backbone (NCBIP:81502)
A; Note: Second from NCBI backbone (NCBIP:81502)
A; Note: Sequence extracted from NCBI backbone (
                                                   A;Molecule type: mRNA
A;Residues: 1-1172 <LAB>
A;Cross-references: UNIPROT:P35442; UNIPARC:UP10000046680; GB:L12350; NID:g307505; PIDN:
                                                                                                                                                                                 FilaBell, T.L.; Milewicz, D.J.; Disteche, C.M.; Byers, P.H. Genomics 12, 421-429, 1992

Genomics 12, 421-429, 1992

A;Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression A;Reference number: A42173; MUD:92217961; PMID:1559694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression during cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42587; A39851
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J; Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression du.
A;Reference number: A42587; MUID:92147683; PMID:1371115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: fibroblast
A, Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
C, Genetics:
A, Gene: GDB:THBS2; TSP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.4%; Score 38; DB 1; Length 1172;
58.3%; Pred. No. 33;
ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 560-1172 <LA2>
A;Cross-references: UNIPARC:UPI00001742C1; GB:M81339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: GDB:128789; OMIM:188061
A,Map position: 6q27-6q27
C,Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chrombospondin 2 precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|:||:|
FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-873 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A39851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
Cona pellucida glycoprotein A - dog
C;Species: Canis lupus familiaris (dog)
C;Accession: S70397
R;Harris, J.D.; Hibler, D.W.; Fontenot, G.K.; Hsu, K.T.; Yurewicz, E.C.; Sacco, A.G.
NNA Seq. 4, 361-393, 1994
A;Fitle: Cloning and characterization of zona pellucida genes and cDNAs from a variety of A;Reference number: S70396; MUID:95143578; PMID:7841460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross_references: UNIPROT:P47983; UNIPARC:UPI000013C45A; EMBL:U05779; NID:g458274; PIDP C;Superfamily: sperm-binding glycoprotein ZP2; ZP domain homology
F;368-628/Domain: ZP domain homology <ZPH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPARC:UP100001190B3; EMBL:U00061; GSPDB:GN00008; MIPS:YHR063w-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YHR063w-a - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 19-Oct-1995 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
< VWC>
                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 8R
C;Superfamily: Saccharomyces probable membrane protein YHR063w-a
C;Keywords: transmembrane protein
F;49-65/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                      Length 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.0%; Score 36; DB 2; Length 111; 50.0%; Pred. No. 7; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 2; Length 715; Pred. No. 31; 0; Mismatches 2; Indels
   repeat homology
                             F;380-431/Domain: thrombospondin type 1 repeat homology <THRI>F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>F;495-494/Domain: thrombospondin type 1 repeat homology <THR3>F;553-588/Domain: Brombospondin type 1 repeat homology <THR3>F;553-588/Domain: EGF homology <EGF1>F;652-691/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, May 1994
A;Description: The sequence of S. cerevisiae cosmid 8025.
A;Reference number: $46731
A;Accession: $52596
                                                                                                                                                                                                                                               Query Match 64.4%; Score 38; DB 2; Best Local Similarity 58.3%; Pred. No. 33; Matches 7; Conservative 3; Mismatches
```

ö

Gaps

```
C; Superfamily: Saccharomyces cerevisiae probable membrane protein YFL025c
                                                            61.0%; Score 36; DB 2; Length 1142; 58.3%; Pred. No. 81; tive 2; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                               5, 2006, 22:44:58
                                                         Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                     | || |:|:| |
887 FTGVCQAVKFSF 898
                                                                                                                                                                                                1 FOGULQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                        Search completed: June
Job time: 14.9655 secs
                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                         g
                                                                                                                      C;Species: Acinetobacter calcoacticus
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 05-Oct-2004
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 05-Oct-2004
C;Accession: C57253
R;Kok, R.G.; van Thor, J.J.; Nugteren-Roodzant, I.M.; Vosman, B.; Hellingwerf, K.J.
J. Bacteriol. 177, 3295-3307, 1995
A;Title: Characterization of lipase-deficient mutants of Acinetobacter calcoaceticus BD4
A;Reference number: A57253; MUID:95286514; PMID:7768830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable negative regulator of vesicle formation - fission yeast (Schizosaccharomyces pd
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1142 <BAR>
A;Cross-references: UNIPROT:Q9UT41; UNIPARC:UPI00006A1AC; EMBL:AL121741; PIDN:CAB57332.
A;Experimental source: strain 972h-; cosmid c824
                                                                tRNA-pseudouridine synthase (EC 5.4.99.-) - Acinetobacter calcoaceticus (fragment)
N;Alternate names: hypothetical protein lipB 5'-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecies: Homo sapiens (man)
Cibate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
Cibate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
Cibacession: T17230
Rikoehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: 218722
A;Reference number: 218722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-931 «KOE>
A;Cross-references: UNIPROT: 09UES6; UNIPARC: UP1000016AC6D; EMBL: AL117432
A;Experimental source: adult testis; clone DKFZp434E066
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-151 <KOK>
A;Cross-references: UNIPARC:UP1000017879A; GB:X80800
C;Superfamily: tRNA pseudouridine synthase B
C;Superfamily: tRNA pseudouridine transferase; isomerase; tRNA modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T39103
R;Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D. submitted to the EMBL Data Library, October 1999
A;Reference number: Z2188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.0%; Score 36; DB 2; Length 993; Best Local Similarity 63.6%; Pred. No. 70; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.0%; Score 36; DB 2; Length 151; 70.0%; Pred. No. 9.6; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: T39103
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein DKFZp434E066.1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 QHILSSLRFVF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 OGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||| ||::|
29 GVLQKVRWLF 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: SPDB:SPAC824.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: DKFZp434E066.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

THIS PAGE BLANK (USPTO)

Jun

Tue

```
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
07SY84 XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        075Y84
ID 07
AC 07
DT 01
DT 01
DT 01
                                                                                                                                                                                                                                                                                                                                                               028194
                                                                                                                                                                                                                                                                                                                                                                                    DDR B 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
brachydanio
tetraodon n
sus scrofa
tetraodon n
tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mus musculu
mus musculu
xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neisseria g
caldicellul
tetraodon n
drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xenopus lae
xenopus lae
shewanella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neisseria m
syntrophoba
celosia sp.
aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q28194 bos taurus
Q7sy84 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ciona intes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nitrosomona
sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bos taurus
                                                                                                         5, 2006, 22:09:41 ; Search time 108.931 Seconds (without alignments) 101.901 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0078784
028178
07396
0311740
080741
080741
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
08096
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                           2849598 segs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q80YQ1 MOUSE
Q8CGB2 MOUSE
TSP1 XENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q28194 BOVIN
Q7SY84 XENLA
TSP1 BOVIN
TSP1 HUMAN
TSP1 MOUSE
Q3TR40 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q3NOH3 9DELT
Q94BI7 9CARY
Q5AVQ8 EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
BRARE
TETNG
PIG
TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLULA
NEIG1
CALSA
TETNG
DROVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q3N8F0_9PROT
Q976Q1_SULTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIOIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q36F14_9GAMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEIMA
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q59E99 F
Q5SPG5 E
Q4S758 T
                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04SHB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4RLR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q5FA21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q2ZGJ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q70BX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6IR63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                            1 FQGVLQSVRFVF 12
                                                                                                                                                                                  US-10-030-735-21
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.11
                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                 .
Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š.
                                                                                                               Run
```

```
ö
                                                                                                     homo sapien
mus musculu
mus musculu
                        banksia men
banksia sce
                                                                           homo sapien
mus musculu
                                                                                                                                                        neurospora
brachydanio
                                                 agrobacteri
agrobacteri
                                                                                                                                           yarrowia li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
 banksia
              banksia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Opposite regulation of thrombospondin-1 and corticotropin-induced secreted protein/thrombospondin-2 expression by adrenocorticotropic hormone in adrenocortical cells.";
J. Cell. Physiol. 167:164-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96331130; PubMed=8698834;
DOI=10.1002/(SICI)1097-4652(199604)167:1<164::AID-JCP19>3.3.CO;2-0;
Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chambaz E.M.,
                                                                                                                                                                                                                                                   DATA BOVIN

Q28194
BOVIN
Q28194;
Q28194;
Q28194;
Q28194;
Q1-NOV-1996, integrated into UniProtKB/TrEMBL.
O1-NOV-1996, sequence version 1.
O1-NOV-1996, entry version 24.
Thrombospondin-1 (Fragment).
Bos taurus (Bovinne).
Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Procras; Bovidae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                      0552w4
0552w7
08ubii
08ubii
935crfi
935crfi
003360
05ri52
06cg21
06cg21
06cg21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 2; Length 229;
Pred. No. 0.012;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 229 229 229 AA; 25015 MW; 90D9EBCE4E6B669C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X89511; CAA61682.1; -; mRNA.
PIR; S57957; S57957.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR013129; ConA like subgrp.
InterPro; IPR03129; Laminin_G_TSP_N.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.078784 XENLA PRELIMINARY; PRT; 496 AA. 078784.
078784.
01-007-2003, integrated into UniProtKB/TrEMBL. 01-007-2003, sequence version 1.
         G52ZW0_9WAGN
G52ZW4_9WAGN
G52ZW4_9WAGN
G8UBII_AGRT5
G7CRFI_AGRT5
TSP2_HUMAN
TSP2_MOUSE
G5RI52_HUMAN
G7TMT3_MOUSE
                                                                                                                                         Q6CH81_YARLI
Q9C229_NEUCR
Q5PZ43_BRARE
                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGULQSVRFVF 12
[1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
```

```
214 FOGVLONVRFVF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGF-beta
셤
                                                                                                                                                                                     Straubberg R.L., Feingeld E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
B stapleton M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Roufigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W. Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
T and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Whole;
BEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, BC054970; AAH54970.1; -; mRNA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007185; P:cell adhesion; IEA.
InterPro; IRR013320; ConA like subgrp.
InterPro; IRR033129; Laminin G_TSP_N.
InterPro; IRR008084; TSP1.
InterPro; IRR001007; WWF_C.
Pfam; PP00090; TSP 1, 2.
Pfam; PP00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 94.9%; Score 56; DB 2; Local Similarity 91.7%; Pred. No. 0.027; Nes 11; Conservative 1; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1705; TSPIREPEAT.
SMART; SM00209; TSP1; 2.
SMART; SM00210; TSP1; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS50092; TSP1; 2.
PROSITE; PS5018; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
SEQUENCE 496 AA; 54843 MW; E4FD2F07
                Kenopus laevis (African clawed frog)
                                                               Xenopodinae; Xenopus; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                            TISSUE-Aortic endothelium;
Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin stimulatory effect of
                                                                                                                                                                                           STRAIN=Holstein; TISSUE=Tooth; MEDLINE=98173773; PubMed=9507054; DOI=10.1016/S0167-4838(97)00188-X; Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                 Inoue H.; "cDNA cloning of bovine thrombospondin 1 and its expression in
TSPI BOVIN

ID TSP1 BOVIN

AC Q28178; Q28179;
DT 01-DEC-2000, sequence version 2.

DT 01-DEC-2000, sequence version 2.

DT 01-MAR-2006, entry version 56.
                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA] OF 1-18 AND 710-1170.
                                                                                                                                                                                                                                                           odontoblasts and predentin.";
Biochim. Biophys. Acta 1382:17-22(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; $55501; $55501.

HSSP; P07996; 1LSL.

SMR; Q28178; 549-1169.

GlycoSuiteDB; Q28178; -
InterPro; IPR013320; ConA_like_subgrp.
InterPro; IPR006210; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; 19800042; EGF 3.
InterPro; IPR001881; EGF Ca.bd.
InterPro; IPR001881; EGF Like
InterPro; IPR013032; EGF like reg.
InterPro; IPR00312; EGF Like reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB005287; BAA21115.1; -; mRNA.
EMBL; X87618; CAA60950.1; -; mRNA.
EMBL; X87619; CAA60951.1; -; mRNA.
                                                                                        Name=THBS1; Synonyms=TSP-1, TSP1;
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nterPro; IPR003367; tsp_3:
InterPro; IPR008859; TSP_C.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA].
                                                                            Thrombospondin-1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 1. Pfam; PF00090; TSP_1; 3. Pfam; PF02412; TSP_3; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR006209; E
Interpro; IPR013032; E
Interpro; IPR003129; L
Interpro; IPR000884; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008085;
InterPro; IPR003367;
                                                                                                                                                       NCBI_TaxID=9913;
```

Gaps

ö

0; Indels

1 FOGULOSVRFVF 12

à

ന

```
Biochemistry 25:8418-8425(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 1-374
                                                                                                                                    208 FQGVLQNVRFVF 219
  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                       1 FOGULOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins
                                                                                                                                                                                                                                 T 4
HUMAN
                                                                                                       ઠે
                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSP type-3 1.
TSP type-3 2.
TSP type-3 2.
TSP type-3 4.
TSP type-3 5.
TSP type-3 6.
TSP type-3 6.
TSP type-3 6.
TSP type-3 7.
TSP C-terminal.
Heparin-binding (Potential).
Cell attachment site (Potential).
Cell attachment (GICNAC. .) (Potential).
N-linked (GICNAC. .) (Potential).
N-linked (GICNAC. .) (Potential).
Interchain (Probable).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ODD6ADF3E5FA031A CRC64;
                                                                                                                                                                    PROSITE; PS00022; EGF 1; FALSE_NEG.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50020; TSPI; 3.
PROSITE; PS501208; VWFC 1; 1.
PROSITE; PS50184; VWFC 2; 1.
Calcium; Cell adhesion; EGF-11ke domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                        Thrombospondin-1.
/FTId=PRO_0000035841.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2, cal
                                                                                                                                                                                                                                                                                                                                                                                By similarity.
                                                                                                                                                                                                                                                                                                                                                      Heparin-binding, Repeat, Signal.
SIGNAL 1 18 By E
CHAIN 19 1170 Thro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129534 MW;
                       Pfam; PF00093; VWC; 1.
PRINTS; PR01705; TSPIREPEAT.
SMART; SM00181; EGF; 3.
SMART; SM00209; TSPI; 3.
SMART; SM00210; TSPI; 1.
SMART; SM00210; TSPI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                708
1067
1085
270
274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               946 116
805 80
1170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGION
DORAGE STATES AND SELECT STATE
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Endochelial cell;
MEDLINE=87057677; PubMed=2430973; DOI=10.1083/jcb.103.5.1635;
Lawler J., Hynnes R.O.;
"The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=86287276; PubMed=3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
Characterization of a cDNA encoding the heparin and collagen binding domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 1-397.
MEDLINE=87157592; PubMed=3030396;
Kobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.;
"Partial amino acid sequence of human thrombospondin as determined by analysis of CDNA clones: homology to malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laherty C.D., Gierman T.M., Dixit V.M., "Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription."; J. Biol. Chem. 264:11222-11227(1989).
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89139590; PubMed=2918029; DOI=10.1083/jcb.108.2.729; Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L., Baumgartel D.M., Rotwein P., Frazier W.A.; "Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region."; J. Cell Biol. 108:729-736(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 1028-1170.

Ta Fleur M., Jobin C., Gauthier J., Kreis C.G.;

"Expression of thrombospondin in chronic inflammation: neutrophils from synovial fluids synthesize a novel 3.9 kb TSP mRN.";

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441; THR-460; TRP-498 AND THR-507.
TAR-460; TRP-498 AND THR-507.
TISSUE=Platelet;
MEDLINE=21125860; Pubmed=11067851; DOI=10.1074/jbc.M008073200;
Length 1170;
                                      0; Indels
                                                                                                                                                                                                        TSP1 HUMAN STANDARD; PRT; 1170 AA. P07996; Q15667; O1-AUG-1988, integrated into UniProtKB/Swiss-Prot. 01-AUG-1988, sequence version 1. 07-MAR-2006, entry version 78. Thrombospondin-1 precursor. Name-THS1; Synonyms-TSP, TSP1; Homo sapiens (Human).
Score 56; DB 1;
Pred. No. 0.067;
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell Biol. 103:1635-1648(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 1-166.
MEDLINE=89291870; PubMed=2544587;
```

```
R Pfam; PF02412; TSP 3; 12.

R Pfam; PF05735; TSP_C; 1.

R PRIMTS; PR01093; WG; 1.

R PRIMTS; SM00181; EGF; 3.

R SMART; SM00181; EGF; 3.

R SMART; SM00210; TSP1; 3.

R SMART; SM00214; VWC; 1.

R PROSITE; PS01086; EGF 1; FALSE_NEG.

R PROSITE; PS01086; EGF 3; 1.

R PROSITE; PS01086; EGF 3; 1.

R PROSITE; PS01086; WFC 2; 1.

R PROSITE; PS01084; VWC 2; 1.

R PROSITE; PS01084; VWFC 2; 1.

R PROSITE; PS01084; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2.
EGF-like 3.
TSP type-3 2.
TSP type-3 3.
TSP type-3 4.
TSP type-3 5.
TSP type-3 5.
TSP type-3 6.
TSP type-3 6.
TSP type-3 7.
TSP type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=CAR_000210.
O-linked (Fuc. .).
/FTId=CAR_000211.
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .).
Interchain (Probable).
Interchain (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 1; Length 1170;
Pred. No. 0.067;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        Thrombospondin-1.
/FTId=PRO_000035842.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTIG=CAR 000208.
O-linked (Fuc. .).
/FTIG=CAR 000209.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=CAR 000205.
O-linked (Fuc. .).
/FTId=CAR 000206.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               000207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTIG=CAR 0002(
C-linked (Man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  708
1067
270
274
423
428
413
484
489
                                                                                                                                                                                                                                                                                                                                          1170
                                                                                                                                                                                                                                                                                                                                                                                                                     429
490
547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              587
645
690
758
781
817
840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  708
1067
270
274
391
395
406
487
462
504
508
                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                               24
3316
3316
4435
5483
5483
7723
7723
818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOTIF
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
DOMAIN
BOMAIN
                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                            CHAIN
          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
G
                                                                                                                                                                                                                                                       CARBOHYDRATE-LINKAGE SITES ASN-248 AND ASN-1067.

Pubmed=16335952; DOI=10.1021/pro502065;

A Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,

Liu T., Qian W.-J., Smith R.D.;

Moore R.J., Smith R.D.;

"Human plasma N-glycoproteome analysis by immunoaffinity subtraction,

"Human plasma N-glycoproteome analysis by immunoaffinity subtraction,

"Thydraide chemistry, and mass spectrometry.";

J. Proteome Res. 4:2070-2080(205).

"I FINCTION: Adhesive glycoprotein that mediates cell-to-cell and

cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,

lamini, type V collagen and integrins alpha-V/beta-1, alpha-

V/beta-3 and alpha-IIb/beta-3.

"SMULNATIY: Contains 1 TSP C-terminal (TSPC) domain.

"SIMILARITY: Contains 1 TSP V-terminal (TSPN) domain.

"SIMILARITY: Contains 7 TSP type-1 domains.

"SIMILARITY: Contains 7 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                         THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES.
MEDLINE=22338361; PubMed=12450339; DOI=10.1021/Di026463u;
Huwillar K.G., Veetling M.M., Annis D.S., Mosher D.F.;
"Biophysical characterization, including disulfide bond assignments, of the anti-angiogenic type I domains of the most thrombospondin-1.";
Biochemistry 41:14329-14339(2002).
      Hofateenge J., Huwiler K.G., Macek B., Hess D., Lawler J., Mosher D.F., Peter-Katalinic J.; "C-mannosylation and O-fucosylation of the thrombospondin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M25631; AAA36741.1; "RRNA.
EMBL, X14781; CAA28370.1; "RRNA.
EMBL, X14781; CAA28370.1; "RRNA.
EMBL, X14781; AAA61237.1; ALT SEQ, mRNA.
EMBL, J04835; AAA61237.1; ALT SEQ, mRNA.
EMBL, M99425; AAA61178.1; "Genomic_DNA.
EMBL, M99425; AA859366.1; "RNA.
PDB, 1LSL, X-ray; A=434-546.
PDB; 1LSL, X-ray; A=19-233.
PDB; 1Z78; X-ray; A=19-233.
PDB; 1Z78; X-ray; A=19-257.
PDB; 2ERF; X-ray; A=19-257.
PDB; 2ERF; X-ray; A=19-257.
PDB; 2ERF; X-ray; A=19-267.
PDB; 2ERF; X-ray; A=10-267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ensembl; ENSG0000137801; Homo sapiens
                                                                                   Biol. Chem. 276:6485-6498(2001).
                                                                    module.";
```

Ŋ

```
MOTIF
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
PROTEIN SEQUENCE OF 19-37.

A Chen H., Asechlämann D., Nowlen J., Mosher D.F.,

Expression and initial characterization of recombinant mouse
thrombospondin 1 and thrombospondin 3.",

Expression and initial characterization of recombinant mouse
thrombospondin 1 and thrombospondin 3.",

I FEBS Lett. 387:36-41(1996).

-!-FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
laminin, type V collagen and integrins alpha-V/beta-1, alpha-
V/beta-3 and alpha-IIb/beta-3.

-!- SUBUNIT: Homotrimer; disultide-linked.

-!- SIMILARITY: Contains 1 TSP C-terminal (TSPC) domain.

-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

-!- SIMILARITY: Contains 3 TSP type-1 domains.

-!- SIMILARITY: Contains 7 TSP type-1 domains.

-!- SIMILARITY: Contains 7 TSP type-3 domains.

-!- SIMILARITY: Contains 7 TSP type-3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE OF 1-490.

MEDLINE=90375546; PubMed=2198070;

Bornstein P., Alfi D., Devarayalu S., Framson P., Li P.;

"Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";

J. Biol. Chem. 265:16691-16698(1990).
                                                                                                                                                                                                                                                                                                                                                                     "Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development."; J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDINE=22128941; PubMed=1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J., Jenkins N.A.;
                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
BEDEINE=22147683; PubMed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.P.,
Dixit V.M.;
                                                                                                                                                                                                                                                                         "Characterization of the murine thrombospondin gene."; Genomics 11:587-600(1991).
                                                                        01-JUN-1994, integrated into UniProtKB/Swiss-Prot. 01-JUN-1994, sequence version 1. 07-MAR-2006, entry version 57. Thrombospondin-1 precursor. Name-Thbs1; Synonyms-Tsp1; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M62470; AAA50611.1; -; Genomic DNA.
EMBL, M62450; AAA50611.1; JOINED; Genomic DNA.
EMBL, M62451; AAA50611.1; JOINED; Genomic DNA.
EMBL, M62453; AAA50611.1; JOINED; Genomic DNA.
EMBL, M62453; AAA50611.1; JOINED; Genomic DNA.
EMBL, M62454; AAA50611.1; JOINED; Genomic DNA.
EMBL, M62455; AAA50611.1; JOINED; Genomic DNA.
EMBL, M62455; AAA50611.1; JOINED; Genomic DNA.
EMBL, M62459; AAA50611.1; JOINED; Genomic DNA.
EMBL, M62460; AAA50611.1; JOINED; Genomic DNA.
EMBL, M62460; AAA50611.1; JOINED; Genomic DNA.
                                                  PRT; 1170 AA
                                                 STANDARD;
                                                                                                                                                                                               NCBI_TaxID=10090;
```

```
| BY SHI, WG AG AN ASSOCIATION COUNTY, BROWN, BRILL WG AG AG ANASOCIALION CONTROL CONT
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Aorta and vein;
PubMed=16141072; DOI=10.1126/science.1112014;
Carninci P., Kaeukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530055N06 product:thrombospondin 1, full insert sequence.
.) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 1; Length 1170;
Pred. No. 0.067;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0443E493615E7F06 CRC64;
                Interchain (Probable).
Interchain (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-0CT-2005, integrated into UniProtKB/TrEMBL 11-0CT-2005, sequence version 1. 07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                          PRT; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1170 AA; 129647 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q3TR40 MOUSE PRELIMINARY;
Q3TR40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLOSVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Thbs1;
                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                       DISULFID
                                            DISULFID
                                                                 DISULFID
                                                                                      DISULFID
                                                                                                                                                          DISULFID
                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                               DISULPID
                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
1037R40
MO
10 11-0
DT 11-0
DT 11-0
DT 11-0
DT 11-0
DT 11-0
DE Clon
DE Clon
GN MUB
OC ENLB
OC MUB
OC NUI
CO NUI
C
ద
```

```
Bensell W. Bensell W. Berede K.W. Beledel K.W. Baressoor T. Bonch H., Chalk A.W.,
Ching K.P. Choudhery. The Erical K.W. Ching Coffee J. A. Collitechhock D. Bonch H. Chall B. Della Grate G. H.

Crowe M.L. Della E. Della E. Della C. B. Della Grate G. H.

B. Bolletter C.F. Fulunhian T. Regarron P. Fagicilini M., Fallkher G.,
Georgi-Herming P. Gingers T.R. Gorjobori T. Green R.E.,
B. Milletter M. W. Large M. Bayshi Y. Benebri T.K. Hirokewa N.,
B. Milletter M. W. Large M. Washare W. Ranghold M.,
B. Milletter M. W. Large M. Washare W. Narchionni L.,
B. Marchell H. Mateurawa S. Wiki H. Wignone F. Migake S. Worris K.
B. Mischell H. Mateurawa S. Wiki H. Wignone F. Migake S. Worris K.
B. Mischell H. Mateurawa S. Wiki H. Wignone F. Migake S. Worris K.
B. Mischell H. Mateurawa S. Wiki H. Wignone F. Migake S. Worris K.
B. Mischell H. Mateurawa S. Wiki H. Wignone F. Migake S. Worris K.
B. Mischell H. Mateurawa S. Wiki H. Wignone F. Migake S. Worris K.
B. Mischell H. Mateurawa S. Wiki H. Wignone F. Migake S. Worris K.
B. Mischell H. Mateurawa S. Wiki H. Wignone F. Migake S. Worris K.
B. Mischell H. Mateurawa S. Wiki H. Wignone F. Migake S. Worris K.
B. Mischell H. Mateurawa S. Wiki H. Wignone F. Migake S. Worris K.
B. Mischell H. Mateurawa S. Mischell H. S. Ghengel C. Grane B. Mischell H. S. Ghengel C. Grane B. Mischell H. S. Ghengel C. Mischell H. S. Ghengel C. Grane B. Mischell H. S. Ghengel C. Mischell H. S. Mischell H. S. Mischell H. S. Mischell H. S. Ghengel C. Mischell H. S. Mischell M. Mischell H. Mischell H. S. Mischell H. S. Mischell M. Mischell H. Mischell H. S. Mi
```

```
Name=Tsp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q71SA3
     50 OR 10 OR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE-2108560; PubMed=11217851; DOI-10.1038/3505500;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
Kawai T., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda T., Cissi C., King B., Kochiwa H.,
Kadota K., Matsudi T., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whynibaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Narabhizaki V., V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Aorta and vein; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komo H., Okazadi Y., Muramateu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateminoto H., Sakaguchi S., Ikegami T., Kabhiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matemira B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matemira M., Ohara E., Watahiki M., Vacaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
STRAIN=C5/BL/6J; TISSUE-Aorta and vein;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Immanuza K., Imceni K., Itch M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AK163092; BAE37190.1; -; mRNA.
MGI; MGI:98737; Thbs1.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0005615; P:negative regulation of angiogenesis; IDA.
InterPro; IPR006210; EGF.
InterPro; IPR000742; EGF.
InterPro; IPR001881; EGF.
InterPro; IPR001881; EGF.
InterPro; IPR013032; EGF.like_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
```

```
Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
           STRAIN=Sprague-Dawley;
Iwabu A., Hirohata S., Kusachi S., Nakamura K., Murakami T.,
Ninomiya Y., Tsuji T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.9%; Score 56; DB 2; Length 1170; 91.7%; Pred. No. 0.067; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF309630; AAQ14549.1; -; mRNA.

SNR; QT15A3; 834-1169.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005576; F:calcium ion binding; IEA.

GO; GO:0005189; F:calcium ion binding; IEA.

R InterPro; IPR001320; ConA_like_subgrp.

R InterPro; IPR00181; EGF.

R InterPro; IPR00181; EGF.

R InterPro; IPR00181; EGF.

R InterPro; IPR00181; EGF.

R InterPro; IPR01302; EGF_like.

R InterPro; IPR013032; EGF_like.

R InterPro; IPR03129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           071SA3 RAT PRELIMINARY; PRT; 1170 AA. 071SA3; 05-UUL-2004, integrated into UniProtKB/TrEMBL.
Laminin G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 9. Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008085; TSP_1.
InterPro; IPR003367; tsp_3.
InterPro; IPR008859; TSP_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGULOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
```

```
Ensembl; ENSWINGSGON00040152; Mus musculus.

R G0; G0:0005615; C:extracellular space; RCA.

G0; G0:0005615; C:extracellular space; RCA.

G0; G0:0005615; C:extracellular space; IDA.

R G0; G0:0005615; C:extracellular space; IDA.

R InterPro; IPR01330; ConA_like_subgrp.

R InterPro; IPR001801; EGF_3.

R InterPro; IPR001801; EGF_1.

R InterPro; IPR001801; EGF_1.

R InterPro; IPR00181; EGF_Ca bd.

R InterPro; IPR00181; EGF_Tike_reg.

R InterPro; IPR00181; EGF_1ike_reg.

R InterPro; IPR001801; VWF_C.

R Ffam; PF000100; TSP_1; 3.

R Pfam; PF002012; TSP_1.

R Pfam; PF002013; TSP_C; 1.

R Pfam; PF002013; VWF_C.

R Pfam; PF00313; VWF_C.

R Pfam; PF00313; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.9%; Score 56; DB 2; Length 1171; 91.7%; Pred. No. 0.067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                1171 AA; 129690 MW; 12E077B50C64B2D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBCGB2_MOUSE PRELIMINARY; PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1705; TSPIREPEAT.
SMART; SM00181; EGF; 3.
SMART; SM00210; TSP1; 3.
SMART; SM00210; TSP1; 3.
SMART; SM00214; VWC; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50026; TSP1; 3.
PROSITE; PS50128; VWCC 1; 1.
PROSITE; PS5014; VWFC 2; 1.
SEQUENCE 1171 AA; 129690 MW; 12507;
          EMBL; BC050917; AAH50917.1; -; mRNA.
HSSP; P07996; 1LSL.
SWR; Q80YQ1; 835-1170.
                                                                                                                                                                                                                                                                                                                 C; 1.
TSP1REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8CGB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                         Length 1170;
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                1170 AA; 129671 MW; 6F38D3DCE733060F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE.
STRAIN-CSTBL/6, TISSUE=Brain;
Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                         94.9%; Score 56; DB 2; 91.7%; Pred. No. 0.067; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003, integrated into UniProtKB/TrEMBL. 01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                              QBOYO1 MOUSE PRELIMINARY; PRT; 1171 AA.
QBOYO1;
         Pfam: PF00008; EGF; 2.

Pfam: PF00109; TSP 1; 3.

Pfam: PF02412; TSP 2; 12.

Pfam: PF02412; TSP 2; 12.

Pfam: PF02412; TSP C; 1.

Pfam: PF020093; VWC; 1.

PRINTS; PR01705; TSPLREPEAT.

SMART; SM00181; EGF; 3.

SMART; SM00181; EGF; 3.

SMART; SM00210; TSP1; 3.

SMART; SM00210; TSP1; 3.

SMART; SM00210; TSP1; 3.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01266; EGF 3; 2.

PROSITE; PS50026; EGF 3; 2.

PROSITE; PS50126; WWFC 2; 1.

PROSITE; PS501284; VWFC 2; 1.

PROSITE; PS501284; VWFC 2; 1.

PROSITE; PS501284; VWFC 2; 1.
 InterPro; IPR001007; VWF_C
                                                                                                                                                                                                                                                                                        208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                           1 FQGVLQSVRFVF 12
                                                                                                                                                                                                             Query Match
Best Local Similarity
Local 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                    용
```

Gaps

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauener R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
OSCGB2;
01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 22.
Thrombospondin 1 (Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN fu.
length enriched library, clone:G930018021 product:thrombospondin
full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
```

σ

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lux, Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Suchertield Y.S.M., Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Greet than 15,000 full-length human and initial analysis of more than 15,000 full-length human TISSUE=Mammary gland; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously; Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999). mouse cDNA sequences. NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE Hayashizaki and

RC TISSUE-Mammary gland;

RD Publed=1614072; DOI=10.1126/science.1112014;

RD SQUARMAR TASSUE AND T "The transcriptional landscape of the mammalian genome. Science 309:1559-1563(2005).

NUCLEOTIDE SEQUENCE.

RA Meade I., Osato N., Salto R., Suzuki H., Yamanaka I., Kiyosawa H., Raddo I., Osato N., Salto R., Suzuki H., Yamanaka I., Kiyosawa H., Argin K., Tomatu Y., Hasegawa Y., Nogami A., Schonbach C., Golobori T., Raddo I., Osato N., Salto R., Suzuki H., Yamanaka I., Kiyosawa H., Raddo I., Osato N., Hasegawa Y., Nogami A., Schonbach C., Golobori T., Raddorill R., Hall D.P., Bult C., Hume D.A., Quackenbush J., Raddorill R., Bradt D. Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Bradt D. Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Banai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Marchiomi L., McKenzie L., Miki H., R. Maglott D.R., Maltais L., Marchiomi L., McKenzie L., Miki H., R. Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Pertovsky N., Pillai R., Pontius J.U., Rang B.Z., Ringwald M., Ravasi T., Reed J.C., Reed D.J., Reid J., Ramachandran S., Sultana R., Takenaka Y., Taylor M.S., Tesadale R.D., Tomita M., Salto R., Sultana R., Takenaka Y., Taylor M.S., Tesadale R.D., Tomita M., Salto K., Shilmaga M., Yang L., Wunning L.G., Wynshaw-Boris A., Yana Z., Zavolan M., Zhu Y., Zimmer A., Bakakawa T., Rukuda S., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shirada A., Hashizume W., Imotani K., Ishiragawa A., Hayashizaki Y., Sawai D., Shibata K., Shiragawa A., Hayashizaki Y., Sawai D., Shibata K., Shiragawa A., Burney B., Hayashizaki Y., Shirada Y., Lander E.S., Rogers J., Birney B., Hayashizaki Y., Shirada Y., Lander B.S., Rogers J., Shirada Y., Shi TISSUE-Mammary gland;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005). TISSUE=Mammary gland; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266; NUCLEOTIDE SEQUENCE

NUCLEOTIDE SEQUENCE

Nature 420:563-573(2002)

RESURE-Mammary gland;

REDINE-2108560; PubMed=11217851; DOI=10.1038/3505500;

REDINE-2108560; PubMed=11217851; DOI=10.1038/3505500;

REDINE-2108560; PubMed=11217851; DOI=10.1038/3505500;

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Anawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Raito T., Okazaki Y., Golbobri T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Rahl P., Lewis S., Matsudo I., Resole G., Quackenbush J., Rothin D., Morido T., Puruno M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Barah J., Bult C., Floricher C., Fujita M., Gariboldi M., Rathorich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyon P., Marchioni L., Mashima J., Mordone P., Ringyald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suruki H., Toyo-oka K., Wang K.H., Weitz C., Whitcher C., Wilming L., Marshizaki Y.;

R. Punctional annotestion of a full-length mouse cDNA collection.";

R. Marther A. Ord, SAR, Leon.

Nature 409:685-690(2001).

NUCLEOTIDE SEQUENCE.

TISSUE=Mammary gland;
MEDINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Garninci P. Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombospondin-1.
/FTId=PRO_0000035844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
                                                  HSSP, D04278; -; NOT_ANNOTATED_CDS; mRNA. HSSP, P07996; 1LSL.
SMR; P35448; 552-1172.
InterPro; IPR01320; Cona_like_subgrp.
InterPro; IPR006210; EGF.3.
InterPro; IPR000742; EGF.3.
InterPro; IPR01881; EGF_Ca_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-linked
N-linked
                                                                                                                                            EGF 3.
EGF Ca bd.
EGF like.
EGF like reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heparin-binding; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR006209; B
Interpro; IPR013023; B
Interpro; IPR00129; L
Interpro; IPR00884; T
Interpro; IPR00886; T
Interpro; IPR00886; T
Interpro; IPR00885; T
                                                                                                                                                                                                                                                                                                           InterPro; IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIĞNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGION
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                    MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Suninch H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matuminoto H., Sakaguchi S., Ikegami T., Kashiiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.

TISSUE-Mammary gland;
Arakwa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Arakwa T., Carninci P., Fukuda S., Hori F., Itch M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Submitted (WAR-2004) to the EWBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=thbāl; Synonyms=tspl;
Renopus laevis (African clawed frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.9%; Score 56; DB 2; Length 1171; 91.7%; Pred. No. 0.067; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC042422; AAH42422.1; -; mENA.
EMBL; AK145202; BAE26293.1; -; mENA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994, sequence version 1: 07-MAR-2006, entry version 54. Thrombospondin-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FOGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 91.7
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSP1 XENLA
P35448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
TSP1 XENLA
TO 11-YSP1 XENLA
DT 01-JUN
DT 01-JUN
DT 01-JUN
DT 01-JUN
DT 01-JUN
DE Thromb
DE Thromb
DE C Amphib
OC Amp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                           [10]
```

6 셤

```
Type type-1 1.

TSP type-1 2.

TSP type-1 3.

EGF-like 2; calcium-binding (Potential).

EGF-like 3.

TSP type-3 1.

TSP type-3 2.

TSP type-3 4.

TSP type-3 5.

TSP type-3 6.

TSP type-3 6.

TSP type-3 6.

TSP type-3 7.

TSP type-3 7.

TSP type-3 7.

TSP type-3 6.

TSP type-3 7.

TSP C-terminal.

TSP C-terminal.

TSP C-terminal.

TSP C-terminal.

TSP C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-linked (GlcNAc. .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GlcNAc. .) (Potential). (GlcNAc. .) (Potential). (GlcNAc. .) (Potential).
| PEGNO | PEGN
```

us-10-030-735-21.rup

g ઠે

```
Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collagen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-DEC-2004, integrated into UniProtKB/TrEMBL.
21-DEC-2004, sequence version 1.
21-DEC-2006, entry version 12.
Novel protein similar to vertebrate thrombospondin 1.\n\ (Fragment).
ORFNames=DKEY-11823.1-001;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Caniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBL_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                R PÉAM; PEPO0008; EGF; 2.

R PÉAM; PEPO0008; TSP 1; 3.

R PÉAM; PEPO035; TSP 2; 1.2.

R PÉAM; PEPO035; TSP C; 1.

R PÉAM; PEPO035; VWC_1.

R PARIYS; PRO1705; TSP1REPEAT.

R SMART; SM00210; TSP1; 3.

R SMART; SM00210; TSP1; 3.

R SMART; SM00210; TSP1; 3.

R SMART; SM00214; VWC; 1.

R PROSITE; PS50026; EGF 2; 1.

R PROSITE; PS50026; EGF 2; 1.

R PROSITE; PS50184; VWFC_1; 1.

R PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 2; Length 1225;
Pred. No. 0.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barker D.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL928866; CAI20599.1; -; Genomic_DNA.

SMR; Q5SPG5; 751-804, 754-1089.

Ensembl; ENSDARGO00001010785; Danio rerio.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:000510; F:heparin binding; IEA.

GO; GO:000511; F:protein binding; IEA.

GO; GO:000515; F:grotein binding; IEA.

GO; GO:000519; F:sprotein binding; IEA.

GO; GO:000519; F:erructural molecule activity; IEA.

GO; GO:0007155; P:cell adhesion; IEA.

InterPro; IPR00210; EGF.

InterPro; IPR006210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1090 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF Ca bd.
EGF Tike.
EGF Tike reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSSPGS_BRARE PRELIMINARY;
QSSPGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.9%;
    InterPro; IPR001007; VWF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 FQGVLQNVRFVF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 91.7
Les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001881;
InterPro; IPR006209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR013032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR008085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSSPGS
    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Aorta endothelial cell;
procki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 1; Length 1173;
Pred. No. 0.067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       A9F036D6516C0F24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB209912; BAD93149.1; -; mRNA.

SMR; Q59E99; 886-939, 889-1225.

Ensembl; ENSGORO0137801; Homo sapiens.

GO; GO: 0005576; C: extracellular region; IEA.

GO; GO: 0005509; F: calcium ion binding; IEA.

GO; GO: 000519; F: proretin binding; IEA.

GO; GO: 000519; F: proretin binding; IEA.

GO; GO: 0005115; P: cell adhesion; IEA.

InterPro; IPRO1519; F: cell adhesion; IEA.

InterPro; IPRO06210; EGF. 3.

InterPro; IPRO06210; EGF. 3.

InterPro; IPRO06209; EGF Ca bd.

InterPro; IPRO06209; EGF Like.

InterPro; IPRO06209; EGF Like.

InterPro; IPRO06209; EGF Like.

InterPro; IPRO06219; EGF Like.

InterPro; IPRO06209; EGF Like.

INTERPRO*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-2005, integrated into UniProtKB/TrEMBL
                                            similarity.
similarity.
similarity.
                                                                                                           similarity.
similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                        similarity.
similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q59E99_HUMAN PRELIMINARY; PRT; 1225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                        similarity
similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-2005, sequence version 1.
21-FEB-2006, entry version 10.
Thrombospondin 1 variant (Fragment).
94.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; IPRO00884; TSP1.
; IPRO08085; TSP_1.
; IPRO03367; tsp_3.
; IPRO08859; TSP_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 FÓGVLÓNVRFVF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 91.7
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGULOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                          1173
                                                                   595
602
623
653
660
660
708
721
757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                              DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                          DISULFID
                                              DISULFID
                                                                                                                                                                                                                                                DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                        DISULFID
                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                059E99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
1059899 HJW
10708999 HJW
10708999 HJW
10708999 HJW
107089999 HJW
1070899999 HJW
10708999999 HJW
107089999999 HJW
1070899999999 HJW
107089999999 HJW
107089999999 HJW
107089999999 HJW
10708999999 HJW
107089999999 HJW
10708999999 HJW
107089999999 HJW
10708999999 HJW
1070899999 HJW
1070899999 HJW
1070899999 HJW
1070899999 HJW
10708999999 HJW
1070899999 HJW
107089999 HJW
107089999 HJW
107089999 HJW
107089999 HJW
107089999 HJW
10708999 HJW
10708999 HJW
107089999 HJW
10708999 HJW
10708999 HJW
10708999 HJW
1070899 HJW
10708999 HJW
1070899 HJW
107089 HJW
10708 HJW
107089 HJW
107089 HJW
10708 HJW
1070
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51, DB 2; Length 1193;
Pred. No. 0.71;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang K., Mauco G., Hauet T.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1193 AA; 133256 MW; 6E8781648FCEC7F2 CRC64;
                                                                                                 GO; GO: 0005576; C: extracellular region; IEA.
GO; GO: 0005576; C: extracellular region; IEA.
GO; GO: 0005509; F: calcium ion binding; IEA.
GO; GO: 0005201; F: heparin binding; IEA.
GO; GO: 0005515; F: protein binding; IEA.
GO; GO: 000515; F: protein binding; IEA.
GO; GO: 000515; F: protein binding; IEA.
InterPro; IPRO00742; EGF.
InterPro; IPRO01801; FGF.
InterPro; IPRO00804; TSP1.
InterPro; IPRO00804; TSP1.
InterPro; IPRO00804; TSP1.
InterPro; IPRO00806; TSP2.
                                                 EMBL; CAAE01014723; CAG03524.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DBC-2004, integrated into UniProtKB/TrEMBL.
07-DBC-2004, sequence version 1.
07-FEB-2006, entry version 7.
Thrombospondin 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY773342; AAV38110.1; -; mRNA.
InterPro; IPR000884; TSP1.
InterPro; IPR0018085; TSP 1.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01186; EGF 2; UNKNOWN 1. PROSITE; PS50026; EGF 3; 2. PROSITE; PS50092; TSP1; 3. PROSITE; PS01208; VWFC 1; 1. PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00008; EGF; 2.
Pfam; PF00008; TSF 1; 3.
Pfam; PF002412; TSP 1; 1.
Pfam; PF005735; TSP 2; 1.2.
Pfam; PF00033; VWC; 1.
PRINTS; SM00101; EGF; 2.
SMART; SM00210; TSP1; 3.
SMART; SM00210; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 FMGVLONVRFVF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 83.3
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q50903_PIG
Q50903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
Q5U903_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
      The property of the property o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
21-FBB-2006, entry version 8.
21-FBB-2006, entry version 8.
Chromosome 14 SCAF14723, whole genome shotgun sequence. (Fragment). ORFNames-GSTENG0002297601,
Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontoidea, Tetraodont.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.4%; Score 51; DB 2; Length 1090; 83.3%; Pred. No. 0.64; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 1090 AA; 120978 MW; 5A9320504A22D836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q4S758 TETNG PRELIMINARY; PRT; 1193 AA. 04S758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                          SMART; SM00181; EGF; 2.
SWART; SM00210; TSP1; 2.
SMART; SM00210; TSP1; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS00018; EF_HAND_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                         PROSITE; PSO1186; EGF_2; I.
PROSITE; PSO1026; EGF_3; 2.
PROSITE; PS50092; TSP1; 2.
PROSITE; PS501208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
Cell adhesion; EGF-1ke domain.
NON_TER
                                                                Pfam; PF00008; EGF; 1. — Pfam; PF00090; TSP 1; 2. Pfam; PF02412; TSP 3; 12. Pfam; PF05735; TSP C; 1. Pfam; PF00093; VWC; 1. PRINTS; PR01705; TSPIREPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 FMGVLQNVRFVF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

Gaps

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A PubMed-15496914, DOI=10.1038/nature03025,
A Jaillon O. Aury J.-M., Brunet P., Petit J.-L., Stange-Thomann N.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Cruaud C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL -2005, sequence version 1.
21-FEB-2006, entry version 1.
21-FEB-2006, entry version 1.
Chromosome 10 SCAFT5019, whole genome shotgun sequence. (Fragment).
ORFNames-GSTENG0032374001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Tetradontoidea; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                            84.7%; Score 50; DB 2; Length 249; 90.9%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                    249 AA; 27560 MW; 465D664BE0329C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7. Q4RLR5; 834-867, 837-1171.
GG:0005576; Cestracellular region; IEA.
GG:0005209; F:calcium ion binding; IEA.
GG:0008201; F:heparin binding; IEA.
GG:0005515; F:protein binding; IEA.
GG:000518; F:structural molecule activity; IEA.
GG:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; CAAE01015019; CAG10667.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4RLR5_TETNG PRELIMINARY; PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the early vertebrate proto-karyotype."
Nature 431:946-957(2004).
                                                    PRINTS; PR01705; TSPIREPEAT SMART; SMO209; TSP1; 1. SMART; SMART; VWC; 1.
                                                                                                                                          PROSITE; PS50092; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGVLQNVRFVF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
04 RLRS TETT
10 AC GARLR
AC GARLR
DD 19-JU
DT 19-JU
DT 19-JU
DT 19-JU
DT 21-FE
DE Chrom
OC Bukar
OC Acant
OC Acant
OC Acant
OC Acant
OC Acant
OC Acant
CO Acat
CO Ac
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.7%; Score 50; DB 2; Length 1171;
83.3%; Pred. No. 1.1;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1171 AA; 129304 MW; 865F3749693F7FCE CRC64;
EGF 3.
EGF Ca bd.
EGF like reg.
Laminin G TSP N.
                InterPro; IPROUGHS, ESG-Ca bd.
InterPro; IPROUGHS, ESG-Ca bd.
InterPro; IPROUGHS, ESG-Tike reg.
InterPro; IPROUGHS, ESG-Tike reg.
InterPro; IPROUGHS, TSP1.
InterPro; IPROUGHS, TSP1.
InterPro; IPROUGHS, TSP1.
Ffam; PPOOGHS, TSP1.
Pfam; PPOOGHS, TSP1, 3.
Pfam; PPOOGHS, TSP-1; 3.
Pfam; PPOOGHS, TSP-1; 3.
Pfam; PPOOGHS, TSP-1; 3.
Pfam; PPOOGHS, TSP-1; 3.
SWART; SWOOLS, TSP1; 3.
SWART; SWOOLS, TSP1; 3.
SWART; SWOOLS, TSP1; 3.
SWART; SWOOLS, TSP1; 3.
PROSITE; PSOOUGS, EGF-2; UNKNOWN-1.
PROSITE; PSOOUGS, EGF-2; UNKNOWN-1.
PROSITE; PSOOUGS, EGF-2; UNKNOWN-1.
PROSITE; PSOOUGS, TSP1; 3.
PROSITE; PSOOUGS, TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 FTGVLÓNVRFVF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell adhesion.
```

Search completed: June 5, 2006, 22:42:38 Job time: 110.931 secs

THIS PAGE BLANK (USPTO)

```
Sequence 6333, Ap
Sequence 17510, A
Sequence 5, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 482, App
Sequence 97, Appl
Sequence 98, Appl
Sequence 20, Appl
Sequence 2, Appli
Sequence 350, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10, Appl
10, Appl
10, Appl
10, Appl
10, Appl
7, Appli
6, Appli
6, Appli
6, Appli
116180, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18826, A
Sequence 11112, A
Sequence 19, Appl
                                                                                                 5, 2006, 22:43:07; Search time 23.8966 Seconds (without alignments) 43.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/HCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/iaa/Rackfiles1.pep:*/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-002-482
US-09-939-853A-97
US-09-313-2888-98
US-08-313-2888-98
US-09-657-472-2
US-09-949-002-350
US-09-949-016-11112
US-08-313-2888-19
US-09-259-94A-18826
US-09-949-016-6333
US-09-258-634-5
US-09-258-634-5
US-08-484-1588-10
US-08-484-9538-10
US-08-484-9538-10
US-08-484-9538-10
US-08-484-9538-10
US-08-484-9538-10
US-08-484-9538-10
US-08-488-711-10
US-08-414-643-6
                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-09-800-170-16
                                                                                                                                                                                                                                                                                               650591 segs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
                                                                                                                                                                                                          1 FQGVLQSVRFVF 12
                                                                                                                                                                      US-10-030-735-21
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB &
Maximum DB &
                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
8
```

```
Sequence 482, Application US/09949002
; Sequence 482, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
    TITLE OF INVENTION: AND USES THEREOF
    TITLE OF INVENTION: AND USES THEREOF
    FILE REFERENCE: CLO00790
    CURRENT APPLICATION NUMBER: G0/231,401
    FRIOR FILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 10823
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 482
    LENGTH: 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97, Application US/09939853A

Patent No. 6989232

GENERAL INFORMATION:

APPLICANT: Burgess et al.

TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-099

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR APPLICATION NUMBER: 60/269,961

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                  61802, A
15, Appl
15, Appl
                                                                                                                                                                                                                                                                       46234, A
5578, Ap
3511, Ap
42057, A
                                                                                       26, Appl
22, Appl
22, Appl
3, Appli
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                       Sequence Sequence
                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                              Sequence
                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 2; Length 825;
Pred. No. 0.0076;
1; Mismatches 0; Indels
                                                           US-08-271-364A-7
US-08-227-715B-26
US-08-222-715B-26
US-09-144-643-22
US-09-144-643-22
US-09-341-3
US-09-34-20-5
US-09-270-767-61802
US-09-270-767-61802
US-09-270-767-6134
US-09-134-0000-5578
US-09-134-0000-5578
US-09-134-0000-3511
US-09-270-767-42057
US-09-2710-279-154
US-08-222-71364A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 FQGVLQNVRFVF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGULQSVRFVF 12
Query Match
Best Local Similarity
661.0
661.0
661.0
661.0
661.0
661.0
661.0
661.0
661.0
661.0
67.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
681.0
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Human
US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-939-853A-97
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
```

ð

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Cargill, Michele
APPLICANT: Lander, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Doley, George Q.
APPLICANT: Moley, George Q.
APPLICANT: Moley, George Q.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT PILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/123,357
PRIOR PELLING DATE: 1999-09-10
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.9%; Score 56; DB 1; Length 1170;
91.7%; Pred. No. 0.011;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.9%; Score 56; DB 2; Length 1170; 91.7%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION INPORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212) 278-0400
TELEPRAX: (212) 391-0526
TELERAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-002-350
; Sequence 350, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     20:
                                                                                                                                                                                                                                                                                                                  LENGTH: 1170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 FQGVLQNVRFVF 219
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                         Generoe 98, Application US/09939853A

Fadence 98, Application US/09939853A

Fatent No. 6989232

GENERAL INFORMATION:

FAPLICANT: Burgess et al.

TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099

CURRENT PAPLICATION NUMBER: 60/228,191

FRIOR APPLICATION NUMBER: 60/228,191

FRIOR APPLICATION NUMBER: 60/228,191

FRIOR APPLICATION NUMBER: 60/267,300

FRIOR FILING DATE: 2001-02-08

FRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOFTWARE: PATENTIN VET. 2.1

FROM FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                            94.9%; Score 56; DB 2; Length 831; 91.7%; Pred. No. 0.0076; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.9%; Score 56; DB 2; Length 831; 91.7%; Pred. No. 0.0076; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/08313288B

Patent No. 5750502

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, P-SPONDIN NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                             1; Mismatches
                SOFTWARE: Patentin Ver. 2.1;
SEQ ID NO 97;
ENGTH: 831;
TYPE: PRT;
ORGANISM: Homo sapiens
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                    1||||:|||||
208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FQGVLQNVRFVF 219
                                                                                                                                                                            Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                       1 FOGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVLOSVRFVF 12
NUMBER OF SEQ ID NOS: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mus musculus
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

g ò

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                      Length 1045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1172;
                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATORNEY/AGEN INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                   Score 38; DB 2
Pred. No. 47;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Pred. No. 53; 3; Mismatches
  PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11112
LENGTH: 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 6333, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                      64.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1172 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 391-0526
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.3
Parameter 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|:||:| ||
202 FRGLLQNVHLVF 213
                                                                                                                                                                                                      Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                       281 FRGLLQNVHLVF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSES: Cooper & DU
STREET: 1185 Avenue of
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                           1 FOGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGULOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                              ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10036
                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-313-288B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-313-288B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18826, Application US/09252991A

Patent No. 6551795
GENERAL INCOMPATION:

GENERAL INCOMPATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
FRIOR SEQID NOS: 33142
SEQID NO 18826
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT APPLICATION NUMBER: 06/231,401
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 350
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WS-09-949-016-11112

Sequence 11112, Application US/09949016

Sequence 11112, Application US/09949016

Sequence 11112.

Sequence 11112, Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3

PRIOR PILING DATE: 2000-10-3

PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                              Length 1170,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.4%; Score 38; DB 2; Length 175; 63.6%; Pred. No. 6.2; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 2;
Pred. No. 0.011;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                   94.98;
91.78;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||| :|:|
41 QGVLDAVQFLF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-18826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-18826
                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human
US-09-949-002-350
                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
```

ઠે

ઠ

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-484-993B-10

Sequence 10, Application US/08484993B

Patent No. 5837497

GENERAL INFORMATION:

APPLICANT: Harris Ph.D., Jeffrey D.

APPLICANT: Podolski, Joseph S.

TITLE OF INVENTION: Materials and Methods for Immunocontraception Number OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                          Score 37; DB 2; Length 287; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.7%; Score 37; DB 1; Length 715; 80.0%; Pred. No. 49; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CADITY BORGOTO THE COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,993B
FILING DATE: 09-NOV-1993
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION NUMBER: 07/973,341
RILING DATE: 09-NOV-1993
RILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                2; Mismatches
CURRENT APPLICATION NUMBER: US/09/258,634A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Sears Tower, 233 Sout CITY: Chicago STATE: Illinois COUNTRY: Uniced States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REPERENCE/DOCKET NUMBER: 31745
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
                     CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 287
                                                                                                                                                                                                                                  62.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 312/474-6653
312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 715 amino acids
amino acid
                                                                                                                              ; TYPE: PRT; Candida albicans US-09-258-634-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    Query Match 62.7
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                              1 FOGULOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                          45 FOSVLKSLRKVF 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLOSVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-484-993B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PORD 132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR PELLOR DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17510
LENGTH: 158
                   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
RURENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09258634A
Sequence 5, Application US/09258634A
Sequence 5, Application US/09258634A
Sequence 5, Applicant No. 6875655
APPLICANT: Roberts, David
APPLICANT: Wan, Sizhuang
TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences Of
TITLE OF INVENTION: Hemoglobin-Response Genes In Candida Albicans And The
TITLE OF INVENTION: Use Of Reagents Derived From These Sequences In The
TITLE OF INVENTION: Discount Of disseminated Candida Albicans Infection
FILE REFERENCE: 2026-4301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 2; Length 1172;
Pred. No. 53;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 2; Length 158; Pred. No. 8.8; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-248-796A-17510
; Sequence 17510, Application US/09248796A
; Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.7%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Candida albicans
US-09-248-796A-17510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|:||:| ||
202 FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 FOSVLKSLRKVF 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-258-634-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
Materials and Methods for Immunocontraception
                                                           ADDRESSE:
ADDRESSE:
ADDRESSE:
STREET: 6300 Sears Tower, 233 South Wacker Drive
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,596A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.7%; Score 37; DB 1; Length 715; 80.0%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June 5, 2006, 22:48:53
Job time: 24.8966 secs
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,223
FILING DATE: 11-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,107
REFERENCE/DOCKET NUMBER: 31745
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 715 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 715 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                        NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 FPCKLOSVŘF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLOSVRF 10
    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-484-596A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 1; Length 715;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                               Sequence 10, Application US/08484158B
Patent No. 5976545
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hau, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Pharmaceutical Compositions for TITLE OF INVENTION: Immunocontraception NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: United States of America

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,158B
FILING DATE: 07-JUNE-95
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/149,223
FILING DATE: 09-NOV-93
PRIOR APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-93
RIOR APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-93
RIOR APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-92
ATTORNEY/AGENT INFORMATION:
NAME: Clough, DATA #3,107
REFERENCE/DOCKET NUMBER: 32,107
REFERENCE/DOCKET NUMBER: 32,107
REFERENCE/DOCKET NUMBER: 32794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08484596A
Patent No. 5981228
GENERAL INFORMATION:
APPLICANT: Hauris Ph.D., Jeffrey D.
APPLICANT: Hau, Kuang T.
APPLICANT: Podolski, Joseph S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.7%;
Best Local Similarity 80.0%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 715 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
277 FPGKLQSVRF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 FPGKLÓSVRF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FQGVLQSVRF 10
                                                                                           US-08-484-158B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-484-596A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-484-158B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
셤
```

Gaps

ö

2; Indels

THIS PAGE BLANK (USPTO)

Tue

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Appl Sequence 40, Appl Sequence 1020, Appl Sequence 1022, Appl Sequence 462, Appl Sequence 456, Appl Sequence 456, Appl Sequence 455, Appl Sequence 461, Appl Sequence 461, Appl Sequence 461, Appl Sequence 461, Appl Sequence 1, Appli Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Appl
Sequence 482, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appl
                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA Main: *

: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                      5, 2006, 23:46:43; Search time 78.6207 Seconds (without alignments) 70.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 114,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-474-213-28

US-10-419-462-40

US-10-741-600-1020

US-10-741-600-1022

US-10-741-600-1022

US-11-043-806-454

US-11-043-806-454

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-451

US-10-043-806-451

US-10-043-806-451

US-11-043-806-451

US-11-043-806-451

US-11-043-806-451

US-10-296-733-1

US-10-296-733-1

US-10-296-733-1

US-10-20-114-12

US-10-020-114-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-295-027-1170
US-10-211-462-38
US-10-231-956A-482
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          2097797 seqs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           protein search, using sw model
                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                                1 FQGVLQSVRFVF 12
                                                                                                                                          US-10-030-735-21
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
                                                                                         June
                                                                                                                                                                                                                                                                                                                        seq
seq
                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein
                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
```

```
NSOLISE OF A PAPICATION US/10419462
Sequence 40, Application US/10419462
Sequence 40, Application No. US20040053392A1
Sequence 40, Mailiams, Publication No. US20040053392A1
GENERAL INFORMATION:
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents;
TITLE OF INVENTION: US/10/419,462
CURRENT APPLICATION NUMBER: US/10/419,462
CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOCTWARE: PatentIn version 3.2
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Roberts, David D
APPLICANT: Roberts, David D
APPLICANT: Krutzsch, Henry C
TITLE OF INVENTION: CASE
TITLE OF INVENTION: CASE
FILE REFERENCE: 224329
CURRENT APPLICATION NUMBER: US/10/474,213
CURRENT APPLICATION NUMBER: PCT/US02/10535
PRIOR PILING DATE: 2002-04-03
PRIOR PILING DATE: 2002-04-06
PRIOR APPLICATION NUMBER: 06/281,994
PRIOR PILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                       548, App
1376, Ap
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
  Sequence
Seq
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.9%; Score 56; DB 4; Length 12; llarity 91.7%; Pred. No. 0.00074; Conservative 1; Mismatches 0; Indels
US-10-419-462-38

US-10-741-600-1018

US-10-741-600-1019

US-10-741-600-1021

US-10-849-88-38

US-10-849-88-44

US-10-831-697-2

US-10-831-997-2

US-10-995-561-594

US-10-995-561-596

US-11-095-561-596

US-11-046-64-28

US-11-046-64-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic peptide
US-10-474-213-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-474-213-28
; Sequence 28, Application US/10474213
; Publication No. US20040214248A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOGVLONVRFVF 12
                           11170
11170
11170
11170
11170
11170
11170
11170
11170
11170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 11; Conserv
```

```
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Uncleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: Lhereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 462
LENGTH: 459
                                                                                                                                                                                                            Sequence 1022, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1022
                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.9%; Score 56; DB 6; Length 459; 91.7%; Pred. No. 0.038; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                           0; Indels
Pred. No. 0.036;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 5;
Pred. No. 0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)...(432)
CTHER INFORMATION: Xaa = Any Amino Acid
US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-925-301-1047
; Sequence 1047, Application US/09925301
; Patent No. US2002062308A1
; GRNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-043-806-462

'Sequence 462. Application US/11043806

'Publication No. US20060051774A1

'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||:|||||
208 FQGVLQNVRFVF 219
                                                                                               208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 FOGVLONVREVE 219
    Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 91.7
Matches 11; Conservative
                                                                     1 FOGULOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
                                                                                                                                                                                   RESULT 5
US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-043-806-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
                                                                          ò
                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                 USC-10-782-968-40

| Sequence 40, Application US/10782968
| Sequence 40, Application Wools 124A1
| Sequence 40, Application No. US20050065324A1
| Publication No. US20050065324A1
| Publication No. US20050065324A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Kevin J.
| TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents | FILE REFERENCE: W1107-2008 |
| TITLE NEFERENCE: W107-2008 | US/10/782,968 |
| CURRENT FILING DATE: 2004-02-20 |
| PRIOR PILING DATE: 2003-04-21 |
| NUMBER OF SEQ ID NOS: 53 |
| SOFTWARE: PatentIn version 3.2 |
| SEQ ID NO 40 |
| LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1020, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
TUTLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INPARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1020

LENTH: 432
                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                          ; OTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-419-462-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Thrombospondin Region plus N-terminal domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 240;
                                                                                                                                                                Length 240;
                                                                                                                                                                                                          0; Indels
                                                                                                                                                              Score 56; DB 4;
Pred. No. 0.019;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.9%; Score 56; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 5;
Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1) ... (432)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.9%;
91.7%;
                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                              Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                      1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-782-968-40
      LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

```
Sequence 452, Application US/11043806
Publication No. US20060051774A1
Publication No. US20060051774A1
Publication No. US20060051774A1
APPLICANT: Compugen Ltd
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: Lhereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 455, Application US/11043806
Publication No. US20060051774A1
Publication No. US20060051774A1
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT APPLICATION NUMBER: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 6; Length 685;
Pred. No. 0.059;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.9%; Score 56; DB 6; 91.7%; Pred. No. 0.07; iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 453, Application US/11043806
; Publication No. US20060051774A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.77,
Best Local 11; Conservative
                                                                       208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FOGVLONVRFVF 219
                                1 FOGULOSVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLOSVREVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-11-043-806-453
                                                                                                                                          RESULT 10
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 453
LENGTH: 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 454, Application US/11043806

Sequence 454, Application Wo. US20060051774A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Compugen Ltd

TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT APPLICATION DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 456, Application US/11043806

Sequence 456, Application US/11043806

Publication No. US20060051774A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: 1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575

LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 09/9-03-12
NUMBER OF SEQ ID NOS: 1694
SEQ ID NO 1047
LENGTH: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.9%; Score 56; DB 6; Length 578; Best Local Similarity 91.7%; Pred. No. 0.049; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                    Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 3;
Pred. No. 0.039;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 6;
Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    94.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 FQGVLQNVRFVF 272
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FOGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGULQSVRFVF 12
                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Homo sapiens
US-11-043-806-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-043-806-456
                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
```

ò 셤 us-10-030-735-21.rapbm

```
208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 91.7
Matches 11; Conservative
                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                1 FOGVLOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: June
Job time: 78.6207 secs
  US-09-939-853A-98
                                                                                                                                                                                                                                                                 US-11-043-806-461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-043-806-461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                          Sequence 97, Application US/09939853A

Bublication No. US20040039163A1

GENERAL INPORMATION:

GENERAL INPORMATION:

TITLE OF INVENTION:

FILE REFERENCE: 21402-099

CURRENT APPLICATION NUMBER: US/09/939,853A

CURRENT FILING DATE: 2000-08-27

FRIOR APPLICATION NUMBER: 60/228,191

PRIOR FILING DATE: 2000-08-27

PRIOR FILING DATE: 2000-08-27

PRIOR PELING DATE: 2000-08-26

PRIOR PELING DATE: 2001-02-09

FRIOR PILING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOFTWARE: PATENTIN VET: 2.1

SEQ ID NO 97

LENGTH: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98, Application US/09919853A

Publication No. US20040039163A1

GENERAL INFORMATION:

APPLICANT: Burgess et al.

TITLE OF INVENTION:

FILE REFERENCE: 21402-099

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 98

LENGTH 831
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                            Gaps
                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                         Score 56; DB 6; Length 828;
Pred. No. 0.072;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 3; Length 831;
Pred. No. 0.072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                           Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.9%;
91.7%;
                                                                                                                                                                                                                              208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                   1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLOSVRFVF 12
; LENGTH: 828
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
Sequences, Application US/11043806

Bublication No. US20060051774A1

GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods:
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: UNMERS: US/11/043,806
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
BENGTH: 855

WARRENT HEADER SECONDER SEC
                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
94.9%; Score 56; DB 3; Length 831; 91.7%; Pred. No. 0.072; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.9%; Score 56; DB 6; Length 855; 91.7%; Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6, 2006, 00:00:09
```

```
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-10-953-349-9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-505-928-662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-505-928-662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ~
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 662, App
Sequence 232, App
Sequence 1159, App
Sequence 1157, App
Sequence 2004, App
Sequence 9203, App
Sequence 9203, App
Sequence 2452, App
Sequence 1264, App
Sequence 1282, App
Sequence 1282, App
Sequence 15282, App
Sequence 15282, App
Sequence 2569, App
Sequence 2402, App
Sequence 2402, App
Sequence 2402, App
Sequence 2402, App
Sequence 3401, App
Sequence 1518, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179, App
33070, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEMC Celerra SIDS3/prodata/1/pubpaa/US09_NEW_PUB.pep:*
EMC Celerra SIDS3/prodata/1/pubpaa/US06_NEW_PUB.pep:*
EMC Celerra SIDS3/prodata/1/pubpaa/US06_NEW_PUB.pep:*
FEMC Celerra SIDS3/prodata/1/pubpaa/US08_NEW_PUB.pep:*
FEMC Celerra SIDS3/prodata/1/pubpaa/US08_NEW_PUB.pep:*
FEMC Celerra SIDS3/prodata/1/pubpaa/US10_NEW_PUB.pep:*
FEMC Celerra SIDS3/prodata/1/pubpaa/US10_NEW_PUB.pep:*
FEMC Celerra SIDS3/prodata/1/pubpaa/US11_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                     6, 2006, 00:00:38; Search time 3.72414 Seconds (without alignments) 37.266 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-505-928-662

US-10-953-349-9347

US-10-953-349-1159

US-10-953-349-1159

US-10-953-349-1159

US-10-953-349-1157

US-10-953-349-9203

US-10-953-349-9203

US-10-953-349-9203

US-10-953-349-9203

US-10-953-349-9203

US-10-953-349-15283

US-10-953-349-15283

US-10-953-349-3401

US-10-953-349-3401

US-11-293-697-3323

US-11-297-349-3401

US-11-297-349-3401

US-11-297-349-3401

US-11-297-349-3401

US-11-297-349-3401

US-11-297-349-3401

US-10-953-349-3401

US-10-953-349-3401

US-10-953-349-3401

US-10-953-349-3401

US-10-953-349-3401

US-10-953-349-3401

US-10-953-349-3401
                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_AA_New:*
                                                                                                                                                                                                                                                                                                        58871 segs, 11565156 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                     protein search, using sw model
                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                            US-10-030-735-21
59
1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 08
Maximum Match 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00

    0.00
  </tr
                                                                                                         June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is
score greater
                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq
Maximum DB seq
                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein
                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
```

```
Sequence 93477, Application US/10953349
Publication No. US20060107345A1
Publication No. US20060107345A1
Publication No. US20060107345A1
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579Pr02
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9347
LIENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
    34818, A
2388, App
2380, App
33069, A
31561, Ap
2387, Ap
34817, Ap
34817, Ap
14600, A
14599, A
23111, A
21132, Ap
21132, Ap
21132, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                              Sequence Seq
        Sequence
                                            Sequence
                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Length 1504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ludwig Institute for Cancer Research et ITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Parentin 3.2
LENGTH: 1504
US-10-953-349-34818

US-10-953-349-178

US-10-953-349-177

US-10-953-349-3069

US-10-953-349-365

US-10-953-349-3662

US-10-953-349-3662

US-10-953-349-366

US-10-953-349-3661

US-10-953-349-3661

US-10-953-349-3661

US-10-953-349-3131

US-10-953-349-21132

US-10-953-349-21132

US-10-953-349-21132

US-10-953-349-21132

US-10-953-349-21131

US-10-953-349-21131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB
Pred. No. 28;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 662, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.0%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :| |:||||
751 QHILSSLRFVF 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Homo sapiens
      444444444444444444
```

~

ö

```
Sequence 9204, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: 2004-09-30
NUMBER OF SEO ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ALEXANIROV, NICKOLAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILLE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILLING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 6; Length 315;
Pred. No. 49;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                Score 31; DB 6; Length 249;
Pred. No. 38;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 6; Length 250;
Pred. No. 38;
2; Mismatches 4; Indels
                 FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1158
LENGTH: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1157, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9204
                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.5%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                |: |: || ||
167 FEAVVDRVRLVF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 FEAVVDRVRLVF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                      1 FOGULOSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGULQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-953-349-9204
                                                                                                                                                                                                           US-10-953-349-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-953-349-1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1157
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1159, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1158, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
DB 6; Length 298;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                             1; Indels
                                                                                                                                                                                            US-10-505-928-282
Sequence 282, Application US/10505928
Sequence 282, Application US/10505928
Publication No. US20060088532A1
GENERAL INPORMATION:
APPLICANT: Ludwig Institute for Cancer Research et TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 2896/739178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT APPLICATION NUMBER: US 60/363,019
PRIOR PILING DATE: 2004-08-27
PRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.5%; Score 31; DB 6; 50.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 6;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 24;
2; Mismatches
                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
    Score 33;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Arabidopsis thaliana
    55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 POGLLVSTIFCF 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 FEAVVDRVRLVF 93
                                                                                                             :|::| |:|:
87 EGIIQGVKFI 96
                                                                                       2 QGVLQSVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-953-349-1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-953-349-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-953-349-1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                         ઠ
                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Woodward, Robert
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Morshor, Seeven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: MORBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR PELING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 6; Length 1043;
Pred. No. 1.8e+02;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                          Score 31; DB 6; Length 820;
Pred. No. 1.4e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 104, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICANTON NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR FILING DATE: 2002-03-07
FILE REFERENCE: 259358USO
CURRENT APPLICATION NUMBER: US/10/982,908
CURRENT FILING DATE: 2004-11-08
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.3
SEQ ID NO 26
LENGTH: 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 2452, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
                                                                                                                                                                                                                                                                  52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wohlgemuth, Jay
Fry, Kirk
Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 40.0
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                          1 FOGULQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|:: :|:|
696 GILRTFKFIF 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GVLQSVRFVF 12
                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-908-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-511-937-2452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-511-937-2452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-10-505-928-104
                                                                                                                                                                                                                                                                                                                                                                                                       <del>a</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                         APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUSZ
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9203
LENGTH: 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9202, Application US/10953349
Publication No. US20060107345A1
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-10-982-908-26
Sequence 26, Application US/10982908
Sequence 26, Application No. US20060099603A1
Sequence 26, Application No. US20060099603A1
GENERAL INFORMATION:
APPLICANT: DAVI, FREDERIC
APPLICANT: DIWAS, GERARD
APPLICANT: STTEGRANA, CATHERINE
APPLICANT: STTEGRANA, CATHERINE
APPLICANT: WASCONCELOS PINHEIRO, YURI
TITLE OF INVENTION: METHOD OF DIAGNOSIS/PROGNOSIS OF HUMAN CHRONIC LYMPHOCYTIC
TITLE OF INVENTION: LEUKEMIA COMPRISING THE PROFILING OF LDL/ADAM GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.5%; Score 31; DB 6; Length 400; Best Local Similarity 50.0%; Pred. No. 63; Matches 6; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.5%; Score 31; DB 6; 50.0%; Pred. No. 64; tive 2; Mismatches
                                                                                                                                            Sequence 9203, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Arabidopsis thaliana
US-10-953-349-9203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: |: || ||
167 FEAVVDRVRLVF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 FEAVVDRVRLVF 179
  |: |: || ||
82 FEAVVDRVRLVF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FQGVLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                      US-10-953-349-9203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-10-953-349-9202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEO ID NO 9202
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
```

ò 셤 g

```
us-lu-slu-sy-1-239.

sequence 2992, Application US/10511937

publication No. US20060088836A1

publication No. US20060088836A1

general information:

APPLICANT: EXPRESSION DIAGNOSTICS, INC.

APPLICANT: Fry, Kirk

APPLICANT: Fry, Kirk

APPLICANT: Produced, Robert

APPLICANT: Prentice, James

APPLICANT: NOWBER: US/10/511,937

CURRENT APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24

PRIOR FILING DATE: 2003-04-24

PRIOR FILING DATE: 2002-04-24

PRIOR FILING DATE: 2003-04-24

PRIOR FILING DATE: 2003-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.8%; Score 30; DB 6; Length 1333; 50.0%; Pred. No. 3.8e+02; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6, 2006, 00:12:55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 FRGVLEQLRW 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLQSVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June Job time: 3.82414 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-511-937-2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15283, Application US/10953349
Sequence 15283, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE OF THERBY
FILE REPERENCE: 2750-15799US2
CURRENT APPLICATION WHORE: US/10/953,349
CURRENT APPLICATION WHORE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 15283
LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15282, Application US/10953349
Sequence 15282, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                            52.5%; Score 31; DB 6; Length 3460; 54.5%; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.8%; Score 30; DB 6; Length 77; 55.6%; Pred. No. 16; 2; Mismatches 2; Indels tive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.8%; Score 30; DB 6; Length 74; 55.6%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2173 FEĞQLESDRFL 2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.8
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                Query Match 52.5
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   1 FQGVLQSVRFV 11
NUMBER OF SEQ ID NOS: 866
                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::| ||| |
24 IVQGVRFAF 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VLQSVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::| ||| |
21 IVQGVRFAF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VLQSVRFVF 12
                           SOFTWARE: Patentin 3.2
SEQ ID NO 104
LENGTH: 3460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-15282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Glycine max US-10-953-349-15283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-10-953-349-15283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-953-349-15282
                                                                                                                                                                                              US-10-505-928-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 15282
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

ö

Gaps

```
15-JUL-1999;
                                                                                                                                                                                                                                                                                RESULT 1
                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                        (without alignments)
60.201 Million cell updates/sec
                                                              5, 2006, 22:08:53 ; Search time 68.3534 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                       2589679
                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                 2589679 segs, 457216429 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         - protein search, using sw model
                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                         geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
                                                                                                                                                                                                                                                                                                                                                                               geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                      geneseqp2003as:*
                                                                                                                                                                                                                                                                                                                                                                                          geneseqp2004s:*
geneseqp2005s:*
                                                                                                                                                                                                                                                                                                                                                                                                               geneseqp2006s:*
                                                                                                                                                                                                                                                                                                      A_Geneseq_8:*
1: geneseqp1980s:*
                                                                                                                                                                                                                                                                                                                                                           geneseqp2002s:*
                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                        US-10-030-735-22
40
                                                                                                                            1 XGVLQNVRF 9
                                                                                                                                                   BLOSUM62
                                                                                                                                                   Scoring table:
                                                                                                        Title:
Perfect score:
                                         OM protein
                                                                                                                                                                                                                                                                                                        ••
                                                                                                                              Sequence:
                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                      Database
                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ž
```

Aab54450 Human var Aab50800 Human she Aae25301 Human thr Aby5780 Human thr Aby574673 Human COP Abu013474 Angiogene Abg74673 Human THB Abc82059 Human THB Abc82059 Human Thr Adr39852 Cancer/an Adj75296 Marker ge Adj75296 Marker ge Adj3594 Human thr Adl35874 Human thr Add38348 Human myo Adq39356 Human myo Adq39356 Human myo	B Thromb 1 Human 1 Human
AAB74450 AAB90800 AAB90800 AAU75315 AAU75315 ABU04474 ABU74673 ABR26228 ABR26228 ABR26228 ABR26228 ABR39852 ADV70639 ADV39858 ADQ39356 ADQ39355	ADZ21688 AEB87781 AEB46751
11111111111111111111111111111111111111	1170 9 1170 9
	0 100.0 0 100.0 0 100.0
4 2 9 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	

ALIGNMENTS

Alpha3betal integrin binding peptide #40. AAB35375 standard; peptide; 9 AA. (first entry) 08-MAY-2001 AAB35375;

Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.

Synthetic.

WO200105812-A2.

25-JAN-2001.

12-JUL-2000; 2000WO-US018986.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

99US-0144549P.

Krutzsch HC; Roberts DD,

WPI; 2001-182656/18.

New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and cancer.

Claim 4; Page 34; 84pp; English.

The present invention provides a number of peptides which bind to alphalbetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention

Sequence 9 AA;

```
Roberts DD, Krutzsch HC,
                                                                                                                                                                                                                                                                                                                                                                                                                      GVLQNVRF 10
                                                                                                                                                                                    WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    2 GVLQNVRF
                                                                                                                                                                                                                                                                                                                        the invention
                                                                                                                                                                                                                                                                                                                                           Sequence 11 AA;
                                                                    WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200105812-A2
                                                                                                                             15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999;
                                                                                                                                                                  Roberts DD,
                                                                                      25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2001
                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB35357;
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                      cancer.
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB35357
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention
                                                                                                                                                                                   Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                               New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 40; DB 4; Length 10; 100.0%; Pred. No. 0.058; rive 0; Mismatches 0; Indel8
100.0%; Score 40; DB 4; Length 9; 100.0%; Pred. No. 2.1e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                  Alpha3betal integrin binding peptide #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha3betal integrin binding peptide #25.
                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                         AAB35355 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB35360 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 34; 84pp; English.
          ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                    12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                       99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Pest Local Similarity luv.
A: Conservative
                                                                                                                                                                                                                                                                                                                                            Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVLONVRF 10
                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-182656/18.
                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVLQNVRF 9
 Query Match
Best Local Similarity
Matches 8; Conserv
                                                   GVLQNVRF
                                        GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 AA;
                                                                                                                                                                                                                                              WO200105812-A2
                                                                                                                                                                                                                                                                                                       15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-2001
                                                                                                                                               08-MAY-2001
                                                                                                                                                                                                                                                                  25-JAN-2001
                                                                                                                                                                                                                           Synthetic.
                                       N
                                                                                                                             AAB35355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB35360;
                                                                                                                                                                                                                                                                                                                                                                                                                cancer.
                                                                                      RESULT 2
                                                                                               AAB35355
ID AAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB35360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXEXEXE
Executive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of peptides which bind to alpha3beta1 integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid archritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
Alpha3beta1 integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 40; DB 4; Length 11; 100.0%; Pred. No. 0.064; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha3betal integrin binding peptide #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB35357 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
```

```
The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid archritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                             New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 4; Length 11; 100.0%; Pred. No. 0.064; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha3betal integrin binding peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB35352 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 34; 84pp; English.
                                                                                                                                Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-182656/18.
             WPI; 2001-182656/18
                                                                                                                                                                                                                                                                                                                                                                                   2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       GVLONVRF
                                                                                                                                                                                                                                                  of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention
                                                                                                                                                                                                                                                                                  Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB35352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer
                                                                                                                                                                                                                                                                                                                                                  Matches
셤
                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

Sequence 12 AA;

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, disbetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                       Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides that bind to or are recognized by alpha3-betal integrins,
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
           100.0%; Score 40; DB 4; Length 12; 100.0%; Pred. No. 0.071; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 40; DB 4; Length 12; larity 100.0%; Pred. No. 0.071; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                Alpha3betal integrin binding peptide #31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB35370 standard; peptide; 12 AA.
                                                                                                                                                                AAB35366 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
8; Conserv
                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                   2 GVLQNVRF
                                                                                             GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                            WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999;
                                                                                                                                                                                                                       08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                           AAB35366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB35370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB35370
                                                                                           g
                                                                                                                                                                  셤
                                                                   8
                                                                                                                                                                                                                                                                                          ö
```

```
The present invention provides a number of peptides which bind to alphaibetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention
                                                                                                                                                                                                                              The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alphaibetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 40; DB 4; Length 12; 100.0%; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha3betal integrin binding peptide #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                             Example 2; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 31; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB35347 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 100.8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-182656/18.
                                            WPI; 2001-182656/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVLONVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                  of the invention
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999;
Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB35347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                       cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB35347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of peptides which bind to alpha3beral integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                     Alphalbetal integrin; anglogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 40; DB 4; Length 12; 100.0%; Pred. No. 0.071; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha3betal integrin binding peptide #43.
  Alpha3betal integrin binding peptide #35.
                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB35378 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0144549P
                                                                                                                                                                                                                                                             12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                     99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
```

GVLONVRF 10

RESULT 8 AAB35378 08-MAY-2001

AAB35378;

WO200105812-A2.

Synthetic

Z B X B X B X B X B X B X B X B X B X X X X X X B

25-JAN-2001

15-JUL-1999;

σ

GVLQNVRF

N

ð g

Local Similarity

Best Loc Matches

Query Match

Sequence 12 AA;

the

ö

Gaps

Krutzsch

Roberts DD,

15-JUL-1999;

WO200105812-A2.

Synthetic.

25-JAN-2001

WPI; 2001-182656/18.

cancer.

RESULT 10

ઠે

AAB35369

```
The invention relates to diagnosing cancer other than prostate cancer in a male mammal, comprising assaying a test sample for increased level of semenogelin, or cancer in a female by assaying for the presence of semenogelin, according a semenogelin protein or polypeptide fragment or a semenogelin. Administering a semenogelin protein or polypeptide fragment or a semenogelin-specific antibody or active fragment, or a recombinant vector expressing the protein or antibody, is useful for inducing an immune response to a cancer in a mammal, where the cancer is not prostate cancer, particularly of epithelial origin such as lung cancer, papillary renal cell carcinoma, colon cancer, especially small-cell lung cancer (SCLC), or a melanoma. The present sequence represents the amino acid sequence of the thrombospondin-1 sequence containing synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new diagnosis for cancer other than prostate cancer in a mammal useful to detect cancer including lung cancer, particularly small cell lung cancer and melanoma comprises detecting semenogelin in a sample.
                                                    Human; thrombospondin-1; cytostatic; immunostimulant; cancer; epithelial cancer; lung cancer; papillary renal cell carcinoma; colon cancer; small-cell lung cancer; SCLC; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 40; DB 6; Length 12; 100.0%; Pred. No. 0.071; ive 0; Mismatches 0; Indele
                  Thrombospondin-1 sequence containing synthetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Heparin binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Heparin binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human thrombospondin-1 N-terminal domain.
                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which binds to alpha-3-beta-1 integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL70641 standard; protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 14; 32pp; English.
                                                                                                                                                                                                                                                        03-APR-2002; 2002WO-US010535.
                                                                                                                                                                                                                                                                                             06-APR-2001; 2001US-0281994P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                        Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-103329/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GVLONVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12 AA;
                                                                                                                                                                        WO200281630-A2
                                                                                                                                                                                                                                                                                                                                                                      Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                               7-0CT-2002
                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL70641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL70641
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of peptides which bind to alpha3beral integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid archritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                        Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 40; DB 4; Length 12; 100.0%; Pred. No. 0.071;
                                        DB 4; Length 12;
                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                    0.071;
                                  100.0%; Score 40; DB
100.0%; Pred. No. 0.0
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Alpha3betal integrin binding peptide #34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                      AAB35369 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG72834 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 34; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0144549P
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2003 (first entry)
                                  Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                    GVLONVRF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GVLQNVRF 10
                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 8; Conser
                                                                                                                  2 GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the invention
Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200105812-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                 08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                          AAB35369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG72834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
```

cancer

Matches

RESULT 11 ABG72834

SXXXE

용

ò

ö

Gaps

ø

151. .164 /note= "Fibrinogen binding region"

WO2004018995-A2.

```
(WILL/) WILLIAMS K J.
                 WPI; 2004-226901/21.
                                                                             Sequence 240 AA;
     04-MAR-2004
               Williams KJ
```

The present sequence is that of the N-terminal domain of human thrombospondin-1 (TSP) ADL70639. The invention relates to TSP fragments thrombospondin-1 (TSP) ADL70639. The invention relates to TSP fragment continued assays for cancer and for generation of antibodies and other binding agents. A method that distinguishes TSP fram a TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion of TSP plus TSP fragment or portion; (2) using an epitope present in TSP but not in the fragment or portion; (2) using an epitope present in TSP but not in the fragment or portion; (2) using an epitope present or protein of TSP plus TSP fragment or portion of TSP fragment or portion of SPP but amount of TSP fragment or portion. Suitable epitopes are provided ADL70602-ADL70639 betection or quantification of the TSP fragment or portion of SPP fragment or securities, renal allograft, asthma, diabetes mellitus, myocardial inferction, liver disease, splementowy, diabetes mellitus, myocardial inferction, liver disease, splementowy, diabetes mellitus, framal rallograft, varculities, juvenile rheumatory condition, recondition, are condition, are condition associated with intravascular coagulation, internal coagulation, an ordition and coagulation, and condition and coagulation, and condition and coagulation, and spontane reaction, and condition associated with a cryoglobuli, and a condition associated with a cryoglobuli, and a condition associated w biliary system, pancreas, head, neck, endocrine system, reproductive system male or female), genitourinary system, kidney, urinary tract, sensory system, nervous system, lymphoid organ, blood, a gland, mammary gland, prostate gland, endometrial tissue, mesodermal tissue, ectodermal tissue, endodermal tissue, a poorly-differentiated cancer, a well-differentiated cancer or a moderately differentiated cancer. New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes. Disclosure; SEQ ID NO 40; 76pp; English. 20-AUG-2003; 2003WO-US026023. 23-AUG-2002; 2002US-0405494P. 21-APR-2003; 2003US-00419462.

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single mucleocide polymorphism (SNP) in any one of the nucleocide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises; an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleocides is an SNP given in the specification or its complement and encoding any one of the amino the specification or its complement and encoding any one of the amino caid sequence given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification, an antibody that specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting an anetyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity.
                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction associated gene containing one or more SNP so of the invention. Note: This sequence was not shown in the specification. The sequence has come from
                                                                                                                                                                                                                                                                                                                                    Human myocardial infarction-associated gene derived protein, SEQ ID 1022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                     Gaps
                     ö
                   Indels
                     ;
0
100.0%; Pred. No. 2.2; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; SEQ ID NO 1022; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iakoubova 0;
                                                                                                                                                                                                           ADQ39359 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                    cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DBC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-046412P.
23-SBP-2003; 2003US-0604955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                             18-NOV-2004 (first entry)
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cargill M, Devlin JJ,
                                                                                                    192 GVLQNVRF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-533949/51.
N-PSDB; ADQ38531.
                                                             σ
                                                             2 GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004058052-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                domo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2004.
                                                                                                                                                                                                                                                     ADQ39359;
                                                                                                                                                                    RESULT 13
                                                                                                                                                                                          ADQ39359
                                                               ò
                                                                                                    g
```

7

```
RESULT 15
                                                                                                                                                                                                                                                           AAU02916
  88888888888
                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                 The invention relates to a novel method for identifying an individual who cast an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an ancleic acids where the presence of the SNP is correlated with an activate risk for myocardial infarction in the individual. The invention turther comprises: an isolated nucleic acid molecule comprising at least a contiguous nucleotides where one of the nucleotides is an SNP given in the specification, an isolated polypeptide comprising an amino acid sequence given in the specification, an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody comprising an amino acid sequence given in the specification; an inthe specification and which is between about 16 and 1000 nucleotides in the specification and which is between about 16 and 1000 nucleotides in comprising the polymucleotide, and an SNP in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and an enthod for identifying an agent useful in treating or preventing myocardial infarction. The novel detection may be used in gene therapy. The method is useful in identifying an individual who has an increased or
                                                                                ö
                                                                                                                                                                                                                                                                                 Human myocardial infarction-associated gene derived protein, SEQ ID 1020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                            Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.
                                                                                Gaps
an electronic sequence listing downloaded from the WIPO website.
                                                                                ö
                                                     100.0%; Score 40; DB 8; Length 432, 100.0%; Pred. No. 4.4;
                                                                            0; Indels
                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; SEQ ID NO 1020; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iakoubova O;
                                                                                                                                                                                                   ADQ39357 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-050495SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                                                       18-NOV-2004 (first entry)
                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devlin JJ,
                                                                                                                            210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (APPL-) APPLERA CORP
                                                                                                        2 GVLQNVRP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-533949/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADO38529
                           Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                             WO2004058052-A2.
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cargill M,
                                                                                                                                                                                                                             ADQ39357;
                                                     Query Match
                                                                    Best Loc
Matches
                                                                                                                                                                        RESULT 14
ADQ39357
                                                                                                                                g
                                                                                                                                                                                                    ઠ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of garanlocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and vascative intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various discorders including cardiovascular diseases such as arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nontiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarctionassociated gene containing one or more SPP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme (ACEV) splice variant protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 40; DB 8;
100.0%; Pred. No. 4.4;
ive 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU02916 standard; protein; 459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 16; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1999; 99IL-00132978.
10-DEC-1999; 99IL-00133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 GVLONVŘF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS06016.
                                                                                                                                                                                                                                                                                             Seguence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02916;
```

```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

June Run on:

5, 2006, 22:25:22 ; Search time 10.4741 Seconds (without alignments) 82.675 Million cell updates/sec

US-10-030-735-22 40

1 XGVLQNVRF 9 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*

pirl: pir2:* pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ιρ	thrombospondin 1 p	н	chitin synthase (E	hypothetical prote	chitin synthase (E	conserved hypothet	iron-sulfur cofact		chitin synthase (E		chitin synthase (E	chitin synthase (E	probable 3-oxoacyl	3-oxoacyl-[acyl-ca	malate dehydrogena	leukocidin chain l	leukotoxin LukE [i	phosphoglycerate k	tryptophan oxygena	phosphoglucomutase	H+-transporting tw							
SUMMARIES	ID	795	TSHUP1	A40558	S53801	T50315	JC6015	B82877	860953	B75421	B45190	H45189	G45189	A45190	A64590	B71923	D81399	JC5468	C89968	TVECG	AD0875	E91103	H85948	AB0113	F82317	KIBSGM	C69675	G02022	N	D84938
	DB	7	Н	~	7	7	7	7	N	7	~	N	7	7	-	N	N	0	7	н	~	~	7	N	αi	н	7	N	7	0
	Query Match Length	229	1170	1170	207	780	889	1413	156	186	189	195	198	198	247	247	300	308	311	387	387	387	387	387	392	394	394	406	446	467
d	Query		100.0	100.0	80.0	80.0	80.0	80.0	77.5	77.5	77.5	77.5	77.5	77.5	77.5	•	77.5	77.5	77.5	77.5	•	•	77.5	•	77.5	77.5	77.5	٠	•	77.5
	Score	40	40	40	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
	Result No.	-	7	m	4	S	9	7	80	σ	10	11	12	13	14		16		18	19	20	21	22	23	24	25	56	27	28	59

two component resp	probable transcrip	chitin synthase (E	chitin synthase (E	p63 related protei	leukocidin chain F	probable outer mem	hypothetical prote	hypothetical prote	gamma-hemolysin co	synergohymenotropi	leukocidin chain S	leucocidin chain S	leucocidin R S com	leukocidin chain S	gamma-hemolysin co
AE2929	A98353	JC6016	JC2315	T49517	835697	F64066	G84013	S77023	C49238	S68225	T00160	832211	A49234	JN0626	E90043
7	~	~	~	~	~	7	N	N	~	7	~	~	7	~	7
747	783	911	916	1114	54	70	102	192	286	310	312	312	315	315	315
77.5	77.5	77.5	77.5	77.5	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0
31	31	31	31	31	30	30	30	30	30	30	30	30	30	30	30
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 S57957 Lhrombospondin 1 - bovine (fragment) C;Species: Bos primigenius taurus (cattle) C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004 C;Accession: S57957	R;Lafeuillade, B.; Pellerin, S.; Keramidas, M.; Chambaz, E.M.; Feige, J.J. submitted to the EMBL Data Library, July 1995 A;Pescription: Opposite regulation of thrombospondin-1 and CISP/thrombospondin-2 expressi A;Reference number: S57955	A;Status: praliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Ross-references: UNIPROT:Q28194; UNIPARC:UPI00008740A; EMBL:X89511; NID:g899228; PIDN C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor	Query Match 100.0%; Score 40; DB 2; Length 229; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	2 GVIQNVRP 9	192 GVLONVRF 199
RESULT 1 S57957 thrombosponc C;Species: E C;Date: 13-0 C;Accession:	R;Lafeuillac submitted to A;Descriptic A;Reference	A;Status: D; A;Molecule t A;Residues: A;Cross-refe C;Superfamil	Query Matc Best Local Matches	ò	DD 19

CiSpecies: Homo sapiens (man)
CiAccession: A56155; A34274; Ā30140; A25812; A65172; A42927
Ricall Biol. 10; Hynes, R.O.
A; Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple Call Ricession: A26155; MUD:87057617; PMID:2430973

A; Molecule type: mRNA A; Residues: 1-1170 <LAW> A; Cross-references: UNIPROT: P07996; UNIPARC: UPI0000046821; GB: X04665; NID: g37137; PIDN: CJ A; Cross-references: UNIPROT: P07996; UNIPARC: UPI0000046821; GB: X04665; NID: g37137; PIDN: CJ A; Note: parts of this sequence, including the amino end of the mature protein, were deter R; Laherty, C.D.; Gierman, T.M.; Dixit, V.M. J; Biol. Chem. 264, 11222-11227, 1989 A; Fitle: Characterization of the promoter region of the human thrombospondin gene. DNA 8¢ A; Reference number: A34274; MUID: 89291870; PMID: 2544587

A;Accession: A34274 A;Molecule type: DNA A;Residues: 1-166 <LAH>

A;Cross-references: UNIPARC:UPI00001742BF; GB:J04835 R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, f Aj Cell Biol. 108, 729-736, 1989 A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the

a

```
chitin synthase (BC 2.4.1.16) chsC - Aspergillus fumigatus (fragment)
C;Species: Aspergillus fumigatus
C;Species: Aspergillus fumigatus
C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C;Accession: S53801
R;Mellado, E.; Aufauvre-Brown, A.; Specht, C.A.; Robbins, P.W.; Holden, D.W.
Mol. Gen. Genet. 246, 353-359, 1995
A;Title: A multigene family related to chitin synthase genes of yeast in the opportunistial A;Reference number: S53799; MulD:95157525; PMID:7854320
                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1170 <LAW>
A; Cross-references: UNIPROT: P35441; UNIPARC: UPI0000028012; GB: M62449; GB: M62450; GB: M6245
A; Cross-references: UNIPROT: P35444; GB: M62465; GB: M62466; GB: M62467; GB: M62468; GB: M62465; GB: M62463; GB: M62464; GB: M62464; GB: M62463; GB: M62463; GB: M62463; GB: M62463; GB: M62463; GB: M62464; GB: M624644; GB: M62464; GB: M624644; GB: M62464; GB: M62464; GB: M62464; GB: M62464; GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 19-26, 'X', 28-37 < CHE>
A; Residues: 19-26, 'X', 28-37 < CHE>
A; Crogs-references: UNIPARC: UPI0000177A97
C; Complex: homotrimer, disulfide linked
C; Complex: homotrimer, disulfide linked
C; Superfamily: thrombospondin 1; BGF homology; thrombospondin type 1 repeat homology; vor C; Reywords: calcium binding; glycoprotein; homotrimer
C; Reywords: calcium binding; glycoprotein; homotrimer
C; Reywords: calcium binding; glycoprotein; homology vor S; 19-1170/Product: thrombospondin 1 #status predicted < NAT>
F; 19-1170/Promain: thrombospondin type 1 repeat homology < THR2>
F; 1317-375/Domain: thrombospondin type 1 repeat homology < THR2>
F; 19-547/Domain: thrombospondin type 1 repeat homology < THR3>
F; 19-547/Domain: BGF homology < RGR>
F; 18-648/Domain: BGF homology < RGR>
F; 18-848/Domain: BGF homology < RGR>
F; 248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPARC:UPI000016D076; GB:J05605; GB:J05606; NID:g201991; PIDN:AAA404 R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M. J. Balol. Chem. 267, 3274-3281, 1992 A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and characterization of mouse thro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar A;Reference number: S68787; MUID:96234006; PMID:8654563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-1152, 'P',1154-1170 <1AH5
A;Cross-references: UNIPARC:UP10000177A96; GB:M87276
A;Note: sequence extracted from NCBI backbone (NCBIP:81501)
R;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                          A,Title: Characterization of the murine thrombospondin gene. A,Reference number: A40558; MUID:92128941; PMID:1774063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-207 <MEL>
A;Cross-references: UNIPROT:Q9URD7; UNIPARC:UPI000006C612
A;Experimental source: strain H237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 2
100.0%; Pred. No. 1.4;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 GVLONVRF 217
Genomics 11, 587-600, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A37905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <BOR>
                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: B42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S68787
                                                                                                                                                                                      A; Accession: A40558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc C; Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 1-18/Domain: signal sequence #status predicted <MAT>
F; 13-13/Domain: urcombospondin 1 #status predicted <MAT>
F; 13-13/Domain: thrombospondin type 1 repeat homology <THR1>
F; 13-4-49/Domain: thrombospondin type 1 repeat homology <THR3>
F; 44-49/Domain: thrombospondin type 1 repeat homology <THR3>
F; 51-58/Domain: EGF homology <EGF1>
F; 551-58/Domain: EGF homology <EGF2>
F; 526-5928/Region: cell attachment (R-G-D) motif
F; 11-232/Disulfide bonds: #status predicted
F; 11-232/Disulfide bonds: #status predicted
F; 100,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 1051/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                        A; Molecule type: mRNA
A; Residues: 1-83, 4', 85-522, 4', 524-1170 < HENN>
A; Residues: 1-83, 4', 85-522, 4', 524-1170 < HENN>
A; Residues: 1-83, 4', 85-522, 4', 524-1170 < HENS-XI4787; NID:g37464; PIDN:CAA32889.1; PID
A; Cross-references: UNIPARC:UPI0000038AB1; EMBL:XI4787; NID:g37464; PIDN:CAA32889.1; PID
B; Cross-reference: List sequence, including the amino end of the mature protein, were dete
R; Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A; Title: Partial amino acid sequence of human thrombospondin as determined by analysis of A; Reference number: A25812; MUID:87157592; PMID:3030396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: A25812
A,Molecule type: mRNA
A,Residues: 1-83, A', 85-397 <KOB>
A,Cross-references: UNIPARC:UPI000016B0CA, GB:M25631; NID:g538353; PIDN:AAA36741.1; PID:
R;Dixti, V. M.; Hennesey, S. W.; Grant, G. A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A,Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A. Accession: A05172
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Cross-references: UNIPARC: UPI000016B140; GB: M14326; NID: 9340005; PIDN: AA461237.1; PII
A. Note: parts of this sequence, including the amino end of the mature protein, were det
A. Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A. Pritle: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A. Reference number: A42927; MUID: 92348511; PMID: 1379247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42887; S68787
R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 40; DB 1; Length 1170; 100.0%; Pred. No. 1.4; ive 0; Mismatches 0; Indels (
Reference number: A30140; MUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: Cys-992 is shown to have a free sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be incomplete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Gene: GDB:THBS1; TSP1; TSP
A;Cross-references: GDB:120438; OMIM:188060
A;Map position: 15q15-15q15
A;Introns: 23/1
A;Note: the list of introns may be incomplet
C;Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 987-1003 <SUN>
A;Cross-references: UNIPARC:UP100001742C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - monse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombospondin 1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
8, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A42927
```

Function:

RESULT 3

유 ò

m

g Š

```
Cispecies: Ureaplasma urealyticum
Cibate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
Cibate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
Cibate: 18-Aug-2000
Cibate: 18-Aug-2000
Cibate: 18-Aug-2000
Riglass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minj
A;Accession: BB2877
A;Accession: BB2877
A;Accession: Agains
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1413 <GLA>
A;Cross-references: UNIPARC:UPI0000C1CB2; GB:AE002153; GB:AF222894; NID:g6899544; PIDN:/
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-156 <BOY>
A;Residues: 1-156 <BOY>
A;Cross.references: UNIPARC:UP10000658D8; EMBL:Z75133; NID:g1420519; PIDN:CAA99445.1; P)
A;Experimental source: strain S288C
A;Experimental source: strain S288C
B;Galisson, F.; Dujon, B.
Yeast 12, 877-885, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iron-sulfur cofactor synthesis protein nifU homolog YOR226c [similarity] - yeast (Saccha) N;Alternate names: hypothetical protein O5076; hypothetical protein YOR50-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eubmitted to the EMBL Data Library, October 1995
A;Description: Sequence and analysis of a 33 kb fragment from the right arm of chromosome
A;Reference number: S60938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 15R
C;Superfamily: iron-sulfur cluster assembly protein, iscU type; nitrogen fixation proteir
C;Keywords: metalloprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q12056; UNIPARC:UPI0000698D8; EMBL:X92441; NID:g1050762; E
R;Boyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Michaux, G.; Thierry, A.; Dujon, submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV A:Reference number: S71713; MUID:96437977; PMID:8840505 A;Accession: S71728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UPI00000698D8; EMBL:X92441; NID:g1050762; PIDN:CAA63189.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: hypothetical protein 05076; hypothetical protein YOR50-1 C;Species: Saccharomyces cerevisiae C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 31-Dec-2004 C;Accession: $60953; &67119; $71728 R;Galisson, F.; Dujon, B. submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                    conserved hypothetical UU543 [imported] - Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%; Score 32; DB 2; Length 1413; 71.4%; Pred. No. 1.2e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: SGD:S0005752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S67104
                                ||:||||
218 GVMQNVR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||:||
820 ILQNIRF 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-156 <GAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Residues: 1-156 <GAW>
   GVLONVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S67119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: S60953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: SGD: ISU2
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                      RESULT
B82877
ò
                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                         A;Description: catalyzes the alpha-1,4-glycosylation of chitin by UDP-N-acetyl-D-glucosa
C;Superfamily: chitin synthase chsA
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nypothetical protein SPBC1703.02 with ARID DNA-binding domain [imported] - fission yeasd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chitin synthase (EC 2.4.1.16) C - Aspergillus fumigatus
NAlternaese: chitin-UDP N-acetylglucosaminyltransferase C; CHSC protein
C;Species: Aspergillus fumigatus
C;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
R;Mellado, E.; Aufauvre-Brown, A.; Gow, N.A.R.; Holden, D.W.
Mol. Microbiol. 20, 667-679, 1996
A;Title: The Aspergillus fumigatus chsC and chsG genes encode class III chitin synthases
A;Reference number: JC6015; MUID:96347138; PMID:8736545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-889 <MBL)
A;Cross-treferences: UNIPROT:Q92197; UNIPARC:UPI000012794E; EMBL:X94245; NID:g1197185; PI
A;Experimental source: strain 237
C;Comment: This enzyme belongs to class III zymogen-type enzymes, it is a target for and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description: catalyzes the alpha-1,4-glycosylation of chitin by UDP-N-acetyl-D-glucosa
Superfamily: chitin synthase chsA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-780 <MCD>
A;Cross-references: UNIPROT:Q9P7W8; UNIPARC:UPI00006A13D; EMBL:AL136536; PIDN:CAB66446.
A;Experimental source: strain 972h(-); cosmid c1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Information 2. Schizosaccharomyces pombe
C; Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C; Accession: T50315
R; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert, submitted to the EMBL Data Library, January 2000
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keywords: glycoprotein, glycosyltransferase, hexosyltransferase, zymogen, 524,845/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                   Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%; Score 32; DB 2; Length 889; ilarity 85.7%; Pred. No. 70; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB;
Pred. No. 60;
1; Mismatches
                                                                                                                                                Score 32; DB
Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: chsC
A;Introns: 28/3; 169/2; 289/3; 633/2; 844/3
                                                                                                                                                   80.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.08;
75.08;
                                                                                                                                                                             Local Similarity 85.7
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z25061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GILONVYF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                    GVMQNVR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: SPDB:SPBC1703.02
                                                                                                                                                                                                                                                                          2 GVLQNVR 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: T50315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 2
A;Introns: 38/2
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
                                                                                                                                                                                   Best Loc
Matches
```

셤 ઠે

ö

Gaps

PII B.

2

ద

```
A;Molecule type: DNA
A;Residues: 1-198 <BOW>
A;Cross-references: UNIPARC:UP100001753F3; GB:M82955; NID:g169826; PIDN:AAA33920.1; PID:g
A;Note: sequence extracted from NCBI backbone (NCBIP:75854)
A;Note: sequence extracted chsA
C;Superfamily: chitin synthase chsA
C;Keywords: chitin biosynthesis; glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-198 <BOW>
A;Residues: 1-198 <BOW>
A;Cross-references: UNIPARC:UPI00001753F4; GB:M82946; NID:g168142
A;Note: sequence extracted from NCBI backbone (NCBIP:75851); the sequence shown is from I C;Superfamily: chitin synthase chsA
C;Superfamily: chitin biosynthesis; glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1-195 <BOW>
A,Residues: 1-195 <BOW>
A,Cross-references: UNIPARC:UPI00001753EF, GB:M82948; NID:g168248; PIDN:AAA33381.1; PID:
A,Note: sequence extracted from NCBI backbone (NCBIP:75852)
C,Superfamily: chitin synthase chsA
C,Superfamily: chitin bjosynthesis; glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Bowen, A.R.; Chen-Wu, J.L.; Momany, M.; Young, R.; Szaniszlo, P.J.; Robbins, P.W. Proc. Natl. Acad. Sci. U.S.A. 89, 519-523, 1992
A;Title: Classification of fungal chitin synthases.
A;Reference number: A38192; MUID:92115692; PMID:1731323
A;Accession: A45190
A;Status: not compared with conceptual translation
               chitin synthase (EC 2.4.1.16) CHS2 - Ajellomyces capsulata (fragment)
C;Species: Ajellomyces capsulata, Histoplasma capsulatum
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 03-Nov-2000
C;Accession: H45189
Proc. Natl. Acad. Sci. U.S.A. 89, 519-523, 1992
A;Pitle: Classification of fungal chitin synthases.
A;Reference number: A38192; MUID:92115692; PMID:1731323
A;Accession: H45189
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chitin synthase (EC 2.4.1.16) CH83 - Exophiala jeanselmei (fragment)
C;Species: Exophiala jeanselmei
C;Species: Exophiala jeanselmei
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 03-Nov-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 03-Nov-2000
C;Accession: G45189
Froc. Natl. Acad. Sci. U.S.A. 89, 519-523, 1992
A;Ritle: Classification of fungal chitin synthases.
A;Reference number: A38192; MUID:92115692; PMID:1731323
A;Reference number: A38192; MUID:92115692; PMID:1731323
A;Reference number: A38192; MUID:92115692; PMID:1731323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A45190
chithin synthase (EC 2.4.1.16) CHS2 - Rhinocladiella atrovirens (fragment)
cSpecies: Rhinocladiella atrovirens
C;Species: Rhinocladiella atrovirens
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 03-Nov-2000
C;Accession: A45190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 77.5%; Score 31; DB 2; Length 198; Best Local Similarity 71.4%; Pred. No. 22; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match
Local Similarity 71.4%; Pred. No. 22;
Les 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 GVMQNIR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 GVMQNIR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GVLQNVR 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GVLQNVR 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
G45189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:O9RUZ7; UNIPARC:UPI00000D3E03; GB:AE001971; GB:AE000513; NII
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 1-189 <BON>
A,Cross-references: UNIPARC:UPIO0001753F5
A,Cross-references: UNIPARC:UPIO0001753F5
A,Note: sequence extracted from NCBI backbone (NCBIP:75855); the cited accession number, A,Note: the source is designated as Wangiella dermatitidis
C,Superfamily: chitin synthase chsA
C,Keywords: chitin biosynthesis; glycosyltransferase, hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Bowen, A.R.; Chen-Wu, J.L.; Momany, M.; Young, R.; Szaniszlo, P.J.; Robbins, P.W. Proc. Natl. Acad. Sci. U.S.A. 89, 519-523, 1992
A,Title: Classification of fungal chitin synthases.
A,Reference number: A38192; MUID:92115692; PMID:1731323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                               ö
F;60-113/Domain: nitrogen fixation protein homology <NFH>F;61,88/Binding site: iron-sulfur clusters (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chitin synthase (EC 2.4.1.16) CH83 - Exophilia dermatitidis (fragment) C;Species: Exophilia dermatitidis C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Deinococcus radiodurans
C.Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                   ö
                                                                                                                       Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable pilin, type IV - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                               Score 31; DB 2;
Pred. No. 17;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 2
Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB
Pred. No. 21;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.5%;
71.4%;
                                                                                                                       77.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71...
5; Conservative
                                                                                                                   Query Match 77.5
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 77.5
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                           |:::||:|
GIIENVKF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||:||:|
10 GVMQNIR 16
                                                                                                                                                                                                                                                                               GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVLENVR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GVLQNVR 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-186 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVLQNVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: B45190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B75421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: DR1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
```

RESULT 10

ò g RESULT 11

δ

```
Search completed: June 5, 2006, 22:45:04
Job time : 11.4741 secs
                                                                                                                                                                                                                                                                                                        probable 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A64590
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - Helicobacter pylori (strain C; Species: Helicobacter pylori
A; Variety: strain J99
A; Variety: strain J99
C; Date: 12-Peb-1999 #sequence_revision 12-Peb-1999 #text_change 05-Oct-2004
C; Accession: B71923
R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Nature 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Arecession: B71923
A; Arecession: B71923
A; Accession: B71923
A; Anolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-247 <ARN>
A;Cross-references: UNIPROT:Q9ZLSO; UNIPARC:UPI00000D3648; GB:AE001484; GB:AE001439; NIC
A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:AE000511; NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:025286; UNIPARC:UPI00000D3178; GB:AE000570; GB:AE000511; C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology C;Reywords: farty acid biosynthesis; NAD; oxidoreductase
C;Reywords: farty acid biosynthesis; NAD; oxidoreductase
F;6-186/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: fabG
C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology
                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-247 <TOM>
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Keywords: oxidoreductase
F.6-186/Domain: short-chain alcohol dehydrogenase homology <SAD>
Score 31; DB 2; Length 198;
Pred. No. 22;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.5%; Score 31; DB 2; Length 247; 62.5%; Pred. No. 28; 1; Indels rative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 1; Length 247;
Pred. No. 28;
2; Mismatches 1; Indels
     77.5%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.5.
     Query Match 77.5
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 GALRNIRF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |:|:||
173 GALRNIRF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GVLQNVRF 9
                                                                                                                                            ||:||:|
GVMQNIR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GVLQNVRF 9
                                                                                                                  2 GVLONVR 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

THIS PAGE BLANK (USPTO)

```
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 2
03 PIG
050903 PIG
050903;
07-DEC-2004, i
07-DEC-2004, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
028194 BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT SOST DE CONTROL OF CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDT THE SECOND DESCRIPTION OF SECOND DESCRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 porcine rep
porcine rep
porcine rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sus scrofa
xenopus lae
brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prrsv hnl.
prrsv hb-2(
porcine rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xenopus lae
tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ustilago ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thermoanaer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           candida gla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           porcine rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228194 bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bos taurus
                                                                                                                                                                        5, 2006, 22:09:41; Search time 81.6983 Seconds (without alignments) 101.901 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          porcine porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05u903
07sy94
07sy94
02spg75
02spg77
02spg71
071sa3
071sa3
04y7
04sf75
04sf78
05uf8
5.1.9
Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2849598 seqs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  028194_BOVIN
05U903_FTG
05U903_FTG
07SY84_XENLA
05SPG5_BRARE
TYSP1_HUWAN
TYSP1_HUWAN
TYSP1_MOUSE
071SA3_RAT
080YQ1_MOUSE
04CRS2_MOUSE
04CRS2_MOUSE
04CRS2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TETNG
HUMAN
USTMA
THEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TETNG
CANGA
PRRSV
PRRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRRSV
PRRSV
PRRSV
PRRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRRSV
PRRSV
PRRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8QQW9_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSUUF8
OFPR43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q6TC18
Q91F53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9WBQ4_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6QDR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7TF56
Q99AV5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        048758
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9DY97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4P665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q3CJK9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                US-10-030-735-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                       1 XGVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     704
1549
1034
1172
1457
1457
1457
1457
1457
                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
97.5
97.5
                                                                                                                                                                              June
                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                    OM protein
                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
No.
```

```
ö
Q99bus porcine rep
Q9e8m9 porcine rep
Q9enk5 porcine rep
Q9dln9 porcine rep
Q9dln8 porcine rep
Q9dln8 porcine rep
Q9dlp0 porcine rep
Q9dlp1 porcine rep
Q9p12 preplicase
Q9yn02 preplicase
Q9xn02 preplicase
   porcine rep
porcine rep
porcine rep
porcine rep
p replicase
                                                                                             porcine rep
porcine rep
p replicase
p replicase
burkholderi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige J.J.;
"Opposite regulation of thrombospondin-1 and corticotropin-induced secreted protein/thrombospondin-2 expression by adrenocorticotropic hormone in adrenocortical cells.";
J. Cell. Physiol. 167:164-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96331130; PubMed=8698834;
DOI=10.1002/(SICI)1097-4652(199604)167:1<164::AID-JCP19>3.3.CO;2-0;
Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chambaz E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25015 MW; 90D9EBCE4E6B669C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, X89511; CAA61682.1; -; mRNA.
PIR; S57957; S57957.
G0, G0:0005199; F:erructural molecule activity; IEA.
G0, G0:001155; P:cell adhesion; IEA.
InterPro; IPR013320; ConA like subgrp.
InterPro; IPR003129; Lamimin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                          Q28194 BOVIN PRELIMINARY; PRT; 229 AA. Q28194; 01-NOV-1996, integrated into UniProtKB/TrEMBL. 01-NOV-1996, sequence version 1. 07-FBB-2006, entry version 24. Thrombospondin-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 40; DB 2
llarity 100.0%; Pred. No. 2.2;
Conservative 0; Mismatches
 099BUS_PRRSV

09EBM9_PRRSV

09BLN9_PRRSV

09DLN9_PRRSR

09DLN0_PRRSV

09DLP0_PRRSV

09DLP1_PRRSV

09DLP1_PRRSV

RPOA_PRRSB

RPOA_PRRSB

RPOA_PRRSB

0451709_9BURK

04411M9_9BURK
                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence version 1. entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
   1463
1463
1463
39956
39960
39960
713
713
1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00210; TSPN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||||
192 GVLQNVRF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
   9990.0
9900.0
9900.0
9900.0
9900.0
877.5
877.5
877.5
877.5
```

N

```
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 GVLQNVŘF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GVLQNVRF 9
                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyprinidae; Danio.
NCBI TaxID=7955;
                                                                                                                                                                                                                                                 initiative.";
                                                                                                                                                                                                                                                                                                                                         rissum=whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSSPGS 10 OSS 10
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A KITAUSDERMINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muxzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Halting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blatebley R.W., Touchman J.W., Grene E.D., Dickson M.C.,
Blatebley R.W., Touchman J.W., Grene E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                     Chordata, Craniata, Vertebrata, Euteleostomi,
Laurasiatheria, Cetartiodactyla; Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 40; DB 2; Length 249; 100.0%; Pred. No. 2.4; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                        Zhang K., Mauco G., Hauet T.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 AA; 27560 MW; 465D664BE0329C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY; PRT; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                    EMBL, AY773342; AAV38110.1; -; mRNA.
InterPro; IPR000884; TSP1.
InterPro; IPR018085; TSP 1.
InterPro; IPR010101; VWF C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003, sequence version 1.
07-FEB-2006, entry version 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1705; TSPIREPEAT.
SMART; SM0209; TSP1; 1.
SMART; SM0214; VWC, 1.
PROSITE; PS5092; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS5184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus; Xenopus
      Thrombospondin 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00090; TSP_1; 2. Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                           Name≃Thbs1;
Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GVLQNVRF 9
                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGC64438 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
                                                                                                                                       NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7SY84_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
         ઠ
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barker D.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collegen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-2004, integrated into UniProtKB/TrEMBL.
21-DEC-2004, sequence version 1.
21-DEC-2006, entry (Fragment) .
21-DEC-2006, entry (Fragment) .
21-DEC-2006, entry version 1.
21-DEC-2006,
                                                                                                                                                                                                                                                                                                                                                                        Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 40; DB 2; Length 496;
; Pred. No. 5;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                          MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, BC054970; AAH54970.1; -; mRNA.

GO; GO: 0005198; F: structural molecule activity; IEA.

GO; GO: 0007155; P: cell adhesion, IEA.

InterPro; IPR013120; ConA. like subdrp.

InterPro; IPR003129; Laminin_G_TSP_N.

InterPro; IPR008084; TSP_1.

InterPro; IPR0080884; TSP_1.

Pfam; PP00090; TSP_1.

Pfam; PP00090; TSP_1.

PRINTS; PR01705; TSP_1.2.

PRINTS; SM00219; TSP_1.2.

SMART; SM00210; TSPN; 1.

SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50092; TSPI; 2.
PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; UNKNOWN 1.
SEQUENCE 496 AA, 54843 MW, B4FD2F07CB7EF51B CRC64;
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 40; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSSPGS_BRARE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
nes 8; Conservative
```

;

```
TISSUE=Aortic endothelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221
373
429
490
547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [MRNA].
STRAIN=Holstein; TISSUE=Tooth;
MEDLINE=98173773; PubMed=9507064; DOI=10.1016/S0167-4838(97)00188-X;
UGHOO A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
Inoue H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSPI BOVIN STANDARD; PRT; 1170 AA. 028178; Q28178; Q28179; Q1-NOV-1997, integrated into UniProtKB/Swiss-Prot. 01-DEC-2000, sequence version 2. Q7-MAR-2006, entry version 56. Thrombospondin-1 precursor. Thrombospondin-1 precursor. Bos taurus (Bovine). TSP1; Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bos. Bos. Company 2. Decora; Bovidae; Bos. Company 2. Decora; Bovidae; Bovinae; Bovidae; Bovinae; Bos. Company 2. Decora; Bovidae; Bov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 40; DB 2; Length 1090; 100.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1090 AA; 120978 MW; 5A9320504A22D836 CRC64;
                                EMBL; AL928866; CAI20599.1; -; Genomic_DNA.
SMR; OSSPG5; 751-804, 754-1089.
Ensembl; ENSPG6000001010785; Danio rerio.
GO; GO:0005509; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0008210; F:heparin binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:000515; P:cell adhesion; IEA.
InterPro; IPR013120; ConA_like_subgrp.
InterPro; IPR002048; EF hand_Ca_bd.
InterPro; IPR002010; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000865; TSP 1.
InterPro; IPR000865; TSP 1.
InterPro; IPR000865; TSP 1.
InterPro; IPR000865; TSP 2.
InterPro; IPR000865; TSP 2.
Pfam; PF00096; EGF; 1.
Pfam; PF00091; TSP 1; 2.
Pfam; PF00093; TSP 2; 1.
Pfam; PF00093; TSP 2; 1.
PRMART; SM00181; EGF; 2.
SWART; SM00210; TSP1; 2.
PROSITE; PS01066; EGF 2; 1.
PROSITE; PS01066; EGF 2; 1.
PROSITE; PS01066; EGF 2; 1.
PROSITE; PS01066; TSP1; 2.
PROSITE; PS01066; UWFC 1; 1.
                                                                                                                                                                                                                                                                        InterPro; IPR000742; EGF 3.
InterPro; IPR001881; EGF Ca bd.
InterPro; IPR00509; EGF like.
InterPro; IPR013032; EGF like reg.
InterPro; IPR03129; Laminin G TSP N.
InterPro; IPR00884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 GVLONVRF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSP1_BOVIN

ID TSP1_BG
DT 01-NOV
DT 01-NDR
DT 01-NDR
DT 07-MAR
DE Thromb
GN Name=T
CO Eukary
OC PECOTA
OC PECOTA
OC PECOTA
OC NAMMA
IN [1]
RP NUCLEC
RC STRAIN
RA UBDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
The Good of Device thromospondin 1 and its expression in doctonologues and predentin. 19

Good of Device the thromospondin 1 and its expression in doctonologues and predentin. 19

Richalm. Biophys Acca 1382;17-22(139).

Richalm. Since the Sacurage (Wesh) or 1-1a AND 710-1170.

Richalm. Since the Sacurage (Wesh) or 1-1a AND 710-1170.

Richalm. Since the Sacurage (Wesh) or 1-1a AND 710-1170.

Richalm. Since the Sacurage (Wesh) or 1-1a AND 710-1170.

Richalm. Since the Sacurage (Wesh) or 1-1a AND 710-1170.

Richalm. Since the Sacurage (Wesh) or 1-1a AND 710-1170.

Richalm. Since the Sacurage of Sacurage (Wesh) or 1-1a AND 710-1170.

Colling and sequencing of bovine thromospondin stimulatory effect of Call-to-matrix increations con hind of Educal in darking the Call-to-matrix increations controlled and Administration of Call-to-matrix increations controlled and Call-to-matrix increations controlled and Call-to-matrix increations controlled the Call-to-matrix increations controlled and Call-to-matrix increations increation increatio
```

```
NUCLEOTIDE SEQUENCE OF 1-374.
MEDLINE=86287276; PubMed=3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
"Characterization of a cDNA encoding the heparin and collagen binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 1-166.
MEDLINE=89291870; PubMed=2544587;
Laherty C.D., Gierman T.M., Dixit V.M.;
"Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.";
J. Biol. Chem. 264:11222-11227(1989).
                                                                                                           "The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87157592; PubMed=3030396; Kobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.; "Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=16335952; DOI=10.1021/pr0502065;
Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
Moore R.J., Smith R.D.;
Minan plasma N-glycoproteome analysis by immunoaffinity subtraction,
Hydrazide chemistry, and mass spectrometry.";
J. Proteome Res. 4:2070-2080(2005).
J. Proteome Res. 4:2070-2080(2005).
J. FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
laminin, type V collagen and integrins alpha-V/beta-1, alpha-
                                                                                                                                                                                                                MUCLEOTIDE SEQUENCE.
MEDLINE=89139500; PubMed=2918029; DOI=10.1083/jcb.108.2.729;
Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L.,
Hennessy S.W., Rocwein P., Frazier W.A.;
"Complete thrombospondin mRNA sequence includes potential regulatory
sites in the 3' untranslated region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22338361; PubMed=11450399; DOI=10.1021/bi026463u;
Huwiler K.G., Vestling M.M., Annis D.S., Mosher D.F.;
"Biophysical characterization, including disulfide bond assignments,
of the anti-anglogenic type 1 demains of human thrombospondin-1.";
Biochemistry 41:14329-14339(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLECTIDE SEQUENCE OF 1028-1170.

La Fleur M., Jobin C., Gauthier J., Kreis C.G.;

La Fleur M., Jobin C., Gauthier J., Kreis C.G.;

Expression of thrombospondin in chronic inflammation: neutrophils
from synovial fluids synthesize a novel 3.9 kD TSP mRNA.";

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21125860; PubMed=11067851; DOI=10.1074/jbc.M008073200; Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J., Mosher D.F., Peter-Astalinic J.; "C-mannosylation and O-fucosylation of the thrombospondin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYDRATE-LINKACE SITES TRP-385; SER-394; TRP-438; TRP-441; THR-450; TRP-498 AND THR-507.
TISSUE=Platelet;
  [1]
NUCLECTIDE SEQUENCE.
TISSUB=Endothelial cell;
MEDLINE=87057617;
Pubmed=2430973; DOI=10.1083/jcb.103.5.1635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYDRATE-LINKAGE SITES ASN-248 AND ASN-1067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 276:6485-6498(2001).
                                                                                                                                                                            Cell Biol. 103:1635-1648(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 25:8418-8425(1986).
                                                                                                                                                                                                                                                                                                                                                 Cell Biol. 108:729-736(1989)
                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 1-397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        module."
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapions (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                             calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                           (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                           (Potential)
                                                                                                                                                                                                                                                                                   (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                 (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 40; DB 1; Length 1170;
EGF-like 1.

EGF-like 2. calcium-binding (F
EGF-like 3.

TSP type-3 1.

TSP type-3 2.

TSP type-3 4.

TSP type-3 4.

TSP type-3 4.

TSP type-3 4.

TSP type-3 7.

TSP type-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ODD6ADF3E5FA031A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P07936; 015667;
01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
01-AUG-1988, sequence version 1.
07-MAR-2006, entry version 78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129534 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=THBS1; Synonyme=TSP, TSP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombospondin-1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    833
856
894
930
1167
805
                                                                                                                                                                                                                                                                                                                                708
1067
1085
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413
484
489
474
541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVLONVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451
462
504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISP1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SULFID
                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                     DOMAIN
                                                                                                               DOMAIN
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                             REGION
                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 6
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

ઠે

CXCCCSCCCCCX

Tue Jun

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Engaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                   calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
TSP type-1 3.
EGF-like 1.
EGF-like 2.
EGF-like 2.
EGF-like 3.
EGF-like 3.
TSP type-3 1.
TSP type-3 3.
TSP type-3 3.
TSP type-3 5.
TSP type-3 5.
TSP type-3 6.
TSP type-3 6.
TSP type-3 7.
TSP type-3 6.
TSP type-3 7.
TSP type-3 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCLEOTIDE SEQUENCE.
MEDLINE=92128941; PubMed=1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J., Jenkins N.A.;
"Chakins N.A.; "Characterization of the murine thrombospondin gene.";
Genomics 11:587-600(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 40; DB 1; Length 1170; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
TSP1 MOUSE
TSP2 MOUSE
TSP344;

DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR.2006, entry version 1.
DT 07-MAR.2006, entry version 57.
DE Thrombospondin-1 precursor.
GN MASS muschulus (Mouse).
GN MASS muschulus (Mouse).
GC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu GN MASS muschulus (Mouse).
GC Muschidea; Muridae; Muschontoglires; Glires; Rodentis OC Murchoolea; Muridae; Muschontoglires; Glires; Rodentis NoticeOrldea; Murinae; Muschontoglires; Muschontoglines; Muschontoglines; Muschontoglines; Muschontoglines; Muschontoglines; RN MEDLINE-92128941; PubMed=1774063;
RN MEDLINE-92128941; PubMed=1774063;
RA Johnkins N.A.; Characterization of the murine thrombospondin gene.",
RT "Characterization of the murine thrombospondin gene.",
RL Genomics 11:587-600(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interchain (Probable)
Interchain (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5444423
4423
4484
5444
6414
6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                               438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              708
1067
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507
                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                             DOMAIN
      DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                     DOMAIN
                                                                                              DOMAIN
                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                             DOMAIN
         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
```

ø

```
EGF_like.
EGF_like_reg.
Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                             IPR006209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
926
3248
3248
1067
274
274
4451
4451
462
508
                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISULFID
ISULFID
ISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
REGION
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
       NUCLECTIDE SEQUENCE.

AN EDLINE=92147683; PubMed=1371115;
AN MEDLINE=92147683; PubMed=1371115;
AN EDLINE=92147683; PubMed=1371115;
AN EDLINE=92147683; PubMed=1371115;
AN EDLINE=9214760; PubMed=29800din 2 sequence and expression during cell growth and development.";

A. Biol. Chem. 267:3274-3281(1992)."

B. Biol. Chem. 267:3274-3281(1992)."

AN WEDLINE=9037546; PubMed=2398070;
BOURTEON P., Alfi D., Devarayalu S., Framson P., Li P.;
AN EDLINE=9037546; PubMed=2398070;
BOURTEON P., Alfi D., Devarayalu S., Framson P., Li P.;
AN EDLINE=9037546; PubMed=2398070;
BOURTEON P., Alfi D., Devarayalu S., Framson P., Li P.;
AN ELONGE OF 1-490.

AN EDLINE 9037546; PubMed=2398070;
BOURTEON BOURDE OF 1-937.

AN EDLINE 9037546; PubMed=298070;
BAR PROTEIN SEQUENCE OF 1-937.

AN EXPRESSION and initial characterization of recombinant mouse thrombospondin 1 and thrombospondin 3.";

AN EDLINE 9037546 Glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, 1 am and and initial characterization of recombinant mouse thrombospondin 3.";

FEBS Lett. 387:36-41(1996).

C. Imminn, type V collagen and integrins alpha-V/beta-1, alpha-V/beta-1 and and integrins alpha-V/beta-1.

AND EDLIARITY: Contains 1 TSP V-terminal (TSPN) domain.

C. SIMILARITY: Contains 1 TSP V-type-1 domains.

C. SIMILARITY: Contains 1 TSP V-type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M62450; AAA50611.1; -; Genomic_DNA.

EMBL; M62451; AAA50611.1; -; Genomic_DNA.

EMBL; M62451; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62453; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62453; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62454; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62455; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62457; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62457; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62459; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62460; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62460; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62461; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62461; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62463; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62463; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62464; AAA50611.1; JOINED; Genomic_DNA.

EMBL; M62469; AAA5061.1; JOINED; Genomic_DNA.

EMBL; M62698; AAA4031.1; JOINED; Genomic_DNA.

EMBL; M626
```

```
TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 3.
TSP type-3 2.
TSP type-3 2.
TSP type-3 3.
TSP type-3 4.
TSP type-3 5.
TSP type-3 5.
TSP type-3 6.
TSP type-3 6.
TSP type-3 6.
TSP type-3 7.
TSP ty
INTERPRO 1 FR003229; EGF 134E reg.

RINGERPO; 1PR003129; Laminin G TSP.N.

RINGERPO; 1PR003129; Laminin G TSP.N.

RINGERPO; 1PR003084; TSP.1.

RINGERPO; 1PR000081; TSP.1.

RINGERPO; 1PR00009; TSP.2.

RINGERPO; 1PR00009; EGF 2.

REAM; PF00009; EGF 2.

REAM; PF00009; TSP.3; 12.

REAM; PR0012; TSP.3; 12.

REAM; PR0012; TSP.3; 12.

REAM; SM0210; TSP.3; 13.

REAM; SM0210; TSP.1; 3.

REAM; REAM; SM0210; TSP.1; 3.

REAM; REAM; SM0210; TSP.1; 3.

REAM; REAM; REAM; REG.2; 1.

REAM; REA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombospondin-1.
/FTId=PRO 0000035843.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
```

7

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY STRAIN-CS7BL/60; TISSUE-Aorta and vein;
RX CATHOLE SEQUENCE.

RA CATHINCI P. Kastawama S., Gough J., Frith M.C., Maeda N.,
RA CATHINCI P. Kastawama S., Gough J., Frith M.C., Maeda N.,
RA Cyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Bajic V.B., Brenner S.E., Aldinis V., Allen J.E.,
Bajic V.B., Brenner S.E., Aldinis V., Allen J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N.,
Ransal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chaik A.M.,
RA Crowe M.L., Dalla E., Dalrymple B.P., Fagiolini M., Faulkner G.,
RA Crowe M.L., Dalla E., Dalrymple B.P., Fagiolini M., Faulkner G.,
RA Crowe M.L., Dalla E., Dalrymple B.P., Fagiolini M., Faulkner G.,
RA Georgii-Hemming P., Christoffels A., Cluterbuck D. R.,
R. Farlor C.F., Fukushima T., Puruno M., Pitaki S., Gariboldi M.,
R. Farlor C.F., Fukushima T., Puruno M., Ikeo K., Iwama T.,
R. Marnapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
Alt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
A Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
A Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
A Kurochkin I.V., Lareau L.F., Nakano M., Marchionni L.,
A Kurochkin I.V., Lareau L.F., Dazarevic D., Lipovich L., Liu J.,
A Mctagui-Tabar S., Madan Babu M., Madano M., Marchionni L.,
A Matsuda H., Mashiguchi S., Nishikawa S., Nori F., Ohara O.,
A Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y.,
A Shibata Y., Shimada H., Shimada K., Silva D., Siesla L., Yagi K.,
A Tammoja K., Tan S.L., Taylor M.S., Taylor D., Siesler J., Yagi K.,
A Tammoja K., Tan S.L., Taylor M.S., Tegener J., Taki K.,
A Tammoja K., Tan S.L., Taylor M.S., Taylor M.S., Tegener J., Yagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Musimae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J; TISSUE=Aorta and vein;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530055N06 product:thrombospondin 1, full insert sequence.
                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                            100.0%; Score 40; DB 1; Length 1170; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                        0443E493615E7F06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
Fy similarity.
                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
03TR40 MOUSE
1D Q3TR40_MOUSE PRELIMINARY; PRT; 1170 AA.
AC 93TR40_
                                                                                                                                      L (in Ref
                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2005, sequence version 1. 07-FEB-2006, entry version 5.
                                                                                                                                                      1170 AA; 129647 MW;
                                                                                                                                                                                                            Local Similarity 100.
  774
797
833
856
894
930
1167
                                                                                                                                                                                                                                                                                                           210 GVLQNVRF 217
                                                                                                                                                                                                                                                                       2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Thbs1;
                  DISULFID
                                                                            DISULFID
    DISULPID
                                                                                                              DISULFID
                                                                                                                                                                                              Query Match
                                                          DISULFID
                                                                                                                                                      SEQUENCE
                                                                                                                                    CONFLICT
                                                                                                                                                                                                                  Best Loca
Matches
    27777777
                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                         ઠે
```

As Tramminish H. Zabarrowsky E. Zhu S. Zimmer A. Hidde W. Bulle C.,
Crimonol S. W. Tesadale R.D. Lill B.T. Brusic V. Quackenbush J. B.
Rablested C. Martick C. J.S. Hame D. Lill B.T. Brusic V. Quackenbush J. B.
Rablested C. Martick C. J.S. Hame D. Lill B.T. Brusic V. Quackenbush J. B.
Rablested C. Martick C. J.S. Hame D. K. Statch I. S. Askewa T. B.
Rablested C. Martick C. J. Statch I. S. Statch I. S. Askewa T. B.
Rablested C. Martick C. J. Statch I. S. Statch I. S. Statch I. S. Statch I. S. Martick I. S. Statch I. S. St

ω

ö

Gaps

ö

Indels

ö

0; Mismatches

100.0%;

100.0%; Score 40; DB 2; Length 1170;

```
Best Local Similarity 100.
Matches 8; Conservative
                                                                                210 GVLQNVRF 217
                                                       2 GVLQNVRF 9
                                                                                                                                                                                                                             Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
Query Match
                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                    STRAIN-C57BL/6J; TISSUE-Aorta and vein;
MEDLINE=20499174; PubMed=11042159; DOI=10.1101/gr.145100;
Garninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                              MUCLIALINE STANDARD STRAIN ALTERNAL AND VEIN;
Shibbata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Sumahata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumioto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
"RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Muzata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AK163092; BAE37190.1; -; mRNA.
MGT; MGI:98737; Thbs1.
O; GO:0005615; C:extracellular space; IDA.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0005615; P:negative regulation of angiogenesis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1170 AA; 129619 MW; 55BF04A20D91B194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; irrovozas; Interpro; IRRO 3. Interpro; IRRO 1042; EGF 3. Interpro; IRRO 1041; EGF Cabd. Interpro; IRRO 1302; EGF like reg. Interpro; IRRO 1302; EGF like reg. Interpro; IRRO 1303; EGF like reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01186; EGF 2; UNKNOWN 1. PROSITE; PS50026; EGF 3; 2. PROSITE; PS50092; TSP1; 3. PROSITE; PS01208; VWFC 1; 1. PROSITE; PS01208; VWFC 2; 1. SEQUENCE 1170 AA; 129619 MW; 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000884; TSP1.
InterPro; IPR000805; TSP 1.
InterPro; IPR000805; TSP 2.
InterPro; IPR001007; VWF C.
Pfam; PF001007; VWF C.
Pfam; PF00009; TSP 1; 3.
Pfam; PF02415; TSP 3; 12.
Pfam; PF02415; TSP 2; 12.
Pfam; PF02415; TSP 2; 12.
Pfam; PF05735; TSP C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1705; TSPIREPEAT.
SWART; SMO0181; EGF; 3.
SMART; SMO0209; TSP1; 3.
SMART; SMO0210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006210; EGF
                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley; Iwabu S., Nakamura K., Murakami Iwabu A., Hirohata S., Kusachi S., Nakamura Y., Tsuji T. Tsuji T. Tsuji T. Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129671 MW; 6F38D3DCE733060F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SME OT SERVING TO SERVING THE SERVING THE SERVING TO SERVING TO SERVING THE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 2; 100.0%; Pred. No. 13;
QTISA3 RAT PRELIMINARY; PRT; 1170 AA. Q71SA3.
05-JUL-2004, integrated into UniProtKB/TrEMBL.05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO1186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50022; TSP1; 3.
PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF309630; AAQ14549.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSP1REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Query Match
Best Local Similarity luv.v.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PP00008 EGF; 7. Pfam; PP00009; TSP 1; 3. Pfam; PP00009; TSP 1; 12. Pfam; PP05715; TSP 2; 12. Pfam; PP05735; TSP C; 1. Pfam; PP00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00181; EGF; 3.
SMART; SM00209; TSP1; 3.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

σ

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CSTBL/6; TISSUE-Brain;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B. Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BMBL; BC050917; AAH50917.1; -; mRNA.
HSSP; P07996; ILSI.
SMR; Q807Q1; 835-1170.
Ensembl; ENSMUSG0000040152; Mus musculus.
MGI; MGI:98737; Thbs1.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0016525; P:negative regulation of angiogenesis; IDA.
InterPro; IPR006210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                      01-JUN-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                        \overline{QB} 0 VQ1 MOUSE PRELIMINARY; PRT; 1171 AA. Q80 VQ1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000742; EGF 3.
InterPro; IPR001881; EGF Ca bd.
InterPro; IPR001881; EGF Ca bd.
InterPro; IPR001803; EGF like reg.
InterPro; IPR001803; EGF like reg.
InterPro; IPR000884; TSP1.
InterPro; IPR008859; TSP1.
InterPro; IPR008859; TSP2.
InterPro; IPR008859; TSP2.
                                                                                                                                                                                                              01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00008; EGF; 2.
Pfam; PF00090; TSP_1; 3.
210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                            Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                 Name=Thbs1;
                                                                                                                     MOUSE
                                                                                      RESULT 10
080 YOL
080 YOL
080 YOL
090 
                          셤
```

```
MEDINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hang J., Haieh F., Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Wilalano D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Faby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Malkealey R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., H. Schnerth A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculis (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombospondin 1 (Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library, clone:G930018021 product:thrombospondin 1, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CZECH II; TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 2; Length 1171; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1171 AA; 129690 MW; 12E077B50C64E2D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1. 07-FEB-2006, entry version 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBCGB2 MOUSE PRELIMINARY; PRT; 1171 AA. QBCGB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
Pfam; PF02412; TSP_3; 12.
Pfam; PF06735; TSP_C; 1.
Pfam; PF00093; VWC; 1.
PRINYS; PR01705; TSPEREPEAT.
SMART; SM00181; EGF; 3.
SMART; SM00210; TSPI; 3.
SMART; SM00210; TSPI; 3.
SMART; SM00214; VWC; 1.
PROSITE; PS00024; VWC; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50036; EGF 3; 2.
PROSITE; PS50184; VWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_1; UNKNOWN_1.
SEQUENCE 1171 AA; 129690 MW; 12E077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8CGB2
```

Ambes-Impionabato A., Apweiner R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk G.C., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., A dingersa T.R., Garpinoldi M., Faulkner C.P., Fukushima T., Puruon M., Futaki S., Gariboldi M., Radali D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Attano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Kurochkin I.V., Lareau L.F., Mignon F., Myake S., Morris K., Mutchkin I.V., Lareau L.F., Nakano M., Nakauchi H., Ng P., Mulder N., Nakano M., Nakauchi H., Ng P., Mulder N., Nakano M., Nakauchi H., Ng P., Notlason R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Motaqui-Tabar S., Mulder N., Nakano M., Serosi G., Pevesi G., TISSUE=Manmary gland;

X MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

A MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

A MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

A Mikaido I., Osatoo N., Saitoo R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., A Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Baisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gasterland T., Garsic C., Godzik A., Gough J., Garsic C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D., Armai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., TISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999). Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005). "The transcriptional landscape of the mammalian genome."; TISSUE=Mammary gland; PubMed=16141073; DOI=10.1126/science.1112009; IISSUE=Mammary gland; PubMed=16141072; DOI=10.1126/science.1112014; Science 309:1559-1563(2005) SEQUENCE NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE NUCLEOTIDE

TISSUB-Manmary gland;

KRUINE=2108566) PubMed=11217851; DOI=10.1038/35055500;

KRUINE=2108566) PubMed=11217851; DOI=10.1038/35055500;

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov B., Kochiwa H.,

Kadota K., Matsuda H.P., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mondone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F.,

Narakiawa-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

"Functional annotation of a full-length mouse cDNA collection.", TISSUE-Mammary gland;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of Cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000). Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravaai T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Serou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilmid L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yang L., Yang I., Yang L., Kana T., Komo H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S., Haya A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sakai K. TISSUE=Mammary gland;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K, Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K, Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Sakaguchi S., Kara A., Hayashizaki Y.; Ritkn integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000). Nature 409:685-690(2001). Nature 420:563-573(2002). NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE

```
InterPro; IPR003129;
InterPro; IPR000884;
InterPro; IPR008085;
InterPro; IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell adhesion.
NON TER 1171
SEQUENCE 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSP1 XENLA
P35448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSP1 XENLA
      DAR WAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The pubmed-15495914; DOI-10.1038/nature03025;

The pubmed-15495914; DOI-10.1038/nature0315;

The pail of the pubmed o
                                                                                                                                                                                                                                                                                              ô
                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2006, entry version 8. Chromosome 10 SCAF15019, whole genome shotgun sequence. (Fragment) ORFNames=GSTENG00032374001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                    100.0%; Score 40; DB 2; Length 1171; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; CAAE01015019; CAG10667.1; -; Genomic_DNA.
SMR; QARLRS; 834-897, 837-1171.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0008201; F:heparin binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:estructural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OGRANGE TETNG

OFFICE TETNG

OFFICES TETNG

OFFICES TETNG

OFFICES TETNG

OFFICES TETNG

OFFICES TETNG

DE CHOROSOME 10 SCAF15019, whole genome shotgun see Chromosome 10 SCAF15019, whole genome per chromosome 10 SCAF15019, whole genome shotgun see Chromosome 10 SCAF15019, whole genome ScAF15019, see Chromosome 10 SCAF15019, whole genome ScAF15019, see Chromosome 10 SCAF15019, see Chromosome 10 SCAF15019, see Chromosome Chromosome Chromosome Chromosome Chromosome Chromosome Genome ScAF15019, see Chromosome Chromosome Genome ScAF15019, see Chromosome ScAF15019, see Chromosome ScAF15019, welseenbach JJ, RA MINCKET P., Lander B., Wassenbach JJ, RA MINCKET P., Lander B.S., Wassenbach JJ, ROSE C C CONTIGUE SEQUENCE.

REMBIGGENBARK/DDBJ whole genome shocgun (WGS CC CONTIGUE BEQUENCE TO CONTISS) BA-BBJ, BFSTUCHCENBARK/DDBJ GENOMED SEQUENCE TO CONTISS, PECTICUL SECUENCE SEC
                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                             EMBL; BC042422; AAH42422.1; -; mRNA.
EMBL; AK145202; BAE26293.1; -; mRNA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                     Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                           210 GVLÓNVRF 217
                                                                                                                                                                                                                                                                                                                                                     2 GVLQNVRF 9
2222888
                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                     a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Urry L.A., Ramos J., Duquette M., Desimone D.W., Lawler J.;

"Cloning, characterization and expression of thrombospondin-1 in
"Cloning, characterization and expression of thrombospondin-1 in
"Cloning, characterization and expression of thrombospondin-1 in
"Submitted (May-1993) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
laminin, type V collagen and integrins alpha-V/beta-1, alpha-
V/beta-3 and alpha-IIb/beta-3 (By similarity).

-!- SUBUNIT: Homotrimer; disulfide-linked.

-!- SIMILARITY: Contains 3 EGF-like domains.

-!- SIMILARITY: Contains 1 TSP C-terminal (TSPN) domain.

-!- SIMILARITY: Contains 3 TSP type-1 domains.

-!- SIMILARITY: Contains 7 TSP type-1 domains.

-!- SIMILARITY: Contains 7 TSP type-3 domains.

-!- SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 40; DB 2; Length 1171; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1171 AA; 129304 MW; 865F3749693F7FCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L04278; -; NOT_ANNOTATED_CDS; mRNA.
HSSP; P07996; 1LSL.
SMR; P35448; 552-1172.
                                                                                                             Pfam; PF00008; EGF; 1.

Pfam; PF00009; TSP; 1.

Pfam; PF00009; TSP; 1.

Pfam; PF00135; TSP; 2.

Pfam; PF00135; TSP; 2.

Pfam; PF00175; TSP; 2.

PRINTS; PR01705; TSP; 2.

SMART; SM00181; EGF; 2.

SMART; SM00219; TSP1; 3.

SMART; SM00214; VWC; 1.

PROSITE; PS01186; EGF; 2; UNKNOWN 1.

PROSITE; PS01008; VWC; 1.

PROSITE; PS01008; VWC; 1.

PROSITE; PS01008; VWC; 1.

PROSITE; PS01008; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR013320; ConA_like_subgrp.
InterPro; IPR006210; EGF.
Laminin_G_TSP_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994, sequence version 1.
07-MAR-2006, entry version 54.
Thrombospondin-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (enopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=thbs1; Synonyms=tsp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 GVLQNVRF 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GVLQNVRF 9
```

ö

```
PUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

PubMed=15496914; DOI=10.1038/nature03025;

A Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

A Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Cruand C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

Parra G., Lardier G., Chapple R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Mincker P., Lander B.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
21-FEB-2006, entry version 1.
Chromosome 14 SCAF14723, whole genome shotgun sequence. (Fragment). ORFNames=GSFENG0002297601;
Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Rukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Tetraodonipa; Acanthognerygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an
-- EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 1; Length 1173; 100.0%; Pred. No. 13; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                      A9F036D6516C0F24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, CAAE01014723; CAG03524.1; -; Genomic_DNA.
SMR; Q48758; 811-1148.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:000515; F:protein binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:structural molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q4S758_TETNG PRELIMINARY; PRT; 1193 AA. 048758;
                               similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                               similarity
similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
681 692 By 93
708 716 By 93
727 741 By 93
757 777 By 93
780 800 By 93
816 836 By 93
839 859 By 93
877 897 By 93
949 1170 By 83
1173 AA, 130020 MW; 2
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100 es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 GVLQNVRF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GVLQNVRF 9
  DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                            DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
Q4S758_TET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HID DRAWN DR
     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
TSP type-1 3.
EGF-like 1.
EGF-like 2.
EGF-like 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 4.
TSP type-3 4.
TSP type-3 6.
TSP type-3 7.
TSP type-3 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heparin-Chinding (Potential).

Cell attachment site (Potential).

N-linked (GlCNAC...) (Potential).

By similarity.

By similarity.
                    InterPro; 1PR000184; EGF Ca bd.
InterPro; 1PR006209; EGF like.
InterPro; 1PR006209; EGF like.
InterPro; 1PR0013129; Edminin_G_TSP_N.
InterPro; 1PR0013129; Laminin_G_TSP_N.
InterPro; 1PR0013129; Laminin_G_TSP_N.
InterPro; 1PR001885; TSP_1.
InterPro; 1PR001805; TSP_1.
InterPro; 1PR001007; VWF_C.
InterPro; IPR001007; TSP_1.3.
INTERPRO; IPR00107; TSP_1.3.
INTERPRO; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombospondin-1.
/FTId=PRO_000035844.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential
EGF 3.
EGF Ca bd.
EGF like.
EGF like reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   feparin-binding; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
```

```
Search completed: June 5, 2006, 22:42:45
Job time : 82.6983 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
    NA CARANTA A CAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Aorta endothelial cell;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 40; DB 2; Length 1193; Local Similarity 100.0%; Pred. No. 13; les 8; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1193 AA; 133256 MW; 6E8781648FCEC7F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB209912; BAD93149.1; -; mRNA.
SMR; Q59E99; 886-939, 889-1225.
Ensembl; ENSGG0000137801; Homo sapiens.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005119; F:protein binding; IEA.
GO; GO:0005119; F:protein binding; IEA.
GO; GO:0005129; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IRR006210; EGF.
InterPro; IRR006210; EGF.
InterPro; IRR006210; EGF.
InterPro; IRR00611; EGF.
InterPro; IRR00811; EGF.
InterPro; IRR008811; EGF.
InterPro; IRR00811; EGF.
INTERPROSENTE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15

059899 HUMAN

TO 058899 HUMAN

DT 26-APR-2005, integrated into UniProtKB/TrEMBL.

DT 26-APR-2005, sequence version 1.

DT 21-EBB-2006, entry version 10.

DE Thrombospondin 1 variant (Fragment).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebr.

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebr.

OC HOMO.

OX NCBL TaxID=9606;

RN 1(1)

RN 1(1)

RN 1(1)

RN 1(1)

RN 10-EBCTIBE SEQUENCE.

RA TOLGEOTIBE SEQUENCE.

RA TOCKI Y. TOYOda A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYOda A., Takeda T., Sakaki X., Tan.

RA TOCKI Y. TOYOda A., Takeda T., Sakaki X., Tan.

RA TOCKI Y. TOYOda A., Takeda T., Sakaki X., Tan.

RA TOCKI Y. TOYOda A., Takeda T., Sakaki X., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki X., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki X., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki X., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki X., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYODA A., Takeda T., Sakaki Y., Tan.

RA TOCKI Y. TOYODA A., TAKEDA T., MANA.

DR GO: GO: 0000510; F: Properin binding; IEA.

DR GO: GO: 0000510; EGF.

DR GO: GO: 00001891; EGF.

DR GO: GO: 00001891; EGF.

DR GO: GO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-2005, integrated into UniProtKB/TrEMBL.
                                       InterPro; IPR000742; EGF 3.
InterPro; IPR001881; EGF_Ca bd.
InterPro; IPR013032; EGF_like reg.
InterPro; IPR003129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01186; EGF 2; UNKNOWN 1. PROSITE; PS0026; EGF 3; 2. PROSITE; PS50026; TSPI; 3. PROSITE; PS501808; VWPC 1; 1. PROSITE; PS50184; VWPC 2; 1.
                                                                                                                                                                                                                       InterPro; IPR000884; TSP1...
InterPro; IPR001005; VWF_C.
Pfam; PP00008; BGF; 2.
Pfam; PP00009; TSP_1; 3.
Pfam; PF005735; TSP_C; 1.
Pfam; PF005735; TSP_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIRITS, PRO1705; TSPREPEAT.
SMART; SM00181; EGF; 2.
SMART; SM00209; TSP1; 3.
SMART; SM00210; TSP1; 3.
SMART; SM00210; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 GVLQNVRF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 40; DB 2; Length 1225; 100.0%; Pred. No. 14; 0; Indels cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1225 AA; 134849 MW; 9888B16E57157B12 CRC64;
EGF like.
EGF like reg.
Laminin G TSP N.
                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50026; TSPĪ; 3.
PROSITE; PS501208; WWFC 1; 1.
PROSITE; PS50184; WWFC 2; 1.
Cell adheaton; EGF-11ke domain.
NON TER 1.25 AA; 134849 MW;
                                        InterPro; IPR003129; Laminin GinterPro; IPR003129; Laminin GinterPro; IPR003129; TSP1.
InterPro; IPR003084; TSP1.
InterPro; IPR003087; tsp3.
InterPro; IPR003087; tsp3.
InterPro; IPR003087; tsp2.
Pfam; PF020129; TSP 1; 3.
Pfam; PF02412; TSP 1; 3.
Pfam; PF02412; TSP 1; 3.
Pfam; PF02412; TSP 3; 12.
Pfam; PF02033; TSP 7; 1.
Pfam; PF02033; TSP 7; 1.
Pfam; PF02033; TSP 1; 3.
SWART; SW00219; TSP1; 3.
SWART; SW00210; TSP1; 3.
SWART; SW00210; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 GVLONVRF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
```

THIS PAGE BLANK (USPTO)

```
US-95-93-93-83-4-97, Application US/09939853A

Sequence 97, Application US/09939853A

Patent No. 6989232

GENERAL INFORMATION:

APPLICANT: Burgess et al.

TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099

CURRENT PAPLICATION NUMBER: US/09/939,853A

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/269,191

PRIOR FILING DATE: 2001-08-25

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 GVLQNVRF 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 482
LENGTH: 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 482, App Sequence 97, Appl Sequence 20, Appl Sequence 20, Appl Sequence 350, Appl Sequence 350, App Sequence 5916, Ap Sequence 5916, Ap Sequence 672, App Patent No. 5405943 Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 58, Appl Sequence 58, Appl Sequence 2342, App Sequence 2342, App Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appli Sequence 15, Appli Sequence 6, Appli Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43314, A
164, App
20870, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                5, 2006, 22:43:07; Search time 17.9224 Seconds (without alignments) 43.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMC_Celerra_SIDS3/ptodata/2/jaa/5_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/jaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5405943-4
US-08-928-692-59
US-08-319-972-59
US-09-319-972-59
US-09-319-972-58
US-09-248-796A-25342
US-10-094-749-3042
US-09-611-616-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-919-853A-98
US-08-313-288B-20
US-09-657-472-2
US-09-949-002-350
US-09-270-767-42057
US-09-248-796A-16180
US-09-621-976-5916
US-09-538-092-752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-670-141-6
US-09-270-767-43314
US-09-769-787-164
US-09-252-991A-20870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-489-039A-11916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-543-681A-6072
                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                           650591 seqs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 08
Maximum Match 10
                                                                                                                                                                                                                              US-10-030-735-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                         1 XGVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                831
11170
11170
11170
11170
731
484
484
486
490
490
911
9116
9116
604
604
604
615
                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
10000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1
                                                                                                                                        June
                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein
                                                                                                                                                                                                                                                                             Seguence:
                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
No.
```

```
Sequence 482, Application US/09949002

Sequence 482, Application US/09949002

Patent No. 690016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: AND USES THERROF

FILE REFERENCE: CLO00790

CURRENT FILING DATE: 2000-01-28

PRIOR PILIAG DATE: 2000-01-28

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                              15, Appl
9, Appli
9, Appli
9, Appli
5053, Ap
                                                                                                                                                                                                                                                                                                                                           4310, Ap
6898, Ap
33134, A
                                                                                                                                                                                                                                                                                                31, Appl
31, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                 Sequence Seq
                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                           Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 40; DB 2; Length 825;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels
US-09-396-149-9
US-08-484-593B-10
US-08-484-594B-10
US-08-484-596A-10
US-08-480-150A-10
US-08-480-150A-10
US-08-419-223A-10
US-08-149-223A-10
US-08-11-86-9
US-08-11-86-9
US-09-11-990-5053
US-09-11-990-5053
US-09-270-767-46705
US-09-239-405-31
US-09-107-532A-4310
US-09-107-532A-43134
US-09-270-767-4898
US-09-270-767-4898
US-09-270-767-48134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
```

ò

```
GURDEACH. IN CACATION:

APPLICANT: Cargill, Michele
APPLICANT: Cargill, Michele
APPLICANT: Cargill, Michele
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, George Q.
APPLICANT: Morariby, George Q.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2021.027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT PILING DATE: 2000-09-010
PRIOR PELICATION NUMBER: US 60/153,357
PRIOR PELICATION NUMBER: US 60/153,357
PRIOR PELICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-08-16
NUMBER OF ESESCE for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 2; Length 1170; 100.0%; Pred. No. 3.7; ive 0; Mismatches 0; Indels 0
                APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
TELEPHAX: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-002-350
; Sequence 350, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-657-472-2; Sequence 2. Application US/09657472; Patent No. 6727063; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       20:
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 GVLONVŘĚ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 98, Application US/09939853A

Sequence 98, Application US/09939853A

Patent No. 6989232

GENERAL INFORMATION:

APPLICANT: BUTGESS et al.

TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-099

CURRENT APPLICATION NUMBER: US/09/939,853A

CURRENT APPLICATION NUMBER: 60/228,191

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 2001-02-08

PRIOR APPLICATION NUMBER: 60/269,961

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOSTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

100.0%; Score 40; DB 2; Length 831;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                            100.0%; Score 40; DB 2; Length 831; 100.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-313-288B-20
; Sequence 20, Application US/08313288B
; Sequence 20, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
    TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
    CITY: New York
                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                            0; Mismatches
NUMBER OF SEQ ID NOS: 159
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 97
LENGTH: 831
TYPE: PRT
                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: Mus musculus
US-09-939-853A-98
                                                                                                                        ORGANISM: Homo sapiens
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                   210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                       2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 98
```

δ

ö

Gaps

ô

ö

Gaps

ö

```
Sequence 752, Application US/09538092
; Sequence 752, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REPRESINCE: 15966-54
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 752
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                               80.0%; Score 32; DB 2; Length 484; 75.0%; Pred. No. 81; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (0). ... (0)
OTHER INFORMATION: Polypeptide Accession Number YOR226C
                                                                                                                                                                                                                                                                                                         RESULT 9
US-09-621-976-5916

Sequence 5916, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Johnas Milne Edwards, J.B.

APPLICANT: Johnas Milne Edwards, J.B.

APPLICANT: Johnas Milne Edwards, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENERE 1054PR2.

CURRENT APPLICATION UNMBER: US/09/621,976

CURRENT PILICATION NUMBER: US/09/621,976

CURRENT PILICATION NUMBER: US/09/621,976

SOFTWARE: Patent.pm

SEQ ID NO 5916

LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 2;
Pred. No. 13;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 5
; OTHER INFORMATION: Xaa = Cys, Asp, Gly, Tyr
US-09-621-976-5916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.5%;
                                                                           Query Match
Best Local Similarity 75.v.
6, Conservative
                             ; ORGANISM: Candida albicans US-09-248-796A-16180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                           |:||:|||
271 GLLQSVRF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |::||| |
12 GIIQNVSF 19
                                                                                                                                                                                                2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: SIGNAL
LOCATION: -15..-1
NAME/KEY: UNSURE
LOCATION: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-538-092-752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                          g
                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-248-796A-16180

US-09-248-796A-16180

Sequence 16180, Application US/09248796A

Sequence 16180, Application US/09248796A

Sequence 16180, Application US/09248796A

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US 60/09/248, 796A

CURRENT FILING DATE: 1999-02-13

PRIOR APPLICATION NUMBER: US 60/096, 409

PRIOR APPLICATION NUMBER: US 60/096, 409

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16180
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
PILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FSSESEQ for Windows Version 4.0
SEQ ID NO 350
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 42057, Application US/09270767

Ratent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburst et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 42057

LENGTH: 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 40; DB 2; Length 1170; 100.0%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.5%; Score 33; DB 2; Best Local Similarity 87.5%; Pred. No. 76; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Xaa means any amino acid US-09-270-767-42057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 GVLQNVDF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-270-767-42057
                                                                                                                                                                                                                                                                                                                                                             US-09-949-002-350
                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

```
GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL1

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-05

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

SEQ ID NOS: 8344

SEQ ID NO 6072
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUDRESSEE: No. 59587270 No. 5958727disk of No. 5958727th America, Inc. STRET: 405 Lexington Avenue CITY: New York STAIR: NY
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATENT NO. 5405943

PATILICANT: COMINGS, DAVID E.

TITLE OF INVENTION: TOURETTE SYNDROM, AUTISM AND ASSOCIATED

BEHAVIORS

NUMBER OF SEQUENCES: 5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/562,596

FILING DATE: 03-AUG-1990

PRIOR APPLICATION NUMBER: 125,577

FILING DATE: 25-NOV-1987

APPLICATION NUMBER: 271,653

FILING DATE: 16-NOV-1987

PILING DATE: 16-NOV-1988

PILING DATE: 12-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Methods for Modifying the Production of a Polypeptide
                                                                                                                                                                                                                                                                                                                              Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 7; Length 436;
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                          Score 31; DB 2; Length 406
Pred. No. 1.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 59, Application US/08928692; Patent No. 5958727; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods fo
TITLE OF INVENTION: a Polypept
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59587270 No.
                                                                                                                                                                                                                                                                   ; ORGANISM: Proteus mirabilis US-09-543-681A-6072
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7-
Berand 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:||||
127 VLENVRF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 GVLQNMR 172
                                                                                                                                                                                                                                                                                                                                                                                                           3 VLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GVLQNVR 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-928-692-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
5405943-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5405943-4
                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-489-039A-11916
US-09-489-039A-11916
Sequence 11916, Application US/09489039A
Parent No. 6610816
GENERAL INFORMATION:
APPLICANT: CARY Breton et. al
APPLICANT: CARY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 19916
                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                     APPLICANT: COMINGS, DAVID E. TITLE OF INVENTION: TOURETTE SYNDROM, AUTISM AND ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 7; Length 238;
Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 400;
                                Score 31; DB 2; Length 156;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 2; Length 400
Pred. No. 1.1e+02;
1; Mismatches 0; Indels
                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/562,596
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 125,577
FILING DATE: 25-NOV-1987
APPLICATION NUMBER: 271,653
FILING DATE: 16-NOV-1988
APPLICATION NUMBER: 410,831
FILING DATE: 22-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-543-681A-6072
; Sequence 6072, Application US/09543681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11916
                                  77.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.5%;
illarity 85.7%;
Conservative
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                       |:::||:|
GIIENVKF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 GVLQNMR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VLENVRF 127
                                                                                                               2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVLONVR
                                                                                                                                                                                                                                                     Patent No. 5405943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 238
US-09-538-092-752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:2
                                                                                                                                                                                                                                                                                                             BEHAVIORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5405943-2
                                                                                                                                                                                                                              5405943-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
COUNTRY: USA

ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Disketce
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPUTER: USOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: VASET: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION NUMBER: 33,728
REFERENCY/DOCKET NUMBER: 4944.200-US
FELECOMPUNICATION INFORMATION:
TELEFAX: 212-878-9655
INFORMATION POR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
INFORMATION POR SEQ ID NO: 2.70+02;
MATCHES SEQUENCE CHARACTERISTICS:
MALCHES SECUENCE CHARACTERISTICS:
MALCHES SEQUENCE CHARACTERISTICS:
MALCHES SECUENCE CHARACTERISTICS:
MALCHES SEQUENCE CHARACTERISTICS:
MALCHES SEQUENCE CHARACTERISTICS:
MALCHES SEQUENCE CHARACTERISTICS:
MALCHES SEQUENCE CHARACTERISTICS:
MALCHES SECUENCE CHARACTERISTICS:
MALCHES SEQUENCE CHARACTERISTICS:
MALCHES SECUENCE CHARACTERISTICS:
MALCHES S
```

Search completed: June 5, 2006, 22:48:56 Job time : 18.9224 secs

2 GVLQNVR 8 ||:||:| 236 GVMQNIR 242

8 8



```
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Appl
Sequence 40, Appl
Sequence 1020, Appl
Sequence 1022, Appl
Sequence 462, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 453, Appl
Sequence 453, Appl
Sequence 453, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 451, Appl
Sequence 451, Appl
Sequence 17, Appli
Sequence 18, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 114, Appli
Sequence 12, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38, Appl
482, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                     5, 2006, 23:46:43 ; Search time 58.9655 Seconds (without alignments) 70.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-474-213-28
US-10-419-466-40
US-10-741-600-1020
US-10-741-600-1022
US-10-741-600-1022
US-09-925-301-1047
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-451
US-10-043-806-451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-295-027-1170
US-10-211-462-38
US-10-231-956A-482
                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA Main:*
                                                                                                                                                                                                                                                                                                 2097797 seqs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 10
                                                                                                                                                                          US-10-030-735-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                             1 XGVLQNVRF 9
                                                                                                                                                                                                                                                BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000.0
1000.0
1000.0
1000.0
1000.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0
                                                                                                         June
                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                      1
                                                                      OM protein
                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
```

```
US-10-474-213-28

US-10-474-213-28

Sequence 28, Application US/10474213

Sequence 28, Application US/10474213

Sequence 28, Application No. US20040214248A1

SEMERAL INFORMATION:

APPLICANT: Roberts, David D

APPLICANT: Roberts, David D

APPLICANT: Roberts, David D

APPLICANT: Roberts, David D

APPLICANTON: USE OF SEMENOGELIN IN THE DIAGNOSIS, PROGNOSIS AND TREATMENT OF TITLE OF INVENTION: CANCER

FILE REPREBENCE: 224329

CURRENT APPLICATION NUMBER: PCT/US02/10535

FRIOR FILING DATE: 2003-04-03

PRIOR FILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.2

SEQ ID NO 28

LENGTH: 12

FAUND APPLICATION OF SEQ ID NOS: 28

SEQ ID NO 28

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-419-462-40
US-10-419-462-40
US-10-419-462-40
Publication No. US20040053392A1
Sequence 40, Application Wollous
Publication No. US20040053392A1
GENERAL INFORMATION
APPLICANT: Milliams, Kevin J.
APPLICANT: Milliams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
TITLE REFERENCE: W107-20005
CURRENT APPLICATION NUMBER: US/10/419,462
CURRENT PILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                      Sequence 28, Appl
Sequence 28, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 30, Appli
                          1018, Ap
1019, Ap
1021, Ap
38, Appl
44, Appl
548, App
1376, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
     Sequence
Seq
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
US-10-419-462-38

US-10-741-600-1018

US-10-741-600-1019

US-10-741-600-1021

US-10-741-600-1021

US-10-741-600-1021

US-10-631-467-1376

US-10-631-467-1376

US-10-631-467-1376

US-10-631-651-594

US-10-995-561-595

US-11-046-644-28

US-11-046-644-28

US-11-046-644-28

US-11-046-644-28

US-11-046-455-28

US-11-046-456-28

US-11-046-456-28

US-11-046-456-28

US-11-046-456-28

US-11-046-456-28

US-10-050-058-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100.0%; Score 40; DB 4; Similarity 100.0%; Pred. No. 0.088; 8; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-750-409-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), OTHER INFORMATION: Synthetic peptide US-10-474-213-28
                          11170
11170
11170
11170
11170
11170
11170
11170
11170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||||||||
GVLQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVLONVRF
```

N

d

```
US-11.0 v. 10 v. 1
                                                                                                                                                                                                                                                                                                                              Sequence 1022, Application US/10741600
| Publication No. US20050026169A1
| CENERAL INFORMATION:
| APPLICANT: CARGILL, MICHEL et al. |
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH |
| TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: MYGER US/10/741,600 |
| CURRENT APPLICATION NUMBER: US/10/741,600 |
| CURRENT FILING DATE: 2003-12-22 |
| NUMBER OF SEQ ID NOS: 73997 |
| SEQ ID NO 1022 |
| SEQ ID NO 1022
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                       Gaps
                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 40; DB 6; Length 459; ilarity 100.0%; Pred. No. 4.9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
Best Local Similarity 100.0%; Pred. No. 4.6; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 40; DB 100.0%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: VARIANT
; LOCATION: (1)...(432)
; CTHER INFORMATION: Xaa = Any Amino Acid
US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1047, Application US/09925301; Patent No. US20020052308A1
GENERAL INFORMATION: APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                  210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 GVLONVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
ses 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-043-806-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                               ò
                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-782-968-40

| Sequence 40, Application US/10782968
| Sequence 40, Application US/10782968
| Sequence 40, Application No. US20050065324A1
| Sequence 40, Application No. US20050065324A1
| Publication No. US20050065324A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Kevin J.
| TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
| TITLE OF INVENTION: UNMBER: US/10/782,968
| CURRENT FILING DATE: 2004-02-20
| PRIOR PPLICATION NUMBER: US/10/419,462
| PRIOR FILING DATE: 2003-04-21
| NUMBER OF SEQ ID NOS: 53
| SOFTWARE: PatentIn version 3.2
| LENGTHARE: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1020, Application US/10741600

Sequence 1020, Application US/10741600

Sequence 1020, Application US/20050026169A1

GENERAL INFORMATION:
APPLICANT: CARCILL, Michele et al.
1TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
1TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
1TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
1CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SEQ ID NO 1020

SEQ ID NO 1020

LENGTH: 432
                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Thrombospondin Region plus N-terminal domain
                                                                                                                                        OTHER INFORMATION: Thrombospondin Region plus N-terminal domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 5; Length 432;
                                                                                                                                                                                                                                        Query Match 100.0%; Score 40; DB 4; Length 240; Best Local Similarity 100.0%; Pred. No. 2.4; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 5; Length 240; 100.0%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
LOCATION: (1)...(432)
OTHER INFORMATION: Xaa = Any Amino Acid
                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 GVLONVRF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 GVLQNVRF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                    2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-741-600-1020
                                                                                                                                                                           US-10-419-462-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-782-968-40
       LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
```

g ઠે

```
Squence 452, Application US/11043806

Publication No. US20060051774A1

GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

STG ID NO 452

LENGTH: 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-11-043-806-455
| Sequence 455, Application US/11043806
| Publication No. US20060051774A1
| Sequence 455, Application US/020060051774A1
| General Information No. US20060051774A1
| APPLICANT: Compugen Ltd
| TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
| TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer
| FILE REFERENCE: 1847.1003
| CURRENT APPLICATION NUMBER: US/11/043,806
| CURRENT PILING DATE: 2005-01-27
| NUMBER OF SEQ ID NOS: 575
| SEQ ID NO 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 6; Length 685; 100.0%; Pred. No. 7.6; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 40; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                       210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 GVLONVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 GVLONVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GVLQNVRF 9
                         2 GVLQNVRF 9
                                                                                                                       RESULT 10
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                           ઠે
                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 454, Application US/11043806

Publication No. US20060051774A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

FILE REFERENCE: 1847.1003

CURRENT APPLICATION UNMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 456, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TIPLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: 1847.1003
CURRENT APPLICATION
CURRENT PILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILLIG DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR PILLIG DATE: 2000-03-08
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Parcentin Ver. 2.0
SEQ ID NO 1047
                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 40; DB 3; Length 466; Best Local Similarity 100.0%; Pred. No. 4.9; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 40; DB 6; Length 578; 100.0%; Pred. No. 6.3; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 40; DB
100.0%; Pred. No. 6;
vative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                 263 GVLONVRF 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-043-806-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-043-806-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 456
```

ઠ 셤

δ g

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-461
                                                                                                                                                                                                                                                                                             210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 GVLQNVRF 217
                                                                                                                                                                                                                    2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GVLQNVRF 9
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                         ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-939-853A-98

i Sequence 98, Application US/09939853A

j Sequence 98, Application US/09939853A

j Publication No. US20040039163A1

j Publication No. US20040039163A1

j TITLE OF INVENTION:

j TITLE OF INVENTION:

j PRIOR APPLICATION NUMBER: US/09/939, 853A

CURRENT FILING DATE: 2001-08-25

j PRIOR APPLICATION NUMBER: 60/228, 191

PRIOR FILING DATE: 2001-02-08

j PRIOR FILING DATE: 2001-02-08

j PRIOR PILING DATE: 2001-02-08

j PRIOR FILING DATE: 2001-02-08

j PRIOR PILING DATE: 2001-02-08

j PRIOR FILING DATE: 2001-03-00

j PRIOR FILING DATE: 2001-03-00

j PRIOR PILING DATE: 2001-03-00

j PRIOR FILING DATE: 2001-03-00

j PRIOR PILING DATE: 2001-03-00

j PRIOR PILING DATE: 2001-03-00

j PRIOR FILING DATE: 2001-03-00

j PRIOR FILING DATE: 2001-03-00

j PRIOR PILING DATE: 2001-03-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 97, Application US/0939853A

| Sequence 97, Application US/0939853A
| Publication No. US20040039163A1
| GENERAL INFORMATION:
| APPLICANT: Burgess et al.
| TITLE COF INVENTION: O. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099
| CURRENT APPLICATION NUMBER: US/09/939,853A
| CURRENT FILING DATE: 2001-08-25
| PRIOR FILING DATE: 2001-08-25
| PRIOR FILING DATE: 2001-02-08
| PRIOR FILING DATE: 2001-03-20
| PRIOR FILING DATE: 2001-03-20
| RIGHTH: 891 |
| SEQ ID NO 97
                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                             Query Match 100.0%; Score 40; DB 6; Length 828; Best Local Similarity 100.0%; Pred. No. 9.3; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 40; DB 3; Length 831; 100.0%; Pred. No. 9.4; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                      210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 GVLQNVRF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                    2 GVLONVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-939-853A-97
LENGTH: 828
                                                                                                                                                                                                                                                                                                                                                                                                      쉽
                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

```
WS-11-043-806-461

Sequence 461, Application US/11043806

Sequence 461, Application No. US20060051774A1

Sequence 461, Application No. US20060051774A1

GENERAL INFORMATION:

TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods

TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer

FILE REFERENCE: 1847.1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT APPLICATION NUMBER: US/11/043,806

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 461

LENGTH: 855
                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 40; DB 6; Length 855; Best Local Similarity 100.0%; Pred. No. 9.7; Matches 8; Conservative 0; Mismatches 0; Indels
  100.0%; Score 40; DB 3; Length 831; 100.0%; Pred. No. 9.4;
                                                           0; Indels
                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 6, 2006, 00:00:11
Job time : 58.9655 secs
Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
```

Tue

```
LENGTH: 525
TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::|||||
463 IVQNVRF 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-10-953-349-31207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-203-828-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Appli
Sequence 31207, A
Sequence 31207, A
Sequence 13367, A
Sequence 13367, A
Sequence 1347, Ap
Sequence 16946, A
Sequence 16946, A
Sequence 16944, A
Sequence 33144, A
Sequence 23129, A
Sequence 23719, A
Sequence 23719, A
Sequence 23719, A
Sequence 23719, A
Sequence 32501, A
Sequence 23718, A
Sequence 23719, A
Sequence 23718, A
Sequence 2319, A
Sequence 2319, A
Sequence 2319, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA New:*

1: /EMC_Celerra_SIDS3/pcodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/pcodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptcodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptcodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptcodata/1/pubpaa/US08_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptcodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptcodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptcodata/1/pubpaa/US11_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                        (without alignments)
37.266 Million cell updates/sec
                                                                                                                                                                                                                  6, 2006, 00:00:38 ; Search time 2.7931 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-203-828-5
US-10-953-349-31206
US-10-953-349-31206
US-10-953-349-13367
US-10-953-349-13367
US-10-953-349-13365
US-10-953-349-13365
US-10-953-349-13365
US-10-953-349-13494
US-10-953-349-16946
US-10-953-349-16946
US-10-953-349-23719
US-10-953-349-32501
US-10-953-349-32499
US-11-293-697-23239
US-11-293-697-23238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58871 seqs, 11565156 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                           US-10-030-735-22
40
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 XGVLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             775.0
7722.5
7722.5
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
7700.0
770
                                                                                                                                                                                                                     June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 6 9 7 8 8 9 7 8 8 9 7 8 8 9 7 8 8 9 7 8 8 9 7 8 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9
```

```
DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Sequence 39138, A Sequence 2388, Ap Sequence 39136, A Sequence 39136, A Sequence 30058, A Sequence 30056, A Sequence 30056, A Sequence 30056, A Sequence 32, Appl Sequence 7, Appl Sequence 20, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6694, Ap Sequence 6694, Ap
                                                                                                                                                                                                                                                                                                                                      WS-11-203-828-5

Sequence 5, Application US/11203828

Sequence 5, Application US/11203828

Publication No. US20060110390A1

GENERAL INFORMATION:

APPLICANT: LEINWAND, LESLIE

APPLICANT: SUCHAROV, CARRIN

TITLE OF INVENTION: INHIBITION OF KU AS A TREATMENT FOR CARDIOVASCULAR

TITLE OF INVENTION: DISEASES

FILE REFERENCE: MYOG:58US

CURRENT APPLICATION NUMBER: US/11/203,828

PRIOR APPLICATION NUMBER: 60/604,435

PRIOR APPLICATION NUMBER: 60/604,435

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 30; DB 7; Length 608; 71.4%; Pred. No. 33; ive 2; Mismatches 0; Indels
                        US-10-953-349-39137
US-10-953-349-39136
US-10-953-349-30136
US-10-953-349-30058
US-10-953-349-30057
US-10-953-349-30056
US-10-953-349-30056
US-10-953-349-30056
US-10-953-349-7069
US-11-316-521-39
US-11-247-437-2
US-11-247-437-2
US-11-501-834-7
US-10-953-349-6694
US-10-953-349-6694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31207, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA 17 TITLE OF INVENTION: ENCONDED THERBY
FILLE REFERENCE: 2750-1579FUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
SUFFRENT FILING DATE: 2004-09-30
SOFTWARE OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 31207
                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
```

N

```
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT APPLICATION NUMBER: 106/4-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN Version 3.3
SEQ ID NO 13366
LENGTH: 212
                                                                                                                                                                                                       Sequence 13357, Application US/10953349
Publication No. US20060107345A1
GREERL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLAI et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN Version 3.3
SEQ ID NO 13367
LENGTH: 202
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
OCGATION: (111)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (128)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (1217..(121)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (138].
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; CCCATION: (165)...(165)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13367
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 202;
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 6;
Pred. No. 27;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-953-349-13366

'Sequence 13366, Application US/10953349

'Publication No. US20060107345A1

; GENERAL INFORMATION:
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3
    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
                                                                                              36 VLONVAF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 GVLONI 145
                                                 3 VLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GVLQNV 7
                                                                                                                                                                                             US-10-953-349-13367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
    Matches
                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 31206
LENGTH: 560
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Morsenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612001014
FILE OF INVENTION: WUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR PELLING DATE: 2003-04-24
PRIOR PELLING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-12-20
NUMBER: PALENTON NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER: PALENTEN DATE: 2002-12-20
NUMBER: PALENTEN DATE: 2002-12-30
NUMBER: PALENTEN OF SEQ ID NOS: 3117
SOFTWARE: PALENTEN VERSION 30.0
                                               72.5%; Score 29; DB 6; Length 525;
nilarity 75.0%; Pred. No. 47;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.5%; Score 29; DB 6; Length 560; Best Local Similarity 75.0%; Pred. No. 50; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 6; Length 175; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3000, Application US/10511937
Publication No. US20060088836A1
GABRAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                                                  Sequence 31206, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Homo sapiens
US-10-511-937-3000
                                                                                                                                                                                             93 GVLDRVŘF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 GVLDRVRF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GVLQNVRF 9
                                                                                                                                                  2 GVLQNVRF 9
                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              JS-10-953-349-31206
    US-10-953-349-31207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-31206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-10-511-937-3000
                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
US-10-953-349-16946
US-10-953-349-16946
Sequence 16946, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROW. NickOlai et al.
APPLICANT: ALEXANDROW.
APPLICANTON WUMBER: US/10/953,349
CURRENT APPLICANT: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Parentin version 3.3
SEQ ID NO 16446
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-953-349-33145

US-10-953-349-33145

Sequence 33145, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

APPLICANT: ALEXANDROV, Nickolai et al.

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERRINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION UNMBER: 2064-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 33145

LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16445, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DEFERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
     6; Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 6;
Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB Pred. No. 43; 2; Mismatches
       B
     Score 28; DB Pred. No. 41; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 43;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Zea mays subsp. mays
US-10-953-349-33145
       70.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%;
71.4%;
  Query Match 70.0
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.0
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                    88 GIIQGVKF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|:||||
24 LLENVRF 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|:||||
24 LLENVRF 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
tes 5; Conserv
                                                                                                      2 GVLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VLQNVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-953-349-16946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-953-349-16945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                      US-10-953-349-13365

Sequence 13365, Application US/10953349

Publication No. US20060107345A1

Publication No. US20060107345A1

SERNEAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION OF SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION OF SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE PARENTIN VERSION 3.3

SEQ ID NO 13365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 3937
LENGTH: 298
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
; NAME/KEY: misc_feature
; IOCATION: (175)...(175)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

NAME/KEY: misc feature

COCATION: (159)...(159)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (196)...(196)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid

COTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-10-953-349-13365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE:
NAME/KEY: misc feature
LOCATION: (1427. (1427. (1427. OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                          Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 233
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.0%; Score 28; DB 6;
83.3%; Pred. No. 31;
tive 1; Mismatches
                                                                                                                               .
9
                                                                                                                     Query Match 70.0%; Score 28; DB Best Local Similarity 83.3%; Pred. No. 28; Matches 5; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9347, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                                       150 GVLQNI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 GVLONI 176
                                                                                                                                                                                                                         2 GVLQNV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-953-349-9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-953-349-9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
```

```
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-157998US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.0%; Score 28; DB 6; Length 436; Best Local Similarity 71.4%; Pred. No. 63; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; DB 6; Length 329;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                               ; Sequence 33143, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-953-349-23958
; Sequence 23958, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6, 2006, 00:12:57
                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Zea mays subsp. mays US-10-953-349-33143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.5%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 71.4 Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Glycine max
US-10-953-349-23958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|:||||
151 LLENVRF 157
151 LLENVRF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 GTĽONLŘ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GVLQNVR 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June Job time: 3.8931 secs
                                                                              US-10-953-349-33143
                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 33143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 23958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NO. USCUDENTION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PALENTIN VERSION 3.3
SEQ ID NO 33144
LENGTH: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-10-953-149-16944
US-10-953-149-16944
Application US/10953349

Sequence 16944, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION UNMERS: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SOFTWARE: 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.0%; Score 28; DB 6; Length 402; Best Local Similarity 71.4%; Pred. No. 58; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                             70.0%; Score 28; DB 6; Length 401; 71.4%; Pred. No. 58; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 6;
Pred. No. 63;
2; Mismatches
                 CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 16945
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-10-953-349-33144
; Sequence 33144, Application US/10953349
; Publication No. US20060107345A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Zea mays subsp. mays
US-10-953-349-33144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%;
illarity 71.4%;
Conservative
  FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                            Query Match
Best Local Similarity 71.**
Then S; Conservative
                                                                                                                                               ; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-16945
                                                                                                                                                                                                                                                                                                                                                         117 LLENVRF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|:||||
117 LLENVRF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Glycine max US-10-953-349-16944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Loca 5; Conserve
                                                                                                                                                                                                                                                                                                                  3 VLQNVRF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VLQNVRF 9
```

3 VLONVRF 9

```
GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                        Copyright
```

model
38
using
search,
protein
•
protein
ĕ

5, 2006, 22:08:53 ; Search time 91.1379 Seconds (without alignments) 60.201 Million cell updates/sec June Run on:

1 FQGVLNNVRFVF 12 US-10-030-735-24 62 Perfect score: Sequence: Title:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

2589679 segs, 457216429 residues Searched: 2589679 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

geneseqp1980s:* geneseqp1990s:* A Geneseq 8:*

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2000s:* geneseqp2001s:* geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

SUMMARIES

Description	Aab35371 Alpha3bet	Aab35352 Alpha3bet	Aab35378 Alpha3bet	-	Adl70641 Human thr	Adq39359 Human myo		Aau02916 Angiotens	Aab43602 Human can	Aau02915 Angiotens		Aau02914 Angiotens	Aau02913 Angiotens	Aab00042 Human thr	Aau74771 Human thr	Abb82285 Human thr	Human	Human	Aae25030 Human thr	Aau75315 Human thr	Abp96780 Human COP	Angiog	Abg74673 Human THB
ΩI	AAB35371	AAB35352	AAB35378	ABG72834	ADL70641	ADQ39359	ADQ39357	AAU02916	AAB43602	AAU02915	ADN02474	AAU02914	AAU02913	AAB00042	AAU74771	ABB82285	AAB74450	AAB90800	AAE25030	AAU75315	ABP96780	ABU03474	ABG74673
h DB	4	2 4	2 4	2 6	0	2	2 8	4	9	4	8 7	5.4	1 4	2 3	2 5	2 5	0	0	0	0	9 0	9 0	9 0
Lengt	-	-	-	-	240	432	432	459	466	546	548	555	731	1152	115	1152	117	117	117	117	1170	1170	1170
% Query Match Length DB	100.0	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3
Score	62	26	26	26	26	99	26	99	99	26	26	26	99	26	26	99		26	56	26		26	26
Result No.	-	7	m	4	S	9	7	80	O)	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Aae36226 Human THB Abr62059 Human thr Adn39852 Cancer/an Adj76124 Marker ge Adj76236 Marker ge Adj76396 Human thr Add26070 Thrombosp Adg24179 Human thr Add39356 Human myo Add39356 Alman thr Aeb87781 Alman thr Aeb87781 Alman thr Aeb87781 Alpha3bet Aab353173 Alpha3bet Aab35344 Alpha3bet Aab35344 Alpha3bet Aab35344 Alpha3bet	Aab35368 Alpha3bet Aab35376 Alpha3bet
	AAB35368 AAB35376
6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	122
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	1 82.3 1 82.3
4 7 7 7 8 9 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	44 45 5

ALIGNMENTS

AAB35371 standard; peptide; 12 AA. (first entry) 08-MAY-2001 AAB35371; RESULT 1 AAB35371

Alpha3betal integrin binding peptide #36.

Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.

Synthetic.

WO200105812-A2.

25-JAN-2001.

12-JUL-2000; 2000WO-US018986.

99US-0144549P. 15-JUL-1999; (USSH) US DEPT HEALTH & HUMAN SERVICES

Krutzsch HC; Roberts DD,

WPI; 2001-182656/18.

New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and cancer.

Claim 4; Page 34; 84pp; English.

The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatolid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention

Sequence 12 AA;

```
Krutzsch HC;
                                                                                                                                                                        WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                    the invention
                                                                                                                                                                                                                                                                                                                      Sequence 12 AA;
                                                               WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200281630-A2
                                                                                                                                                                                                                                                                                                                                        Ma.
Local S...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-APR-2002;
                                                                                                                     15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roberts DD,
                                                                                                                                                        Roberts DD,
                                                                                 25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2002.
                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG72834;
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                      cancer.
                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               ABG72834
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
 유
                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                       Alpha3betal integrin, angiogenesis, cell proliferation, cancer, diabetic retinopathy, restenosis, atherosclerosis, rheumatoid arthritis, macular degeneration, psoriasis, cell adhesion, cell motility.
                                                                                                                                                                                                                                                                                                                                                       New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                   Gaps
                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
100.0%; Score 62; DB 4; Length 12; 100.0%; Pred. No. 7.3e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 4;
Pred. No. 0.001;
); Mismatches
                                                                                                                                                        Alpha3betal integrin binding peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha3beta1 integrin binding peptide #43.
                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                    AAB35352 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB35378 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.3%;
91.7%;
                                                                                                                                                                                                                                                                 12-JUL-2000; 2000WO-US018986
                                                                                                                                      (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                      Roberts DD, Krutzsch HC;
                   Conservative
                                     1 FOGVLNNVRFVF 12
                                               Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVLONVREVE 12
                                                                                                                                                                                                                                                                                                                                        WPI; 2001-182656/18.
         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 AA;
                                                                                                                                                                                                                             WO200105812-A2
                                                                                                                                                                                                                                                                                   15-JUL-1999;
                  12;
                                                                                                                                      08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2001
                                                                                                                                                                                                                                               25-JAN-2001
                                                                                                                                                                                                             Synthetic.
Query Match
Best Local S
Matches 12
                                                                                                                     AAB35352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB35378;
                                                                                                                                                                                                                                                                                                                                                                                       cancer
                                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB3537
                                                     요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BXXXXX
                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
Alpha3beta1 integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; thrombospondin-1; cytostatic; immunostimulant; cancer; epithelial cancer; lung cancer; papillary renal cell carcinoma; colon cancer; small-cell lung cancer; SCLC; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 4; Length 12;
Pred. No. 0.001;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombospondin-1 sequence containing synthetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG72834 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2001; 2001US-0281994P.
                                                                                                                                                                                                                                                                                                                                                     12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0144549P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FQGVLQNVRFVF 12
```

The invention relates to diagnosing cancer other than prostate cancer in a male mammal, comprising assaying a test sample for increased level of semenogelin, or cancer in a female by assaying for the presence of semenogelin. Administering a semenogelin protein or polypeptide fragment or a semenogelin specific antibody or active fragment, or a recombinant vector expressing the protein or antibody, is useful for inducing an immune response to a cancer in a mammal, where the cancer is not prostate cancer and semenogelin is a marker. The invention is used to diagnose cancer, particularly of epithelial origin such as lung cancer, papillary renal cell carcinoma, colon cancer, especially small-cell lung cancer (SCLC), or a melanoma. The present sequence represents the amino acid sequence of the thrombospondin-1 sequence containing synthetic peptide which binds to alpha-3-beta-1 integrin A new diagnosis for cancer other than prostate cancer in a mammal useful to detect cancer including lung cancer, particularly small cell lung cancer and melanoma comprises detecting semenogelin in a sample. Score 56; DB 6; Length 12; Pred. No. 0.001; Human; thrombospondin-1; epitope; cancer; diagnosis. /note= "Fibrinogen binding region" /note= "Heparin binding region" 151. .164 23. .32 /note= "Heparin binding region" 0; Mismatches Human thrombospondin-1 N-terminal domain. Location/Qualifiers ADL70641 standard; protein; 240 AA. Example 1; Page 14; 32pp; English. 90.3%; 91.7%; 20-MAY-2004 (first entry) 11; Conservative 1 FQGVLQNVRFVF 12 1 FQGVLNNVRFVF 12 WPI; 2003-103329/09. Best Local Similarity WO2004018995-A2 Sequence 12 AA; Homo sapiens ADL70641; Query Match Region Region Region Matches ò

ö

Gaps

; 0

1; Indels

prostate

```
The present sequence is that of the N-terminal domain of human thromosopondin-1 (TSP) ADL/7639. The invention relates to TSP fragments (G-linical sasays for 20-35 Mam Mol. Wt.) found in plasma, and their use in (BO-100, 40-55 or 20-35 Mam Mol. Wt.) found in plasma, and their use in clinical sasays for cancer and for generation of antibodies and other principal department of portion involves (I) using an epitope shared by TSP and the TSP fragment or portion as a target for a binding molecule, e.g. an antibody, to obtain a quantitation of TSP plus of in the fragment or portion to obtain a quantitation of the amount of TSP fragment or portion of obtain a quantitation of the amount of TSP fragment or portion of the TSP fragment or the TSP fragment o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human myocardial infarction-associated gene derived protein, SEQ ID 1022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue, endodermal tissue, a teratoma, a poorly-differentiated cancer, a well-differentiated cancer or a moderately differentiated cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
or leukemia or as calibrators, indicators, immunogens and analytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56; DB 8; Length 240;
pred. No. 0.029;
0; Mismatches 1; Indels
                                         Disclosure; SEQ ID NO 40; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ39359 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 91.7
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ39359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
ADQ39359
  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXXXXXXXX
```

ö

New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma

23-AUG-2002; 2002US-0405494P 21-APR-2003; 2003US-00419462

WILL/) WILLIAMS K J.

WPI; 2004-226901/21.

Williams KJ;

20-AUG-2003; 2003WO-US026023

04-MAR-2004

Human myocardial infarction-associated gene derived protein, SEQ ID 1020.

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's caltered risk for myocardial infarction in the individual one of altered risk for myocardial infarction in the individual. The invention further comprises an isolated nucleic acid molecule comprising at least sontiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification, an antibody that specification and main and specification; an isolated polypeptide comprising an supplication and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method is useful in identifying an individual who has an increased or comprising the method is useful in identifying an individual who has an increased or commonstation for reventing myocardial infarction may be used in gene therapy. The method is useful in identifying an individual who has an increased or commonstation for reventing myocardial infarction may be used in gene therapy. The method is useful in identifying an individual who has an increased or commonstation for revenenting myocardial infarction may be used in gene therapy. The method is useful in identifying myocardial infarction may be used in gene therapy. The method is useful in revenenting myocardial infarction may be used in gene therapy. The method is useful in identifying myocardial infarction method is proparating and myocardial infarction method is used in gene in the inventor myocardial infarction method is used in gene in the inventor myocardial infarction 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; SEQ ID NO 1022; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cargill M, Devlin JJ, Iakoubova O;
                                                                                                                                                                                                                                                      20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504665P.
                                                                                                                                                                                                22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                                                                                                                                      (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-533949/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADQ38531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 432 AA;
                                                                                 WO2004058052-A2
                              Homo sapiens.
                                                                                                                                          15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

RESULT 8 AAU02916 ö Gaps ;; 0 90.3%; Score 56; DB 8; Length 432; 91.7%; Pred. No. 0.055; ive 0; Mismatches 1; Indels ADQ39357 standard; protein; 432 AA. 18-NOV-2004 (first entry) 208 FQGVLQNVRFVF 219 11; Conservative 1 FOGVLNNVRFVF 12 Best Local Similarity Matches 11; Conserv ADQ39357; RESULT 7 ADQ39357 EXXXE. ð

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nuclectide polymorphism (SNP) in any one of the nucleic acids, where the presence of the SNP is correlated with an or altered risk for myocardial infarction in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The individual curther comprises: an isolated nucleic acid molecule comprising at least a contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino the specification and in the specification; an intibody that specificatly binds to the polypeptide or its antigen-binding that specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and method for identifying an agent useful in treating or preventing an composition for treating or preventing myocardial infarction. The novel detection method has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction. This sequence was not shown in the specification for the invention. Note: This sequence was not shown in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                    Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 8; Length 432;
Pred. No. 0.055;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; SEQ ID NO 1020; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Iakoubova 0;
                                                                           cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                    20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.3%;
91.7%;
                                                                                                                                                                                                                                 22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91...
Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGULNINVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                            Cargill M, Devlin JJ,
                                                                                                                                                                                                                                                                                                                                                                       (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-533949/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADQ38529
                                                                                                                                                      WO2004058052-A2
                                                                                                                 Homo sapiens.
                                                                                                                                                                                          15-JUL-2004.
```

S

```
Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; rand disease; diabetic nephropathy; muscular disease; immune diseorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACBV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                  nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                               Angiotensin converting enzyme (ACEV) splice variant protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Khosravi R, Bernstein J;
AAU02916 standard; protein; 459 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 16; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           Levine Z, David A, Azar I,
                                                                                                                                                                                                                                                                                                                                             L7-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                      99IL-00132978
99IL-00133455
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-336004/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS06016.
                                                                                                                                                                                                                                                                                      WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                             Homo sapiens.
                                                      12-SEP-2001
                                                                                                                                                                                                                                                                                                                  25-MAY-2001
                           AAU02916;
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelat-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary atterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as abestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis
```

90.3%; Score 56; DB 4; Length 459; 91.7%; Pred. No. 0.059; ive 0; Mismatches 1; Indels Local Similarity 91.7 hes 11; Conservative Sequence 459 AA; Query Match Matches

1|||| |||||| 208 FQGVLQNVRFVF 219 1 FOGVLANVRFVF 12 ઠે

RESULT 9

ö

Gaps

ö

261 FOGVLONVREVE 272

11; Conservative 1 FOGVLANVRFVF 12

Matches

ö

Gaps

ö

è 셤

```
include: cytostatic; prolliferative, vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antidiabetic; antiasthmatic; antirheumatic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; coortropic; vasotropic; antiporiatic and antianglogenic. The coortropic; antiporiatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or coortropic; polynucleotides, polypeptides can be used for preventing, treating or corpustion may be used to treat immune disorders by activating the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune clicancers, allergic reactions, graft versus host disease and organic rejection, modulate haemostatic or thrombolytic activity, modulate confirmation, cancers, cardiovascular disorders, nucleotides, antibodies, bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                         Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiarchritic; antidativitic; antidativitic; antidativitic; antidativitic; antidativitic; antidativitic; antidation; antidation; antiphyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 3; Length 466;
Pred. No. 0.06;
0; Mismatches 1; Indels
                                                                                                                                 Human cancer associated protein sequence SEQ ID NO:1047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 1636-1638; 2352pp; English.
AAB43602 standard; protein; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000; 2000WO-US005882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA, Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC77811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200055350-A1.
                                                                                        08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2000.
                                             AAB43602;
```

ADN02474 standard; protein; 548 AA.

RESULT 11

4DN02474

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy,
                                                                                                                                                                                               Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders such as immune complex nephritis, multiple sclerosis,
                                                                                                                                                               Angiotensin converting enzyme (ACEV) splice variant protein #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 4; Length 546;
Pred. No. 0.072;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abnormality such as deep vein thrombosis
                                    AAU02915 standard; protein; 546 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Fig 15; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levine Z, David A, Azar I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000; 2000WO-IL000766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99IL-00132978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99IL-00133455
                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-336004/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AASO6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-1999;
                                                                                                                        12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001
                                                                               AAU02915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune
RESULT 10
                     AAU02915
```

```
The present invention relates to a novel recombinant adenovirus vector mediated anti-neoplastic composition is prepared through cloning the cDNA sequence from the human peripheral blood cell by specific primer and reverse transcription-polymerase chain reaction (RT-PCR) method for coding TSF polypeptide, construction in human embryonic kidney cell 293 by AdBasy system, and packaging and expressing the recombinant adenovirus vector of TSF. It can suppress the growth and transfer of cancer. The present sequence represents the TSF polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocyte colony strumlating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor suppressing polypeptide TSF and gene therapy vector composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiotensin converting enzyme (ACEV) splice variant protein #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                     adenovirus vector; anti-neoplastic; TSF polypeptide; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56; DB 7; Length 548; Pred. No. 0.072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                  (TAID-) TAIDA LIFE SCI TECH RES CENT HEMATOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 1; 13pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU02914 standard; protein; 555 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                21-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                               11-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.3%;
91.7%;
                                                 17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FOGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 91.7
es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-469302/45
                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADN02475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 548 AA;
                                                                                    TSF polypeptide
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                             12-MAR-2003.
                                                                                                                                                                                           CN1401387-A
              ADN02474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU02914;
                                                                                                                                                                                                                                                                                                                                                                     Han Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02914
d
```

ö

ö

Gaps

ö

208 FOGVLONVRFVF 219

11; Conservative 1 FOGVLNNVRFVF 12

Best Local Similarity Matches 11; Conserv

Query Match

```
(ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1c, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated mucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, cancer, sarcoidosis, nonarcoidocic pulmonary granulomatous diseases such as such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidocic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection; glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                      Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents an angiotensin converting enzyme splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB 4; Length 731;
Pred. No. 0.099;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                           David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361. .416
/label= Type 1 repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB00042 standard; protein; 1152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 13; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human thrombospondon-1 (TSP-1).
    vascular disorder; asbestosis.
                                                                                                                                                                                             99IL-00132978
99IL-00133455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.3%;
                                                                                                                                                        17-NOV-2000; 2000WO-IL000766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guery Match
Bust Local Similarity 91...

....a 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FÓGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                       COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                  WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS06013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 731 AA;
                                                                              WO200136632-A2
                                                                                                                                                                                             17-NOV-1999;
10-DEC-1999;
                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                    25-MAY-2001
                                                                                                                                                                                                                                                                                           Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB00042
    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THERESEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; mycorardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                        Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin converting enzyme (ACEV) splice variant protein #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB 4; Length 555;
Pred. No. 0.073;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                           Levine Z, David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU02913 standard; protein; 731 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 14; 519pp; English
vascular disorder; asbestosis
                                                                                                                                                        17-NOV-2000; 2000WO-IL000766
                                                                                                                                                                                               99IL-00132978
99IL-00133455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yu.s
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FOGVLONVREVE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                       (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                  WPI; 2001-336004/35
                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS06014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 555 AA;
                                                                              WO200136632-A2
                                            Homo sapiens
                                                                                                                                                                                             17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2001
                                                                                                                    25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU02913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU02913
    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

ö

Gaps

ω

```
label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-106273/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200191781-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawler JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carrier.
             Key
Region
                                                  Domain
                                                                                       Domain
                                                                                                                                          Domain
                                                                                                                                                                  Region
                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
  New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TYE (transforming growth factor)-beta acityvation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerase chain reaction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful of or treating angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. Anti-cancing human immunodeficiency virus (HIV) infection. Anti-cancing human immunodeficiancy be not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombospondin-1; TSP-1; cytostatic; angiogenesis; vasotropic; vulnerary; necvascularisation; cell proliferation inhibitor; cancer; solid tumour; haemangioma; acoustic neuromas; neurofibroma; trachoma; acoustic neuromas; retroma; trachoma; retropachic granulomas; rheumatoid arthritis; ocular angiogenic disease; retinopathy; psoriasis; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rebebosis; angiofibroma; Osler-Webber syndrome; myocardial angiogenesis; haemophiliac joints; plaque neovascularisation; telangiectasia; wound granulation; apoptosis.
                                                                                                                                                                                                                                           Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.3%; Score 56; DB 3; Length 1152; 91.7%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
417. .473
/label= Type 1 repeat region
/label= Type 1 repeat region
/label= Type 1 repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                  (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU74771 standard; protein; 1152 AA
                                                                                                                                                                                                                                                                                               Disclosure, Fig 1, 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  does not induce drug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human thrombospondin-1 (TSP-1).
                                                                                                                 01-FEB-2000; 2000WO-US002482
                                                                                                                                          99US-0118053P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                   WPI; 2000-514823/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1152 AA;
                                                               WO200044908-A2
                                                                                                                                          01-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-2002
                                                                                         03-AUG-2000
                                                                                                                                                                                           Lawler JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU74771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
 Region
                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
  à
```

```
The invention describes a composition comprising cDNA encoding fragments of human thrombospondin-1 (TSP -1), a type 1 repeat polypeptide and potent inhibitor of tumour growth and anglogenesis. The composition is useful for killing cancerous cells (preferably tumour); for reducing volume or inhibiting growth of a tumour (inhibiting neovascularisation the tumour); for decreasing proliferation of tumour cells; in the treatment of diseases and conditions associated with anglogenic activity or misregulated growth and anglogenesis-mediated diseases such as cancer, solid tumour, tumour metastasis, benign tumour, (e.g. haemangloma, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Type_3_repeat_domain
/note= "This region contains 7 type 3 repeats, from
residues 698-733, residues 734-756, residues 757-792,
residues 793-815, residues 816-853, residues 854-889 and
residues 890-925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition useful for treatment of cancer comprises cDNA encoding amino acids of human thrombospondin-1 or its conservative variant and a
                                                                                                                                                                            John 1930
Jabola Type 1 repeat domain
Anotes "This region contains 3 type 1 repeats, from
residues 361-416, residues 417-473 and residues 474-530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 531. .673
/label= Type_2_repeat_domain
/note= "This region contains 3 type 2 repeats, from
residues 531-571, residues 572-629 and residues 630-673"
                                                                                                                                                                                                                                                                                                                                                                                                           note= "Necessary and sufficient for activation of ransforming growth factor beta (TGF beta)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118. .423
|Jabel= TGF-beta_and_fibronectin_binding_domain
|note= "Transforming growth factor"
                                                                                                                label= Procollagen_homology_domain
note= "Required in_inhibition of anglogenesis"
                                                     Procollagen_homology_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-angiogenesis domain
                                                                                                                                                                                                                                                                                                .64. .370
/label= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20. .426
|abel= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calcium_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               413. .415
/label= RFK motif
/note= "Necessary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 7; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2001; 2001WO-US017250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000; 2000US-0207994P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .434
/label= rr<sup>7</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .491
| label= 7
                         , 1abel= Pr
                                                                                    309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570. .601
/label= Ca
```

```
rheumatoid arthritis, psoriasis, ocular angiogenic diseases (e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, necvascullar glaucoma, retrolental fibroplasias, rebeosis), Osler-Webber syndrome, myocardial angiogenesis, telangiectasia, plaque neovascularisation, haemophiliac joints, angiofibroma or wound granulation. The composition induces apoptosis and inhibits neovascularisation in the tumour cells. This amino acid sequence represents human thrombospondin-1 (TSP-1), on which the recombinant proteins of the invention are based
                                                                                                                                                                                                                                                                                                                                                                 Query Match

90.3%; Score 56; DB 5; Length 1152;
Best Local Similarity 91.7%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                Sequence 1152 AA;
            888888888888
```

; 0

Gaps

o'

Search completed: June 5, 2006, 22:24:58 Job time: 94.1379 secs

1 FQGVLNNVRFVF 12 ||||||||||| 190 FQGVLQNVRFVF 201

ઠે

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

Run on:

5, 2006, 22:25:22 ; Search time 13.9655 Seconds (without alignments) 82.675 Million cell updates/sec

US-10-030-735-24 62 Perfect score:

1 FOGVLNNVRFVF 12 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	thrombospondin 1	Н	thrombospondin 1 p	rot	ribose/galactose A	probable receptor	probable membrane	thrombospondin 2 p	thrombospondin 2 p	the	valy1-tRNA synthet	excinuclease ABC c	excinuclease ABC,	hypothetical prote	H+-transporting tw		hypothetical prote	thrombospondin pre	5-oxoprolinase (AT	mannuronan C-5-epi	probable 3-oxoacyl	3-oxoacyl-[acyl-ca	hypothetical prote					probable integral	reverse gyrase (to
SUMMARIES		957	TSHUP1	A40558	B82881	F70184	B96693	AC0347	TSHUP2	A42587	AB1631	AH1268	C97893	F95021	S56224	D84938	T48484	G90095	A39804	T42756	S77626	A64590	B71923	C72207	869659	873396	T23843	S75664	T39891	377
	ΩI	. 85	TSH	A40	B82	F70	B96	ACO	TSH	A42	AB1	AH1	C97	F95	S 26	D84	T48	690	A39	T42	877	A64	B71	C72	869	873	T23	375	T39	H69
	BB	7	-	7	7	~	7	7	Н	7	7	~	7	~	7	~	7	~	н	7	~	Н	7	7	7	~	~	~	7	7
	* Query Match Length	i on	1170	1170	597	311	876	465	1172	1172	882	883	943	943	385	467	569	755	1178	1288	1839	247	247	271	316	440	265	603	834	1054
4	Query Match	90.3	90.3	90.3	64.5	65.9	65.9	61.3	61.3	61.3	59.7	59.7	59.7	59.7	58.1	58.1	58.1	58.1	58.1	58.1	58.1	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5
	Score	- 26	26	26	40	39	39	38	38	38	37	37	37	37	36	36	36	36	36	36	36		35	35		35		35	35	35
	Result No.		7	m	4	S	9	7	œ	σ	10	11	12		14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

tricorn proteinase	probable exported	sulfonylurea recep	hypothetical prote	hypothetical prote	genome polyprotein	DNA-activated prot	probable membrane	enterotoxin Yentl	probable pilin, ty	imidazoleglycerol-	probable imidazole	probable aryl phos	hypothetical prote	transcription regu	cell surface prote
T43255	AD0428	A56248	AE1864	T34274	GNVSTV	A57099	S52596	B89969	B75421	B64363	D81929	A75009	T34271	B96922	F89883
N	N	~	N	~	Н	ď	~	~	N	N	~	~	N	~	~
071	1305	1582	1829	2018	3005	4096	111	133	186	198	212	262	304	306	350
Ä															
56.5 1	56.5	56.5	56.5	56.5	56.5	56.5	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8
35 56.5 10		35 56.5	35 56.5	35 56.5	35 56.5		34 54.8								

ALIGNMENTS

RESULT 1 S57957 thrombospondin 1 - bovine (fragment) C;Species: Bos primigenius taurus (cattle) C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004 C;Accession: S57957 R;Lafeuillade, B: Pellerin, S: Keramidas, M.; Chambaz, E.M.; Feige, J.J.
Budmitted to the Embi Data Library, July 1993 A;Description: Opposite regulation of thrombospondin-1 and CISP/thrombospondin-2 expressi A;Reference number: S57955
A;Accession: S57957 A;Status: preliminary A;Molecule type: mRNA A:Residues: 1-29 <1AF>
A;Cross-references: UNIPROT:Q28194; UNIPARC:UP1000008740A; EMBL:X89511; NID:g899228; PIDN C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
Query Match 90.3%; Score 56; DB 2; Length 229; Best Local Similarity 91.7%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 FOGVLNNVRFVF 12 à

190 FQGVLQNVRFVF 201 g

RESULT 2

thrombospondin 1 precursor - human

Cipecides: Homo sapiens (man)
Cipace: 23-Aug-1997 #sequence revision 03-Aug-1995 #text change 09-Jul-2004
Cipace: 23-Aug-1997 #sequence revision 03-Aug-1995 #text change 09-Jul-2004
Cipaces: 0. Aug-1997 #sequence revision 03-Aug-1995 #text change 09-Jul-2004
Cipaces: 0. Aug-1997 #sequence revision 03-Aug-1995 #text change 09-Jul-2004
Cipaces: 0. Aug-1997 #sequence revision 05-Aug-1996
AyTitle: The structure of human thrombospondin, an adhesive glycoprotein with multiple of AyTitle: The structure of human thrombospondin, an adhesive glycoprotein with multiple of AyRecession: A26155, MulD:87057617; PMID:2430973
AyRecession: A26155
AyRoccession: A34274; MulD:89291870; PMID:2544587
AyRecession: A34274; MulD:89291870; PMID:2544587

A;Molecule type: DNA A;Residues: 1-166 <LMH> A;Cross-references: UNIPARC:UPI00001742BF; GB:J04835 K;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, I J. Cell Biol. 108, 729-736, 1989 A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the

us-10-030-735-24.rpr

```
hypothetical protein UU519 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000 C;Access, J.1.; LefKowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini A;Reference number: A82870 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: preliminary; not compared with conceptual translation
A,Molecule type: mRNA
A,Residues: 1-1152, P'.1154-1170 <LAH>
A,Residues: 1-1152, P'.1154-1170 <LAH>
A,Residues: 1.1152, P'.1154-1170 <LAH>
A,Residues: UNIPARC: UPI0000177A96; GB:M87276
A,Note: sequence extracted from NCBI backbone (NCBIP:81501)
R,Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A,Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar
A,Reference number: S68787; MUID:96234006; PMID:8654563
                                                                                                                                                                                                                                                                                                                                                                                             A);Residues: 1-1170 cLAW>
A);Residues: 1-1170 cLAW>
A);Residues: 1-1170 cLAW>
A);Cross-references: UNIPROT:P35441; UNIPARC:UPI0000028012; GB:M62469; GB:M62469; GB:M62465; GB:M62462; GB:M62463; GB:M62464; GB:M62465; GB:M62465; GB:M62463; GB:M6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 19-26, XY, 28-37 < CHE>
A;Residues: 19-26, XY, 28-37 < CHE>
A;Cross-references: UNIPARC:UPI0000177A97
C;Complex: homotrimer, disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor C;Superfamily: thrombospondin 1; EGF homotrimer
C;Keywords: calcium binding; glycoprotein; homotrimer
F;1-18 Domain: signal sequence #status predicted <SIG>
F;19-1170/Product: thrombospondin 1 #status predicted <AMT>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;431-547/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-547/Domain: EGF homology <EGF>
F;551-586/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UPI00000C1CA3; GB:AE002150; GB:AF222894; NID:g6899515; PIDN:7
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Residues: 1-490 <BOR>
A, Residues: 1-490 <BOR>
A, Cross-references: UNIDARC: UPI000016D076; GB:J05605; GB:J05606; NID:g201991; PIDN:AAA406; A; Cross-references: UNIDARC: Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A, Title: Characterization of mouse thrombospondin 2 sequence and expression during cell §
A, Reference number: A42587; WUID:92147683; PMID:1371115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 2; Length 1170;
Pred. No. 0.025;
0; Mismatches 1; Indels
                                                                A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOGVLNINVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A37905
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-490 <B
                                                                                                                                                                                                         A; Accession: A40558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vd C. Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vd C. Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vd C. F. 19-1170/Product: thrombospondin 1 #status predicted <EGS. F. 19-1170/Product: thrombospondin 1 #status predicted <EGS. F. 19-1170/Promain: von Willebrand factor type C repeat homology <VWC> F. 19-127/Domain: thrombospondin type 1 repeat homology <THR2> F. 19-149/Domain: thrombospondin type 1 repeat homology <THR3> F. 19-147/Domain: thrombospondin type 1 repeat homology <THR3> F. 19-154/Domain: EGF homology <EGFP> F. 19-154/Domain: EGFP homology <EGFP homology <EGFP
                                                                                                                   A; McCecule type: mRNA
A; Residues: 1-83, 'A', 85-522, 'A', 524-1170 < HEN>
A; Residues: 1-83, 'A', 485-522, 'A', 524-1170 < HEN>
A; Residues: 1-83, 'A', 485-522, 'A', 524-1170 < HEN>
A; Cross-references: UNIPARC: UP10000138AB1; EMBL: X14787; NID:g37464; PIDN:CAA32889.1; PID
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
B; Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A; Title: Partial amino acid sequence of human thrombospondin as determined by analysis of
A; Reference number: A25812; MUID:87157592; PMID:303096
A; Accession: A25812
A; MUID:87157592; PMID:303096
A; Residues: 1-83, 'A', 85-397
A; Cross-references: UNIPARC: UP1000016B0CA; GB: M25631; NID: G538353; PIDN: AAA36741.1; PID:
B; Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A; Reference number: A05172;
A; A; Accession: A05172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-83, A', 85-374, 'RC' <DIX>
A; Cross-references: UNIPARC:UPI000016B140; GB:M14326; NID:G340005; PIDN:AAA61237.1; PID:
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
R; Sun, X.; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A; Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A; Reference number: A42927; MUID:92348511; PMID:1379247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787
Ŗ;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
number: A30140; MUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.3%; Score 56; DB 1; 91.7%; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 987-1003 <SUN>
A;Cross-references: UNIPARC:UPI00001742C0
A;Note: Cys-992 is shown to have a free sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: the list of introns may be incomplete C; Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: GDB:THBS1; TSP1; TSP
;Cross-references: GDB:120438; OMIM:188060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 FÓGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Map position: 15q15-15q15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombospondin 1 precursor
```

Intron8: 23/1

RESULT 3

용 ઠે

g ò

```
C;Species: Yersinia pestis
C;Daces: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0347
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; i
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, F. Nature, 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ritabell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
Affitle: Sequence and characterization of the complete human thrombospondin 2 cDNA: poter
A;Reference number: A47379; MUID:94010892; PMID:8406456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Molecule type: mRNA
A;Roseidues: 1.1172 ciAB3.
A;Cross-references: UNIPROT: P35442; UNIPARC: UPI0000046680; GB:L12350; NID:g307505; PIDN:;
A;Cross-references: UNIPROT: P35442; UNIPARC: UPI0000046680; GB:L12350; NID:g307505; PIDN:;
R;LaBell, T.L.; Milewicz, D.J.; Disteche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992.
A;Title: Thrombospondin II: partial CDNA sequence, chromosome location, and expression of A;Reference number: A42173; MUID:92217961; PMID:1559694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Description: participates in cell migration and adhesion, and in platelet aggregation C, Superfamily: thrombospondin 1; BGF homology; thrombospondin type 1 repeat homology; vor C, Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer F;1-18/Domain: signal sequence #status predicted <SIG>-11-172/Product: thrombospondin 2 #status predicted <MAID>-177/Domain: von Willebrand factor type C repeat homology <VWC>-1310-377/Domain: thrombospondin type 1 repeat homology <THRID-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: Q8ZCV8; UNIPARC: UP100000DC696; GB: AL590842; PIDN: CAC92102.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A47379; A42173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AC0347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                              probable membrane protein yegB [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 465,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 560-1172 <LA2>
A;Cross-references: UNIPARC:UP100001742C1; GB:M81339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , DB 2;
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.3%; Score 38; DB Best Local Similarity 70.0%; Pred. No. 26; Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: GDB:128789; OMIM:188061
A,Map position: 6q27-6q27
C;Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: multidrug-efflux transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombospondin 2 precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 FQGMLNALRF 371
                                                                             |:|||||:|
393 FRGVLNNLR 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLNNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-465 <KUR>
                                          1 FOGVLINIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: GDB:THBS2; TSP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A47379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: A42173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: yegB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                       d
                                             ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Figure C. M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Aritle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-311 «KLE»
A,Fresidues: 1-311 «KLE»
A,Cross-references: UNIPROT: 051622; UNIPARC: UPI000005758D; GB: AE001168; GB: AE000783; NID
A,Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Bansen, N.F.; Hughes, B.; Huzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Titles: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribose/galactose ABC transporter, permease protein (rbsC-2) homolog - Lyme disease spird
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable receptor serine/threonine kinase PR5K T4024.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNIPROT: Q9C622; UNIPARC: UP1000004840F; GB: AE005173; NID: g11128393;
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
C;Genetics:
A;Gene: UUS19
A;Genetic Code: SGC3
C;Superfamily: Ureaplasma urealyticum hypothetical protein UU520
                                                                                                                                                                        Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.9%; Score 39; DB 2; Length 876; 77.8%; Pred. No. 33; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: probable ribose ABC transporter rbsC-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.9%; Score 39; DB 2; 50.0%; Pred. No. 11;
                                                                                                                                                                     Score 40; DB 2;
Pred. No. 14;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                     64.5%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | |:|| |:|
131 FDGILNKTSFIF 142
                                                                                                                                                                                                                                                                                                                                                 397 QGILNNPRLVY 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVLANWARFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                          2 QGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                    Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Residues: 1-876 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: F70184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: B96693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: T4024.2
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
```

RESULT 6

셤 ઠે

```
Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 59.7%;
Local Similarity 70.0%;
hes 7; Conservative 1
                                                                                                                                                                                                                                                                                        C,Genetics:
A,Gene: valS
C,Superfamily: valine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                               59.7%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: valine-tRNA ligase
         Schlueter, T.; Simoes,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    838 QCKLNNERFI 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           839 OCKLNNERFI 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QGVLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 OGVLNNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: AH1268
A;Status: preliminary
A,Molecule type: DNA
A;Residues: 1-883 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-943 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: C97893
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: valS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CjAccession: AB1631
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Cglaser, P.; Frangeul, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karet, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A MOLECULE TYPE: MENA
A, Residues: 1-873 -808.
A, Residues: 1-873 -808.
A, Cross-references: UNIPARC: UPI000016D077; GB:M64866; NID:g201994; PIDN:AAA40432.1; PIDD:
A, Cross-references: UNIPARC: UPI000016D077; GB:M64866; NID:g201994; PIDN:AAA40432.1; PID:
C, Superfamily: thrombospondin 1; EGF homology; thrombospondin Cype 1 repeat homology cymC>
C, Keywords: calcium binding; glycoprotein
E, 3191-377 Domain: von Willebrand factor type C repeat homology cymC>
F, 380-431 Domain: thrombospondin type 1 repeat homology cymR1>
F, 436-492 Domain: thrombospondin type 1 repeat homology cymR3>
F, 553-588 Domain: EGF homology comProver 1 repeat homology cymR3>
F, 552-691 Domain: EGF homology comProver 1 repeat homology cymR3>
   F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
F;553-588/Domain: EGF homology <EGF1>
F;552-691/Domain: EGF homology <EGF2>
F;552-691/Domain: EGF homology <EGF2>
F;151,316,330,457,584,710,1069/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;167-226/Disulfide bonds: #status predicted
F;266,270/Disulfide bonds: interchain #status predicted
F;266,270/Disulfide bonds: homology site: carbohydrate (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-1172 < LAMP
A;Residues: 1-1172 < LAMP
A;Residues: 1-1172 < LAMP
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
A;Note: sequence extracted from NCBI backbone (Thbs2) exists in the mouse genome.
A;Reference number: A39851; MUID:91302287; PMID:1712771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C,Accession: A42587, A39851
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
J. Biol. Chem. 267, 3274-3281, 1992
A;Fitche: Characterization of mouse thrombospondin 2 sequence and expression during cell A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: A42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          valyl-tRNA synthetase [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                     Score 38; DB 1; Length 1172;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 2;
Pred. No. 71;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  2: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombospondin 2 precursor - mouse C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                     61.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A39851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
```

```
Valy1-ERNA synthetase [imported] - Listeria monocytogenes (strain EGD-e)
C; Species: Listeria monocytogenes
C; Accession: AH1268
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q8Y6X9; UNIPARC:UPI00000552A3; GB:NC_003210; PIDN:CAC99630.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispecies: Streptococcus pneumoniae
Cispecies: Oct.-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Cispecies: C97893
Ridoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Este, F.; Lemblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.; P.; Sun, P.M.; Winkler, M.B.
J. Bacteriol. 183, 5709-5717, 2001
A, Bacteriol. 183, 5709-5717, 2001
A, Tuthors: Yang, Y.; Younge Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A, Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A, Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q92BG2; UNIPARC:UPI0000CCSDA; GB:AL592022; PIDN:CAC96818.1; A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q97SX7; UNIPARC:UPI0000137E9B; GB:AE007317; PIDN:AAK98975.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
A,Title: Comparative genomics of Listeria species.
A,Reference number: AB1077; MUID:21537279; PMID:11679669
A,Accession: AB1631
A,Status: preliminary
A,Rolecule type: DNA
A,Residues: 1-882 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 2;
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 2; Pred. No. 81; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 81;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain EGD-e
```

```
5, 2006, 22:44:57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGVLNNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|:| |:||
10 FRGILMNLRF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June
Job time: 15.9655 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: fli1; BU076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross.references: 1-943 cKUR>
A;Cross.references: UNIPROT:Q97SX7; UNIPARC:UPI0000137E9B; GB:AE005672; PIDN:AAK74367.1;
A;Experimental source: strain TIGR4
C;Genetics:
C;Genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: F95021
C;Accession: F95021
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <MIR>
A;Cross-references: UNIPROT:P43567; UNIPARC:UPI000013AE1E; EMBL:D50617; NID:g836685; PIC
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        excinuclease ABC, chain A [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein YFL030w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 05-Oct-2004
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
C;Genetics:
A;Gene: uvrA
C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 385;
                                                                                                                                                          Length 943
                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: SGD:S0001864
A;Map position: 6L
C;Superfamily: serine-pyruvate/aspartate aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.1%; Score 36; DB 2;
66.7%; Pred. No. 50;
/ative 0; Mismatches
                                                                                                                                                      Query Match 59.7%; Score 37; DB 2; Best Local Similarity 55.6%; Pred. No. 87; Matches 5; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 2;
Pred. No. 87;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.7%;
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 FORVLKNTRAVF 51
                                                                                                                                                                                                                                                                                                                                                                  |:||:||::
373 FEGVINNIK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 FEGVINNIK 381
                                                                                                                                                                                                                                                                                                                         1 FQGVLNNVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLINNVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: F95021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  æ
                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

```
C;Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain } C;Keywords: hydrolase
H+-transporting two-sector ATPase (EC 3.6.3.14), flagellum-specific [imported] - Buchnera
                                                                                                                                                                                      Ä
                               C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C;Accession: D84938
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A;Reference number: A84930; MUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNS
A;Residues: 1-467 <STO>
A;Residues: UNIPARC:UP1000005E44F; GB:AP000398; GSPDB:GN00144
A;Cross-references: UNIPARC:UP1000005E44F; GB:AP000398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 2;
Pred. No. 62;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain APS
```

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

Run on:

June 5, 2006, 22:09:41 ; Search time 108.931 Seconds (without alignments) 101.901 Million cell updates/sec

US-10-030-735-24 62 1 FQGVLNNVRFVF 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2849598 seqs, 925015592 residues Searched:

2849598 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% '
Maximum Match 100%
Listing first 45 summaries

Database :

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O28194 bos taurus			P07996 homo sapien	P35441 mus musculu	_	Q71sa3 rattus norv	Q80yq1 mus musculu	_	P35448 xenopus lae	Q59e99 homo sapien	Q5spg5 brachydanio	Q48758 tetraodon n	Q5u903 sus scrofa	Q4rlr5 tetraodon n	Q4rg74 tetraodon n	_	Q467v1 methanosarc	_	_	_	_	_	Q44x12 burkholderi		Q4yq55 plasmodium			Q8r808 thermoanaer	Q4dwh6 trypanosoma	Q7z2b9 trypanosoma
	028194 BOVIN	O7SY84 XENLA	TSP1 BOVIN	TSP1_HUMAN	TSP1_MOUSE	Q3TR40_MOUSE	Q71SA3_RAT	Q80YQ1_MOUSE	Q8CGB2_MOUSE	TSP1_XENLA	Q59E99 HUMAN	Q5SPG5_BRARE	Q4S758_TETNG	Q5U903_PIG	Q4RLR5_TETNG	Q4RQ74_TETNG	Q8PRY3 METWA	Q467V1 METBA	Q8TLX6_METAC	Q60XF5_CAEBR	Q83E24_COXBU	Q2L5R0_CLOPE	Q3F1U8_9BURK	Q44XL2_9BURK	Q4LLM8_9BURK	Q4YQ55_PLABE	Q9PPX0 UREPA	Q8RCIO THETN	Q8R808_THETN	Q4DWH6_TRYCR	Q7Z2B9_TRYCR
Length DR		496 2	1170 1	1170 1	1170 1		1170 2			1173 1	•		1193 2	249 2	1171 2	1034 2	727 2	730 2	733 2	84 2	100 2	•		713 2	713 2	•			689 2	· ·	1034 2
& Query March 1	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	82.3	82.3	90.6	90.6	74.2	71.0	71.0	71.0	67.7	67.7	67.7	67.7	67.7	67.7		64.5		64.5		64.5
Springer	95	26	26	99	99	99	26	99	99	26	99	51	51	20	20	46	44	44	44	42	42	42	42	42	42	40	40	40	40	40	40
Result		101	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27		29		31

N

```
214 FOGVLQNVRFVF 225
셤
                                                                                                                                                           TISSUE=Whole;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

W. Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rahla S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rahla S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunbaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Alilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                   Xenopus laevis (African clawed frog).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50092; TSP1; 2.
PROSITE; PS01208; WWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_2; UNKNOWN_1.
SEQUENCE 496 AA; 54843 MW; E4FD2P07CB7EF51B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, BC054970, AAH54970.1, -; mRNA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR0131320; Cona like subgrp.
InterPro; IPR03129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.3%; Score 56; DB 2;
91.7%; Pred. No. 0.085;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 91.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1705; TSPIREPEAT.
SMART; SM00209; TSP1; 2.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP 1.
InterPro; IPR01007; VWF_C.
Pfam; PF00090; TSP 1; 2.
Pfam; PF00090; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             initiative.
```

```
C. I. FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, call-to-matrix interactions. Can bind to fibrinogen, fibronectin, call-to-matrix interactions. Can bind to fibrinogen, fibronectin, call-to-matrix interactions. Can bind to fibrinogen. fibronectin, call-to-matrix alpha-V/beta-1. alpha-V/beta-1. alpha-V/beta-3 and alpha-III/beta-3. May play a role in dentinogenesis and/or maintenance of dentin and dental pulp.

C. I. SUBULAT: Homorrimer; disulfide-linked.

C. I. SIMILARITY: Contains 3 EGF-like domains.

C. SIMILARITY: Contains 1 TSP C-terminal (TSPN) domain.

C. SIMILARITY: Contains 7 TSP type-1 domains.

C. SIMILARITY: Contains 7 TSP type-1 domains.

C. SIMILARITY: Contains 7 TSP type-1 domains.

C. SIMILARITY: Contains 7 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Aortic_endothelium;
Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin stimulatory effect of
                                                                                                                                                                                                                                                                STRAIN=HOlstein; TISSUE=Tooth; MEDLINE=98173773; PubMed=9507054; DOI=10.1016/S0167-4838(97)00188-X; Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                     Indue H.; "cDNA cloning of bovine thrombospondin 1 and its expression in odontoblasts and predentin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
TSPI BOVIN STANDARD; PRT; 1170 AA. 028178; 028179; 01-NOV-1997, integrated into UniProtKB/Swiss-Prot. 01-DEC-2000, sequence version 2. 07-MAR-2006, entry version 56.
                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA] OF 1-18 AND 710-1170.
                                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 1382:17-22(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S55501; S55501.

HSSP; P07996; 11.51.

SMR; Q28178; 549-1169.

GlycoSuiteDB; Q28178; -
InterPro; IPR013320; ConA_like_subgrp.
InterPro; IPR006210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF 3.

EGF Ca bd.

EGF like.

EGF like reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB005287; BAA21115.1; -; mRNA.
EMBL; X87618; CAA60950.1; -; mRNA.
EMBL; X87619; CAA60951.1; -; mRNA.
                                                                                               Thrombospondin-1 precursor.
Name=THBS1; Synonyms=TSP-1, TSP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006209; EGF like
InterPro; IPR01302; EGF like
InterPro; IPR0130129; Laminin,
InterPro; IPR00884; TSP1.
InterPro; IPR00885; TSP1.
InterPro; IPR00885; TSP C.
InterPro; IPR008859; TSP C.
                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00008; EGF; 1.
Pfam; PF00090; TSP 1; 3.
Pfam; PF02412; TSP 3; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000742;
                                                                                                                                    Bos taurus (Bovine).
```

; 0

Gaps

ò

1; Indels

1 FQGVLNNVRFVF 12

ò

11;

```
ઠે
                                                                                                                                                   TSP type-1 1.
TSP type-1 2.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2.
EGF-like 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 4.
TSP type-3 4.
TSP type-3 5.
TSP type-3 7.
TSP C-terminal.
Heparin-binding (Potential).
N-linked (GlCNAc. ..) (Potential).
Interchain (Probable).
                                                                                                EGF-like domain; Glycoprotein;
                                                                                                                       Thrombospondin-1.
/FTId=PRO_0000035841.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity.
Similarity.
                                                                                                                By similarity
                                                                                                                                                                                                                                                                                                                                   similarity
                                                                                                                                                                                                                                                                                                                                                                similarity
similarity
                                                                                                                                                                                                                                                                                                                                                                               similarity
similarity
                                                                                                                                                                                                                                                                                                                                                                                              similarity
similarity
                                                                                                                                                                                                                                                                                                                                                                                                              similarity.
Similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                             similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity
                                                                                                                                                                                                                                                                                                                                           similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity
                                                   PROSITE; PS000022; BGF_1; FALSE_NEG. PROSITE; PS01186; BGF_2; 1. PROSITE; PS00026; BGF_3; 2. PROSITE; PS50092; TSPI; 3. PROSITE; PS01208; WFFC_1; 1. PROSITE; PS50144; WFFC_2; 1. Calcium; Cell adhesion; BGF-like dome
                                                                                                                                               VWFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۰
                                                                                                        Signal.
                                                                                                                                                                                                                                                                                                                                  129534 MW;
        Pfam; PF00093; VWC; 1.
PRINTS; PR01705; TSPIREPEAT.
SMART; SM00181; EGF; 3.
SMART; SM002109; TSP1; 3.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                         Repeat;
Pfam; PF05735; TSP_C; 1.
Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                   1067
1085
270
274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            805 80
1170 AA;
                                                                                                       Heparin-binding;
SIGNAL
CHAIN 19
                                                                                                                                                                                                                                                                                                                                                               451
462
504
508
                                                                                                                                                                                                                                                                                    360
708
1067
1085
270
274
                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                              PARBOHYD
                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                              REGION
MOTIF
                                                                                                                                       DOMAIN
                                                                                                                                               DOMAIN
                                                                                                                                                              DOMAIN
                                                                                                                                                                      DOMAIN
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                        DOMAIN
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE OF 1-374.
MEDLINE=86287276; PubMed=3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
"Characterization of a cDNA encoding the heparin and collagen binding domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 1-397.
MEDIJNE=87157592; PubMed=3030396;
KObayashi S., Eden-Mccutchan F., Framson P., Bornstein P.;
"Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 1-166.

MEDLINE-89291870; PubMed=2544587;
Laherty C.D., Gierman T.M., Dixit V.M.;
"Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.";
J. Biol. Chem. 264:11222-11227(1989).
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VICLEOTIDE SEQUENCE.
TISSUE=Endothelial cell;
MEDLINE=87057617; PubMed=2430973; DOI=10.1083/jcb.103.5.1635;
MEDLINE=87057677; PubMed=2430973; DOI=10.1083/jcb.103.5.1635;
Lawler J., Hynes R.O.;
"The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89139590; PubMed=2918029; DOI=10.1083/jcb.108.2.729; Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L., Baumgartel D.M., Rotwein P., Frazier W.A.; "Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region."; J. Cell Biol. 108:729-736(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE OF 1028-1170.

La Fleur M., Jobin C., Gauthier J., Kreis C.G.;

La Expression of thrombospondin in chronic inflammation: neutrophils from synovial fluids synthesize a novel 3.9 kD TSP mRNB.";

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441; THR-460; TRP-498 AND THR-507.
THR-460; TRP-498 AND THR-507.
TISSUE=platelet;
MEDLINE=21125860; Pubmed=11067851; DOI=10.1074/jbc.M008073200;
                                                         1; Indels
                                                                                                                                                                                                                         TSPI_HUMAN STANDARD; PRT; 1170 AA.
P07956; Q15667;
01-3046-1988, integrated into UniProtKB/Swiss-Prot.
01-AUG-1988, sequence version 1.
07-MAR-2006, entry version 78.
                   DB 1;
                 Score 56; DB 1;
Pred. No. 0.22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins.";
J. Cell Biol. 103:1635-1648(1986)
                                                                                                                                                                                                                                                                                                                      Thrombospondin-1 precursor.
Name=THBS1; Synonyms=TSP, TSP1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochemistry 25:8418-8425(1986)
Query Match
Best Local Similarity 91...
and 11; Conservative
                                                                                                                                208 FOGVLONVREVE 219
                                                                                             1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oroteins.
                                                                                                                                                                                        KESULT 4
TSP1_HUMAN
                                                                                                                                                                                                                               G (in Ref. 2).
ODD6ADF3E5FA031A CRC64;
```

```
Pfam; PF02412; TSP_3; 12.

R Pfam; PF0093; VGZ; 1.

Pfam; PF0093; VMCZ; 1.

R PRINTE; PR01705; TSPLREPEAT.

R SMART; SM00181; EGF; 3.

R MART; SM00219; TSP1; 3.

R MART; SM00214; VWC; 1.

R SMART; SM00214; VWC; 1.

R PROSITE; PS0026; EGF_2; 1.

R PROSITE; PS0026; EGF_2; 1.

R PROSITE; PS0026; EGF_2; 1.

R PROSITE; PS01208; VWFC_1; 1.

R PROSITE; PS01208; VWFC_1; 1.

R PROSITE; PS01208; VWFC_2; 1.

R PROSITE; PS0184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                TSP type-1 1.
TSP type-1 2.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2.
EGF-like 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 4.
TSP type-3 5.
TSP type-3 6.
TSP type-3 7.
TSP type-3 7.
TSP type-3 7.
TSP type-3 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=CAR 000210.
O-linked (Fuc. ..).
/FTId=CAR 000211.
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-linked (GlcNAc. .).
N-linked (GlcNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heparin-binding (Potential).
Cell attachment site (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 56; DB 1; Length 1170;
Pred. No. 0.22;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interchain (Probable)
Interchain (Probable)
                                                                                                                                                                                                                                                                                                                                                   Thrombospondin-1.
/FTId=PRO_0000035842.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=CAR 000205.
O-linked (Fuc. .)
/FTId=CAR 000206.
C-linked (Man).
/FTId=CAR 000207.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=CAR 000208.
O-linked (Fuc. . .)
/FTId=CAR 000209.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 FÓGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 91.7
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1067
270
270
274
423
413
474
541
541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   914
950
1170
232
928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  708
1067
270
274
391
395
406
447
451
504
508
                                                                                                                                                                                                                                                                                                                                                                                              2443
316
433
549
589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         646
723
723
729
729
818
841
841
879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
REGION
MOTIF
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                CARBOHYDRATE-LINKAGE SITES ASN-248 AND ASN-1067.

PubMed=16335952; DOI=10.1021/pr0502065;
Liu T., Qian W.-J., Gariesenko M.A., Camp D.G. II, Monroe M.E.,
Liu T., Qian W.-J., Gariesenko M.A., Camp D.G. II, Monroe M.E.,
A moore R.J., Smith R.D.;
Thydrazide chemistry, and mass spectrometry.";
Thydrazide chemistry, and mass spectrometry.";
J. Proceome Res. 4:2070-2080(205).

J. PROCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
I aminin, type V collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-IIb/beta-3.

Cell-to-matrix: Collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-IIb/beta-3.

Cell-to-matrix: Contains 1 TSP C-terminal (TSPC) domain.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 7 TSP type-1 domains.

SIMILARITY: Contains 7 TSP type-1 domains.

SIMILARITY: Contains 7 TSP type-1 domains.

SIMILARITY: Contains 7 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                          MEDLINE=22338361; PubMed=12450399; DOI=10.1021/bi026463u;
Huwller K.G., Vestling M.M., Annis D.S., Mosher D.F.;
"Biophysical characterization, including disulfide bond assignments,
of the anti-angiogenic type 1 domains of human thrombospondin-1.";
Biochemistry 41:14329-14339(2002).
    Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J., Mosher D.F., Peter-Katalinic J.; "C-mannosylation and O-fucosylation of the thrombospondin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0004866; F:endopeptidase inhibitor activity; TAS.
GO; GO:0004871; F:signal transducer activity; TAS.
GO; GO:0007275; P:development; TAS.
InterPro; IPR013320; ConA.like_subgrp.
InterPro; IPR065210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, M25631, AAA36741.1; "RRNA.
EMBL, X14787, CAA28370.1; "RRNA.
EMBL, X14787, CAA28370.1; "RRNA.
EMBL, X14787, CAA28389.1; "I MLY.
EMBL, M94426; AAA61237.1; ALT. SEO; MRNA.
EMBL, M99425; AAA61178.1; "Genomic_DNA.
EMBL, M99425; AAA61178.1; "Genomic_DNA.
EMBL, M99425; AAA61178.1; "RNA.
PDB, LSL, X-ray; A=434-546.
PDB; LLSL, X-ray; A=834-1170.
PDB; LZ78; X-ray; A=19-233.
PDB; LZ78; X-ray; A=19-257.
PDB; ERF; X-ray; A=19-257.
PDB; ERF; X-ray; A=25-233.
GlycoSuiteDB; P07996; --.
                                                                                                                              THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl; ENSG0000137801; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000742; EGF 3.
InterPro; IPR001881; EGF Ca bd.
InterPro; IPR00209; EGF Like.
InterPro; IPR01312; EGF Like reg.
InterPro; IPR003129; Laminin Grsp N.
InterPro; IPR000884; TSP1.
                                                                                     Biol. Chem. 276:6485-6498(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR008085; TSP 1.
InterPro; IPR008367; tsp 3.
InterPro; IPR008859; TSP C.
InterPro; IPR001007; VWF C.
Pfam; PF00008; EGF; 2.
Pfam; PF00090; TSP 1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC; HGNC:11785; THBS1.
MIM; 188060; gene.
Reactome; P07996; -.
                                                                      module.
```

ö

Gaps

```
24
3316
3316
4435
379
588
646
646
7723
7723
818
818
818
818
                                              M62464;
M62464;
M62465;
M62465;
M62466;
M62467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOTIF
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
REGION
                                                 EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
Pubmed-8654563; DOI=10.1016/0014-5793(96)00460-7;
Chen H., Aeschlimann D., Nowlen J., Mosher D.F.;
Chen H., Aeschlimann D., Nowlen J., Mosher D.F.;
TEXPression and initial characterization of recombinant mouse
Thrombospondin 1 and thrombospondin 3.";
Thrombospondin 1 and thrombospondin 3.";
Thrombospondin 1 and thrombospondin 3.";
Thrombospondin 1.";
TERS Lett. 387:36-41(1996).
Cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type V collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-IID/beta-3.
Cell-to-matrix: and alpha-IID/beta-3.
Cell-to-matrix: contains 3 EGP-like domains.
Cell-to-matrix: Contains 3 EGP-like domains.
Cell-to-matrix: Contains 3 TSP type-1 domains.
Cell-to-matrix: Contains 7 TSP type-1 domains.
Cell-to-matrix: Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukamalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3]
NUCLECTIDE SEQUENCE OF 1-490.
NUCLECTIDE SEQUENCE OF 1-490.
MEDLINE-90375546; PubMed=2398070;
MEDLINE-90375546.
MEDLINE-90375546; PubMed=2398070;
MEDLINE-10 P., Li P.;
Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";
Liberol. Chem. 265:16691-16698 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development."; J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92128941; PubMed-1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
Jenkins N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
MEDLINE-22147683; PubMed-1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of the murine thrombospondin gene.";
                                                                                                                                          01-JUN-1994, integrated into UniProtKB/Swiss-Prot. 01-JUN-1994, sequence version 1. 07-MAR-2006, entry version 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L; M62470; AAA50611.1; -; Genomic_DNA.
L; M62451; AAA50611.1; JOINED; Genomic_DNA.
L; M62451; AAA50611.1; JOINED; Genomic_DNA.
L; M62453; AAA50611.1; JOINED; Genomic_DNA.
L; M62453; AAA50611.1; JOINED; Genomic_DNA.
L; M62454; AAA50611.1; JOINED; Genomic_DNA.
L; M62455; AAA50611.1; JOINED; Genomic_DNA.
L; M62456; AAA50611.1; JOINED; Genomic_DNA.
L; M62459; AAA50611.1; JOINED; Genomic_DNA.
L; M62460; AAA50611.1; JOINED; Genomic_DNA.
L; M62460; AAA50611.1; JOINED; Genomic_DNA.
L; M62460; AAA50611.1; JOINED; Genomic_DNA.
                                                                                                PRT; 1170 AA
                                                                                                                                                                                              07-MAR-2006, entry version
Thrombospondin-1 precursor.
Name=Thbs1; Synonyms=Tsp1;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 11:587-600(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN SEQUENCE OF 19-37
                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                    [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                           TSP1 MOUSE P35441;
                                                                 TSPI MOUSE

TO TASPI MOUSE

TO TASPI MOUSE

DT OT ALLANDAR

OC MAMMANIA

OC MAMMANIA

OC MAMMANIA

RA LANALE

CC CC -1 - 6

CC C -1 -
```

```
| BRBI, M62467, AAA506111, JOINED, Genomic_DRA, M62467, M6
```

us-10-030-735-24.rup

```
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J; TISSUE=Aorta and vein;
PubMed=16141072; DOI=10.1126/science.1112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Baljic V. B., Brenner S. B., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Addinis V., Allen J.E.,
Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CSTBL/67; TISSUE-Aorta and vein;

MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

Carninci P., Aayashizaki Y.;

High-efficiency full-length cDNA cloning.";

Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-00T-2005, integrated into UniProtKB/TrEMBL.
11-0CT-2006, sequence version 1.
07 PEB-2006, entry version 5.
Adult male aorta and vein CDNA, RIKEN full-length enriched library, clone:A530055N06 product:thrombospondin 1, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 1; Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0443E493615E7F06 CRC64;
  N-linked (GlcNAc. . . )
Interchain (Probable).
Interchain (Probable).
By similarity.
N-linked (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129647 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q3TR40 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGULINNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 930
1167
1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Thbs1;
                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
03TR40 MOUSE
10 03TR40 MOUSE
DT 11-0CT-20
DT 11-0CT-20
DF 07-EBB-22
DF 07-EEB-20
DF 07-
                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                        DISULFID
                                                          DISULFID
                                                                              DISULFID
                                                                                                DISULFID
                                                                                                                  DISULFID
                                                                                                                                      DISULFID
                                                                                                                                                        DISULFID
                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

```
REALIMECTORESULOR SEQUENCE.

REALIMECSTREAGUE SEQUENCE.

REALIMECSTREAGUE SEQUENCE.

REALIMECSTREAGUE SEQUENCE.

REALIME SEQUENCE.

REALIME SEQUENCE.

REALIME SEQUENCE.

REALIME SEQUENCE.

REALID SETTING SETTION SETTION SETTION SETTION SETTION SETTION SETTION.

REALIME SETTION 
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
A di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Gistincio B., Harbers T.R., Gojobori T., Garen R.E.,
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikwan T.,
RA Mill D., Huminiecki L., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kalapin B.P., Krashran S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I W., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Matsuda H., Matsuawa S., Miki H., Mignone F., Miyake S., Morris K.,
Antsuda H., Matsuawa S., Miki H., Mignone F., Miyake S., Morris K.,
Antsuda H., Matsuawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mishikawa S., Nori F., Ohara O.,
RA Mottagui-Tabar S., Mishikawa S., Nori F., Ohara O.,
RA Petrovsky N., Piazza S., Miki H., Mignone R., Mishikawa S., Nori F., Ohara O.,
RA Petrovsky N., Sinzberg S.L., Sandelin A., Schneider C., Sensa L., Seno S., Tegner Y., Taki K.,
RA Sperling S., Stupka E., Sugiura K., Silva D., Sinclair B.,
Sperling S., Stupka E., Sugiura K., Silva D., Sinclair B.,
Amanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Tammoja K., Tan S.L., Tang S., Tegner J., Hide W., Bult C.,
RA Tammoja K., Tan S.L., Tang S., Tegner J., Yagi K.,
Amanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Tumond S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Huda J., Maki K., Watahiki A., Okamura-Oho Y., Suzuki H.,
Ragami J., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H.,
Ragami J., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Aorta and vein; PubMed=16141073; DOI=10.1126/science.1112009; RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 109:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 309:1559-1563(2005).
```

Laminin_G_TSP_N

```
IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003367;
InterPro; IPR008859;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Tsp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAT
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
Q71SA3_RA
   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carrallucioning Sequences:

NEDLINE-21085660; PubMed-11217851; DOI=10.1038/35055500;

MEDLINE-21085660; PubMed-11217851; DOI=10.1038/35055500;

MA Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Pukunishi Y., Konno H., Kadchi J., Pukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kaukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Kochiwa H.,

Radota K., Matsuda H.A., Ashburner M., Baldarelli R., Barsh G.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashizaki Y.;

A. Havashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Aorta and vein; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shoromalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/63; TISSUE-Aorta and vein;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATRAIN-CSTBL/6J. TISSUE-Aorta and vein;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK163092; BAE37190.1; -; mRNA.
MGI; MGI:98737; Thbs1.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0005615; P:negative regulation of angiogenesis; IDA.
InterPro; IPR000742; BGF.
InterPro; IPR0001891; EGF.
InterPro; IPR006209; EGF.
InterPro; IPR013032; EGF.like.
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Mětazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.3%; Score 56; DB 2; Length 1170; 91.7%; Pred. No. 0.22; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley;
Iwabu A., Hirohard S., Kusachi S., Nakamura K., Murakami
Ninomiya Y., Tsuji T.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01166; EGF 2; UNKNOWN 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50032; TSP1; 3.
PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS012084; VWFC 2; 1.
SEQUENCE 1170 AA; 129619 MW; 55BF04A20D91B194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMR; Q71SA3; 834-1169.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; P:structural molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0715A3 RAT PRELIMINARY; PRT; 1170 AA. 0715A3; 05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR013320; ConA_like_subgrp_interpro; IPR005420; BGF.
Interpro; IPR00142; BGF.3.
Interpro; IPR001881; BGF_Ca_bd.
Interpro; IPR001323; BGF_like.9.
Interpro; IPR013032; BGF_like.9.
Interpro; IPR013129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF309630; AAQ14549.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 9. Thrombospondin 1.
InterPro; IPR000808; TSP1.
InterPro; IPR0008367; tsp3.
InterPro; IPR0018085; TSPC.
InterPro; IPR001807; VWF_C.
Pfam; PF00008; EGF; 2.
Pfam; PF00412; TSP_1; 3.
Pfam; PF05735; TSP_C;
Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                          PRINTS, PRO1705; TSPIREPEAT.
SWART; SW00181; EGF; 3.
SWART; SW00210; TSP1; 3.
SWART; SW00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
```

```
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS50092; TSPI; 3.
PROSITE; PS01208; VWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01705; TSPIREPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBCGB2_MOUSE PRELIMINARY;
Q8CGB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00181; EGF; 3.
SMART; SM00209; TSP1; 3.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 CGB2

201 CGB2

202 CGB CGB2

203 CGB2

20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 1170 AA; 129671 MW; 6F38D3DCE733060F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
STRAIN=CS7BL/6; TISSUE=Brain;
Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nd mouse cDNA sequences.";
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.3%; Score 56; DB 2;
91.7%; Pred. No. 0.22;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBOYQI MOUSE PRELIMINARY; PRT; 1171 AA.
QBOYQ1;
                Pfam; PF00009; BGF; 2.
Pfam; PF00090; TSP 1; 3.
Pfam; PF00090; TSP 1; 3.
Pfam; PF02012; TSP 2; 1.2.
Pfam; PF020135; TSP 2; 1.2.
Pfam; PF020135; VWC; 1.
PRINTS; PR01705; TSPREEBEAT.
SWART; SW00181; EGF; 3.
SWART; SW00210; TSP1; 3.
SWART; SW00210; TSP1; 3.
SWART; SW00210; TSP1; 3.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01269; VWFC 1; UNKNOWN 1.
PROSITE; PS01269; VWFC 2; 1.
PROSITE; PS01269; VWFC 2; 1.
PROSITE; PS01208; VWFC 2; 1.
PROSITE; PS01269; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003, integrated into Unil
01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OVOLUMENTAL SERVICE SE
     g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombospondin 1 (Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full length enriched library, clone:G930018021 product:thrombospondin 1, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
EMBL; BCG50917; A4450917.1; -; mRNA.

R SNR; G0Y091 835-1170.

R SNR; G0Y00000040152; Mus musculus.

R G0; G070005615; C:extracellular space; RCA.

G0; G0.0005615; C:extracellular space; RCA.

G0; G0.0005615; C:extracellular space; IDA.

R InterPro; IPR001320; ConA_like_subgrp.

R InterPro; IPR001320; ConA_like_subgrp.

R InterPro; IPR001321; EGF.

R InterPro; IPR001321; EGF.

R InterPro; IPR001322; Laminin_G_TSP_N.

R InterPro; IPR001325; Laminin_G_TSP_N.

R InterPro; IPR001365; TSP_C.

R InterPro; IPR001367; tsp_3.

R Pfam; PF000109; TSP_C.

R Pfam; PF001009; TSP_C.

R Pfam; PF001009; TSP_C:

R Pfam; PF001006; TSP_C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56; DB 2; Length 1171; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1171 AA; 129690 MW; 12E077B50C64E2D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003, integrated into UniProtKB/TrEMBL 01-MAR-2003, sequence version 1. 07-FEB-2006, entry version 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
```

σ

```
REC TISSUE-Amammary gland;

RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Carninci P., Rasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Babalo V.B., Brenner S.E., Batalov S., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic V.B., Brenner S.E., Andinis V., Allen J.B., Zavolan M., Ambesi-Impionbaro A., Apweiler R.W., Baleney T.L., Ra Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., R. Britanck D. P., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Al Berrardo D., Down T., Engerrom P., Fagiolini M., Faulkner G., R. Hetcher C.F., Fukushima T., Furuno M., Fletakis V., Garishoffels A., Clutterbuck D.R., Garishoff M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Garisholdi M., Georgii-Hemming P., Katoh M., Kavasawa Y., Katason R.B., Hall D., Huminiecki L., Lacono M., Ikeo K., Iwama A., Ishikawa T., R. Aktanopin A., Katoh M., Kawasawa Y., Katason H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., M. Kurochkin I.W., Lareau L.F., Lazarevic D., Lipovich L., Liu J., M. Aktsuda H., Mateuzawa S., Miki H., Mignone F., Miyake S., Morris K., McMilliam S., McMilliam S., McMilliam S., McMilliam S., McMilliam S., Malando W., Bang K.C., Pavan M.J., Paveti G., Peetole G., Retrowsky N., Pang K.C., Pavan W.J., Paveti G., Senga L., Sheng Y., Shinada H., Shinada H., Shinada K., Sample C.A., Sensa L., Sensa L., Sheng Y., Shinada H., Shinada K., Sample C.A., Sensa L., Sensa L., Sheng Y., Shinada K., Tang S., Taylor M., Silva D., Sinclair B., Shinada H., Shinada K., Tang S., Taylor M., Bult C., Saskij D., Tockman S., Hide W., Bult C., Matlick J., Mathieredt C., Matlick J., Burshin H., Zabarovsky B., Zhu Wan H., Shinada H., Mahlestedt C., Matlick J., Bult G., Matlick J., Bult G., Matlick J., Bult G., Matlick J., Bult G., Thamary M., Hallaste H., Thamary M., Thoh M., Rator T., Raylor H., Malla
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Stanchez R.W., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and many and manae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Mammary gland;
MEDLINE-99279253; PubMed-10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                  cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki
                                                                                                                                                                                                                                                                                                                                                       monge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The
                                                                                                                                                                                                                                                                                                                                                  and
```

Science 309:1559-1563(2005).

NUCLEOTIDE SEQUENCE.

```
RC MUCLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266; RX NUCLEARMMENT YOUND N. KRANUKAWA T., Adachi J., BROND H., KRONDO S., RA OKAZAKI Y., Furunon M., KRANUKAWA T., Adachi J., BROND H., KRONDO S., RA NIKAIGO I., OBACKADURA N., SALTO R., SUZUKI H., YAMMARA H., KRYOBAWA H., YAMMARA T., ADACHI J., GOJODOTI T., RAJACHI J., MATSURA H., BRALLOVS, Beisel K. W., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., ARAGARIA H., BRALLOVS, Beisel K. W., Balder J. R., FILL C., Hume D.A., Quackenbush J., Rahagani T.A., Fletcher C.F., Forrest A., Ferzer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Aranaja A., Kawaji H., Kawasawa Y., Kadzierzki R.W., Brayis E.D., Ranaja A., Kawaji H., Kawasawa Y., Kadzierzki R.W., Perzer K.S., Kawaji H., Xawasawa Y., Kadzierzki R.W., Perser K., Sanglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Rayasahima T., Numater K., Okido T., Pavan W.J., Pertea G., Peeole G., Rayasahima T., Reed J.C., Reed D.J., Reid J., Ramachandran S., Barado R., Pontius J.U., Oli D., Ramachandran S., Solhedae K., Okido T., Pavan W.J., Pertea G., Manglott D.R., Wanghaw-Boris A., Yangie C.A., Secoul M., Shimada K., Salnada M., Yang L., Wang Y., Wall K., Kawai J., Alzawa K., Atakawa T., Fukuda S., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Saka K., Atana X., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Atana A., Hashizume W., Sasaki D., Shibata K., Sakazi K., Sasaki D., Shibata K., Shinagawa A., Hashizaki Y., Sasaki D., Shibata K., Shinagawa A., Hashizaki Y., Waterston R., Lander B.S., Rogers J., Kanala Y., Londor Based on functional annotation of Marter G. Manalysis of the mouse transcriptome based on functional annotation of Marters A., Manalysis of the mouse transcriptome based on functional annotation of Marters A., Manalysis of the mouse transcriptome M., Shinada W., Marterston R., Manalysis of the mouse transcriptome M., Shinada W., Shinada 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Mammary gland;

KEDLINE-2108566; PubMed=11217851; DOI=10.1038/3505500;

KEDLINE-2108566; PubMed=11217851; DOI=10.1038/3505500;

A Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov B., Kochiwa H.,

Richl P., Lewis S., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Puruno M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S.,

Nachonia A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Mammary gland;
MEDILIBE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDILIBE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
TISSUE=Mammary gland;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
    RETT BY REPARABLE REPARABL
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                       EMBL; L04278; -; NOT_ANNOTATED_CDS; mRNA.
HSSP; P07996; 1LSL.
                                                                                            SMR; P35448; 552-1172.
InterPro; IPR013320; ConA_like_subgrp.
InterPro; IPR006210; EGF.
InterPro; IPR000742; EGF.
InterPro; IPR0006209; EGF.
InterPro; IPR005209; EGF_like.
InterPro; IPR001303; EGF_like.
InterPro; IPR001303; EGF_like.
InterPro; IPR001303; EGF_like.
InterPro; IPR000845; TSPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heparin-binding; Repeat; Signal. SIGNAL 1 22 Pot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOTIF
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
DOMAIN
REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                    MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Aktyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.

TISSUB-Mammary gland;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Arakawa T., Carninci P., Fukuda S., Hashizume W., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramateu M., Hayashizaki Y.,
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=thbBl; Synonyms=tspl;
Renopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urry L.A., Ramos J., Duquette M., Desimone D.W., Lawler J., "Cloning, characterization and expression of thrombospondin-1 in Xenopus laevis embryos.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

90.3%; Score 56; DB 2; Length 1171;
Best Local Similarity 91.7%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC042422; AAH42422.1; -; mRNA.
EMBL; AK145202; BAE26293.1; -; mRNA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994, sequence version 1.
07-MAR-2006, entry version 54.
Thrombospondin-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
      NUCLEOTIDE SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSP1 XENLA
AC P35448
DT 01-JUN-1994,
DT 01-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
```

셤 ŝ

```
TSP type-1 1.
TSP type-1 2.
EGF-like 1.
EGF-like 2; calcium-binding (Potential).
EGF-like 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-linked (GlCNAC...) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSP type-3 1.
TSP type-3 2.
TSP type-3 3.
TSP type-3 4.
TSP type-3 4.
TSP type-3 5.
TSP type-3 6.
TSP type-3 7.
TSP type-3 7.
TSP type-3 7.
TSP Cereminal.
Heparin-binding (Potential).
Coll attachment site (Potential).
InterPro; IRRO00805; ISPI.
InterPro; IRRO00806; ISPI.
InterPro; IRRO00806; ISPI.
INTERPRO; ISPI.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombospondin-1.
/FTId=PRO_0000035844.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
By similarity
By similarity.
```

8

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barker D.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collegen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-2004, integrated into UniProtKB/TrEMBL.
21-DEC-2004, sequence version 1.
21-DEC-2004, sequence version 1.
21-DEC-2006, entry version 1.
21-DEC-2006, entry version 1.
21-DEC-2006, entry version 1.
31-DEC-2006, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.3%; Score 56; DB 2; Length 1225; 91.7%; Pred. No. 0.23; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1225 AA; 134849 MW; 9888B16E57157B12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; A1928866; CA120599.1; -; Genomic_DNA.
SMR; Q5SPG5; 751-804, 754-1089.
Ensembl; ENSDARGO000001010785; Danio rerio.
GO; GO: 0005509; F: calcium ion binding; IEA.
GO; GO: 0005509; F: calcium ion binding; IEA.
GO; GO: 0005519; F: heparin binding; IEA.
GO; GO: 0005519; F: protein binding; IEA.
GO; GO: 0005519; F: protein binding; IEA.
GO; GO: 0005519; F: protein binding; IEA.
INTERPRO; IPRO155; P: cell adhesion; IEA.
InterPro; IPRO150549; EF hand_Ca_bd.
InterPro; IPRO0510; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSSPGS BRARE PRELIMINARY; PRT; 1090 AA.
QSSPGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000742; EGF 3.
InterPro; IPR001881; EGF Cabd.
InterPro; IPR001881; EGF Cabd.
InterPro; IPR013032; EGF like reg.
InterPro; IPR003129; Laminin G TSP N.
InterPro; IPR000884; TSP 1.
InterPro; IPR000885; TSP 1.
                                                                                                                                                                                                                                                                                                                  PROSITE; PSO1186; EGF 2; 1.
PROSITE; PSO1026; EGF 3; 2.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS500208; VWFC 1; 1.
PROSITE; PS50184; VWFC 1; 1.
Cell adhesion; EGF-like domain.
NON TER
SEQUENCE 1225 AA; 134849 WW;
                        Pfam; PP00008; EGF; 2. — Pfam; PP00008; EGF; 2. — Pfam; PP002412; TSP_1; 3. Pfam; PP05735; TSP_C; 1. PRINTS; PP07705; TSPLREBEAT. SMART; SM00101; EGF; 3. SMART; SM00209; TSPL; 3. SMART; SM00101; EGF; 3. SMART; SM00101; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 FOGVLONVRFVF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAR WEED BY A TO DE STANK A TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Aorta endothelial cell;
TISCOKI Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 1; Length 1173; Pred. No. 0.22; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130020 MW; A9F036D6516C0F24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005201; F:heparin binding; IEA.
GO; GO:0005515; F:hrotein binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QS9E99_HUMAN PRELIMINARY; PRT; 1225 AA.
                                                                                                              similarity
                                                                                                                                                   similarity
                                                                                                                                                                           similarity.
similarity.
                                                                                                                                                                                                                                      Bimilarity
                                                                                                                                                                                                                                                                                                                               similarity
                                                                                                                                                                                                                                                                                                                                                          similarity
                                                                                                                                                                                                                                                                                                                                                                                      similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity
                                                                                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity
                                                                                                                                                                                                                                                                                                similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB209912; BAD93149.1; -; mRNA.
SMR; Q59E99; 886-939, 889-1225.
Ensembl; ENSG0000137801; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; Irroscotti, BGF.
InterPro; IPR006210; BGF.
InterPro; IPR0172; BGF.
InterPro; IPR01881; BGF.Ca bd.
InterPro; IPR016209; BGF.like.
InterPro; IPR013032; BGF.like.
InterPro; IPR013129; LamInin.G.TSP.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO: 0007155; P:cell adhesion; IEA.
InterPro; IPR013320; ConA_like_subgrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-2005, sequence version 1.
21-FEB-2006, entry version 10.
Thrombospondin 1 variant (Fragment).
   90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 FQGVLQNVRFVF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         913 93
949 117
1173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro; IPR000884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR008859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
5554
559
559
6623
6623
6623
6623
6623
7721
7721
7721
7730
8339
8339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                    DISULPID
                                                                                                                                                                                                    DISULFID
                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q59E99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
Q59E99 HUM
```

DER NEUE DE NEUE

ö

Gaps

Page 12

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51, DB 2; Length 1193;
Pred. No. 2;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang K., Mauco G., Hauet T.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 1193 AA; 133256 MW; 6E8781648FCEC7F2 CRC64;
                                                               EMEL, CAAECOLO14723; CAGG3524.1; -; Genomic_DNA.

R G0; G0:0005576; C:extracellular region; LEA.

G0; G0:0005209; F:calcium ion binding; LEA.

G0; G0:0005201; F:heparin binding; LEA.

G0; G0:0005159; F:errotein binding; LEA.

R G0; G0:0005159; F:errotein binding; LEA.

R InterPro; IPR001881; EGF Ga bd.

R InterPro; IPR013032; EGF like reg.

R InterPro; IPR001884; TSP1.

R InterPro; IPR001884; TSP1.

R InterPro; IPR000884; TSP1.

R InterPro; IPR000988; TSP1.

R Pfam; PF000090; TSP2.; 2.

R Pfam; PF000093; VWC; 1.

R PRINTS; PR01703; TSP2.; 1.

R PRINTS; PR01703; TSP1REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-0903;
07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
07-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY773342; AAV38110.1; -; mRNA.
InterPro; IPR000884; TSP1.
InterPro; IPR000885; TSP 1.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01186; EGF 2; UNKNOWN 1. PROSITE; PS50026; EGF 3; 2. PROSITE; PS50092; TSPI; 3. PROSITE; PS01208; VWFC 1; 1. PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombospondin 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 FMGVLQNVRFVF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 83.3
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SW00181; EGF; 2.
SWART; SW00209; TSP1; 3.
SWART; SW00210; TSPN; 1.
SWART; SW00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Thbs1;
Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSU903 PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-15496914; DOI=10.1038/nature03025;
A Daillon O., Aury J.-M., Brunet F., Perit J.-L., Stange-Thomann N.,
A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
A nathouard V., Jubin C., Castelli V., Katinha M., Vacherie B.,
A nicaud C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
A Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Kellis M., Volff J.-N., Guigo R., Zody M.C., Meeirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2005, sequence version 1.
2-JUL-2006, entry version 8.
Chromosome 14 SCAF14/23, whole genome shotgun sequence. (Fragment)
ORFNames=GSTENG00022976001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopteryydi, Neopeerygli, Teleosteli, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygli, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.3%; Score 51, DB 2; Length 1090;
83.3%; Pred. No. 1.9;
.ive 0, Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1090 AA; 120978 MW; 5A9320504A22D836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY; PRT; 1193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                      PROSITE; PS00018; EF HAND 1; UNKNOWN 1. PROSITE; PS01186; EGF 2; 1. PROSITE; PS00026; EGF 3; 2. PROSITE; PS00025; TSPI; 2. PROSITE; PS01208; WWFC 1; 1. PROSITE; PS01184; WWFC 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell adhesion; EGF-like domain.
  Interpro; IPR003367; tsp_3.
Interpro; IPR008859; TSP_C.
Interpro; IPR001007; VWF_C.
Pfam; PP00000; EGF; 1.
Pfam; PP00000; TSP_1; 2.
Pfam; PP005713; TSP_3; 12.
Pfam; PP005735; TSP_C; 1.
Pfam; PP00093; VWC; 1.
PRINTS; PR01705; TSP_C; 1.
                                                                                                                                                                                                   PRINTS; PR01705; TSPIREPEA
SMART; SM00181; EGF; 2.
SMART; SM00209; TSP1; 2.
SMART; SM00210; TSP1; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 83.3
nes 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q4S758 TETNG
Q4S758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
          DOREST LANGUS AND LANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
```

ö

Gaps

; 0

```
Search cor
Job time
           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whedel5496914; DOI=10.1038/nature03025;

This and the content of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2005, sequence version 1.
21-FBB-2006, entry version 8.
Chromosome 10 SCAF15019, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENGG0032374001;
Tetraodon nigroviridis (Green puffer).
Tetraoton nigroviridis (Green puffer).
Actinopterygii, Neopterygii, Telesostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthomorpha, Acanthomorpha, Acanthomorpha, Acanthomorpha, Tetraodontidae, Tetraodontiformes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 249;
                                                                                                                                                                                                                                                                                                                         249 249 249 249 249 AM; 465D664BE0329C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWR; Q4RLRS; 834-887, 837-1171.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0008201; F:heparin binding; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     80.6%; Score 50; DB 2;
90.9%; Pred. No. 0.58;
iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; CAAE01015019; CAG10667.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. TETNG
QARLES TETNG PRELIMINARY; PRT; 1171 AA.
QARLES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                               PRINTS; PRO1705; TSPIREPEAT.
SMART; SM0209; TSP1; 1.
SMART; SM00204; WC; 1.
PROSITE; PSS0092; TSP1; 1.
PROSITE; PS01208; WWFC 1; 1.
PROSITE; PS01208; WWFC 1; 1.
Pfam; PF00090; TSP_1; 2.
Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 QGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||| |||||
QGVLQNVRFVF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                           NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
       SFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIDDREAD DREAD BREEF BRANK BRA
```

```
DR InterPro; IPRO00742; BGF 3.

DR InterPro; IPRO00742; BGF 3.

DR InterPro; IPRO00742; BGF 3.

DR InterPro; IPRO00181; BGF 7abd.

DR InterPro; IPRO00181; BGF 7abd.

DR InterPro; IPRO00864; TSP1.1.

DR InterPro; IPRO00864; TSP1.1.

DR Ffam; PPO0009; EGF; 1.3.

DR Pfam; PPO0009; EGF; 1.3.

DR Pfam; PPO0009; TSP1.3.

DR PRINTS; BRO1070; TSP1.3.

DR PRINTS; BRO1070; TSP1.3.

DR PRINTS; BRO1070; TSP1.3.

DR SWART; SW00201; TSP1.3.

DR SWART; SW00210; TSP1.3.

DR PROSITE; PS0036; EGF 2; UNKNOWN.1.

DR PROSITE; PS001208; VWFC.1; 1.

DR PROSITE; PS001208; VWFC.2; 1.

COLI adhesion.

FT WON TER 1171 1171

SQ SEQÜENCE 1171 AA; 129304 MW; 865F9749693F7FCE CRC64;

QUETY WAICH 1171 AB; 129304 WW; 865F9749693F7FCE CRC64;

QUETY WAICH 1171 A
```

ö

THIS PAGE BLANK (USPTO)	

```
Sequence 97, Application US/09939853A
; Patent No. 6989232
; GENERAL INFORMATION:
GENERAL INFORMATION:
; TITLE OF INFORMATION:
; TILLE REFERENCE: 21402-099
; CURRENT PAPLICATION NUMBER: US/09/939,853A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/228,191
; PRIOR APPLICATION NUMBER: 60/228,191
; PRIOR FILING DATE: 2001-08-25
; PRIOR APPLICATION NUMBER: 60/269,961
; PRIOR FILING DATE: 2001-02-08
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Appl
Sequence 21, Appli
Sequence 350, Appli
Sequence 11112, Appli
Sequence 6411, Appl
Sequence 6441, Appl
Sequence 334, Appli
Sequence 3340, Appli
Sequence 3340, Appli
Sequence 61396, Appli
Sequence 61396, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11494, A
Sequence 18826, A
Sequence 24789, A
Sequence 45864, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 482, App
Sequence 97, Appl
Sequence 98, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                  June 5, 2006, 22:43:07; Search time 23.8966 Seconds (without alignments) 43.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3264,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RECOMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/RECOMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/RECOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-09-107-433-3340
S-09-270-767-61396
S-09-902-540-11494
S-09-252-991A-18826
S-09-248-796A-24789
S-09-270-767-45864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-11112
US-08-313-288B-19
US-09-949-016-6333
US-09-134-000C-6441
US-09-583-110-4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-540-236-3264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-939-853A-98 US-08-313-288B-20 US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-404-531B-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-671-978A-10
US-09-232-338-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-002-482
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-802-208B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                         650591 seqs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                            1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                      US-10-030-735-24
62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1170
1170
1170
1170
1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
6011.3
60
                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
```

Sequence 2, Appli Sequence 67, Appl Sequence 28, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli	SSOCIATED DISEASE, METHODS OF DETECTION	825; 18 0; Gaps 0;
775 2 US-09-305-640-2 775 2 US-09-348-429C-67 994 1 US-08-404-531B-28 498 1 US-08-404-531B-29 498 2 US-08-476-900A-29 498 2 US-08-476-900A-29 498 2 US-08-476-900A-29 498 2 US-08-476-900A-29 580 2 US-08-76-32 580 2 US-08-76-32 580 2 US-08-76-32 581 1 US-08-76-32 581 2 US-08-76-32 582 1 US-08-76-32 583 2 US-08-76-32 583 2 US-08-76-32 584 2 US-08-76-32 585 3 US-08-76-32 585 3 US-08-76-33 586 3 US-08-76-33 587 3 US-08-76-33 588 3	GNMENTS KNOWN GENES F RY AUTOIMMUNE F 9,002	90.3%; Score 56; DB 2; Length 825 91.7%; Pred. No. 0.043; ttive 0; Mismatches 1; Indels 7F 12
228 330 331 331 331 331 331 331 331 331 331	RESULT 1 US-09-949-002-482 ; Sequence 482, Application US/09949002 ; Sequence 482, Application US/09949002 ; Patent No. 6900016 ; GENERAL INFORMATION: ; TITLE OF INVENTION: POLYMORPHISMS IN KNOW; TITLE OF INVENTION: WITH INFLAMATORY AU; TITLE OF INVENTION: WITH INFLAMATORY AU; TITLE OF INVENTION: AND USES THEREOF ; TILE REFERENCE: CLOO0790 CURRENT APPLICATION NUMBER: 60/231,401 PRIOR APPLICATION NUMBER: 60/231,401 PRIOR PRILING DATE: 2000-01-28 PRIOR APPLICATION NUMBER: 60/231,401 PRIOR PRILING DATE: 2000-09-08 ; NUMBER OF SEQ ID NOS: 10823 ; SOFTWARE: FASTESEQ for Windows Version 4.0 ; SEQ ID NO 482 LENGTH: 825 ; TYPE: PRT US-09-949-002-482	Query Match Best Local Similarity 91. Matches 11; Conservative Qy 1 FQGVLNNVRFVF 12 Db 308 FQGVLQNVRFVF 31

```
US/08/313,288B
                                                                                                      January 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 1170 amino acids TYPE: amino acidd STRANDEDNESS: single TOPOLOGY: linear MOLECTLE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7
Matches 11; Conservative
         CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FQGVLNNVRFVF 12
                                                APPLICATION NUMBER:
FILING DATE: Januar
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 99, Application US/09939853A

Sequence 99, Application US/09939853A

Fatent No. 6989222

GENERAL INFORMATION:

FAPLICANT: Burgess et al.

TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099

CURRENT FILING DATE: 2001-08-27

FRIOR FILING DATE: 2000-08-25

FRIOR APPLICATION NUMBER: 60/267,300

FRIOR FILING DATE: 2001-02-08

FRIOR FILING DATE: 2001-02-08

FRIOR FILING DATE: 2001-02-08

FRIOR FILING DATE: 2001-02-08

FRIOR FILING DATE: 2001-03-08

FRIOR FILING DATE: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.3%; Score 56; DB 2; Length 831; Best Local Similarity 91.7%; Pred. No. 0.044; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 2; Length 831;
Pred. No. 0.044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gequence 20, Application US/08313288B

patent No. 5750502

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
COUNTRY: USA
STATE: New YORK
COMPUTER FRADABLE FORM:
COMPUTER F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.3%;
Best Local Similarity 91.7%;
Matches 11; Conservative
NUMBER OF SEQ ID NOS: 159
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 97
LENGTH: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGULNNVRFVF 12
                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-313-288B-20
                                                                                                                                                                                                                                                                                     US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09657472;
Sequence 2, Application US/09657472;
Patent No. 6727063;
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Lander, James S.
APPLICANT: Ireland, James S.
APPLICANT: Daley, George Q.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE FOLYMORPHISMS IN GENES FILE REFERENCE: 2825.1027.001;
CURRENT APPLICATION NUMBER: US/09/657,472;
CURRENT FILING DATE: 2000-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.3%; Score 56; DB 2; Length 1170; 91.7%; Pred. No. 0.063; 1.ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             90.3%; Score 56; DB 1; Length 1170; 91.7%; Pred. No. 0.063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR PELICATION NUMBER: US 60/153,357
PRIOR PELING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR PELING DATE: 2000-07-26
PRIOR PELING DATE: 2000-07-26
PRIOR PLING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 350, Application US/09949002; Patent No. 6900016; GENERAL INFORMATION:
```

us-10-030-735-24.rai

```
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-03
PRIOR FILING DATE: 2000-00-08
NUMBER OF SEQ ID NOS: 207012
SOUTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6333
LIBNGTH: 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 1; Length 1172;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 2; Length 117
Pred. No. 1.4e+02;
2; Mismatches 3; Indels
                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NOMBER: US/08/313,288B

FLING DATE: January 5, 1995

CLASSIFICATION NUMBER: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/POCKET NUMBER: 40028-A-PCT-US

TELEPHONE: (212) 391-0526

TELEPHONE: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6333, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 1172 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS: si
         STATE: New York
                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-313-288B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FALENCANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FBSESEQ for Windows Version 4.0

SEQ ID NO 11112
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WIDENEST THEREOF

FILE REFERENCE: CLO00790

CURRENT APPLICATION NUMBER: 105/09/949,002

CURRENT FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 2; Length 1170; Pred. No. 0.063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.3%; Score 38; DB 2; Length 104
58.3%; Pred. No. 1.3e+02;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/08313288B
Factor No. 5750502
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: CLONING, EXCRETED PROTEIN, F-SPONDIN NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11112, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 FÓGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|:| || ||
281 FRGLLQNVHLVF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGULANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Human
US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-313-288B-19
                                                                                                                                                                                                                                                            SEO ID NO 350
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
```

ð g

셤

ö

ö

FOR DIAGNOS

```
US-09-270-767-61396

Sequence 61396, Application US/09270767

Sequence 61396, Application US/09270767

Sequence 61396, Application US/09270767

FORENTEAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFERENCE: FILE Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

SOFTWARE: PatentIN Ver. 2.0

SEQ 1D NO 61396

LENGTH: 61
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 2; Length yaz.
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 61;
                                                                                             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.1%; Score 36; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                SOFTWARE: <UNKNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...945
SEQUENCE DESCRIPTION: SEQ ID NO: 3340:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 945 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Drosophila melanogaster
US-09-270-767-61396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3340: SEQUENCE CHARACTERISTICS:
                                              5206
                                                                                                                                           CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.7%;
                                              NUMBER OF SEQUENCES: 5.
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 59.7
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 FEGVINNIK 383
                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FQGVLNNVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-107-433-3340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Sequence 4794, Application US/09583110
| Sequence 4794, Application US/09583110
| Patent No. 6699703
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al.
| APPLICANT: Lynn Doucette-Stamm et al.
| TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| FILE RERERACE: PATHOU-07A
| CURRENT APPLICATION NUMBER: US/09/583,110
| CURRENT PILING DATE: 1998-06-30
| PRIOR FILING DATE: 1998-06-30
| PRIOR PILING DATE: 1998-06-131
| PRIOR PAPLICATION NUMBER: US 60/085,131
| PRIOR PAPLICATION NUMBER: US 60/085,131
| PRIOR PILING DATE: 1997-07-02
| NUMBER OF SEQ ID NOS: 5322
              Sequence 641, Application US/09134000C
Patent No. 617156
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BUTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT PILITING DATE: 1999-08-13
PRIOR FILING DATE: 1997-08-15
PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (11) ... (11)

COTHER INFORMATION: Amino acid 11 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-6441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 2; | Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.7%; Score 37; DB 2; 1
55.6%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-107-433-3340
; Sequence 3340, Application US/09107433
; Patent No. 6800744
; Patent NO. 6800744
; Then No. 1000800744
; The No. 1000800744
; The No. 1000800744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6441
LENGTH: 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 41.7.
Si Conservative
5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 728 FCGILGNINFIY 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.7
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 FEGVINNIK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQGVLNNVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-583-110-4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-583-110-4794
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
```

ò

셤 ઠે

ô

```
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18826
LIBNGTH: 175
                                                                                                                                                                            RESULT 14
US-09-020-540-11494

s Sequence 11494, Application US/09902540

parent No. 683347

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883

PRIOR PLILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 11494

LENGTH: 101

TYPE: PRT

TYPE: PRT

COGANISM: Myxococcus xanthus
US-09-902-540-11494
                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.1%; Score 36; DB 2; Length 101; Best Local Similarity 66.7%; Pred. No. 24; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 2; Length 175; Pred. No. 44; 3; Mismatches 1; Indels
                          3; Indels
Best Local Similarity 58.3%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18826, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June 5, 2006, 22:48:52 Job time: 24.8966 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                    1 FOGVLNNVRFVF 12
                                                                                               44 FFGVVTNVRLLF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||: |:|:|
QGVLDAVQFLF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QGVLNNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 QGMLNRIRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-252-991A-18826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-18826
                                                                         ò
                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ሯ
```

THIS PAGE BLANK (USPTO)

Tue Jun

```
APPLICANT: Kevin J. Williams
APPLICANT: Kevin J. Williams
APPLICANT: Kevin J. Williams, Kevin J.
TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
FITEL SEPRENCE: WILO7-20005
CURRENT APPLICATION NUMBER: US/10/419,462
CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Appl
Sequence 100, Appl
Sequence 1020, Appl
Sequence 1022, Appl
Sequence 1042, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 453, Appl
Sequence 453, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 459, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                     5, 2006, 23:46:43 ; Search time 78.6207 Seconds (without alignments) 70.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-474-213-28
US-10-419-462-40
US-10-782-968-40
US-10-741-600-1020
US-10-741-600-1022
US-10-741-600-1022
US-11-043-806-454
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-295-027-1170
US-10-211-462-38
US-10-231-956A-482
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                     2097797 segs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                           1 FQGVLNNVRFVF 12
                                                                                                                  US-10-030-735-24
62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432
459
666
685
685
6831
831
831
1100
11105
11150
11150
11170
11170
11170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                      Database
                                                                       Run on:
                                                                                                                     Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regult
No.
```

Sequence 38, Appl. Sequence 1018, Ap Sequence 1019, Ap Sequence 1021, Ap Sequence 34, Appl. Sequence 44, Appl. Sequence 248, App Sequence 27, Appl. Sequence 594, App Sequence 595, App Sequence 596, App Sequence 51, Appl. Sequence 28, App Sequence 28, App Sequence 28, Appl.	PROGNOSIS AND TREATMENT	12; 18 0; Gaps 0;
4 US-110-419-442-38 5 US-10-741-600-1018 5 US-10-741-600-1019 5 US-10-741-600-1021 5 US-10-741-600-1021 5 US-10-749-988-38 5 US-10-631-467-548 5 US-10-631-467-1376 5 US-10-995-561-594 5 US-10-995-561-596 6 US-11-046-644-28 6 US-11-046-445-28 6 US-11-046-445-38 6 US-11-046-456-28 6 US-11-046-456-28 7 US-10-285-394-153 8 US-10-285-394-153 9 US-10-285-394-153 9 US-10-285-394-153 1 US-10-285-394-153 1 US-10-285-394-153	ALIGNMENTS n US/10474213 214248A1 vid D Henry C E OF SEMENOGELIN IN THE DIAGNOSIS, NABER: US/10/474,213 203-10-06 ER: PCT/US02/10535 2-04-03 ER: 60/281,994 28 Sion 3.2	%; Score 56; DB 4; Length 12 %; Pred. No. 0.0013; 0; Mismatches 1; Indels
28 56 90.3 1170 31 56 90.3 1170 32 56 90.3 1170 33 56 90.3 1170 34 56 90.3 1170 35 56 90.3 1170 36 56 90.3 1170 37 56 90.3 1170 38 56 90.3 1170 41 56 90.3 1170 42 40 64.5 597 45 45 46 64.5 597	RESULT 1 US-10-474-213-28 US-10-474-213-28 Sequence 28, Application US/10474213 Publication No. US20040214248A1 GENERAL INFORMATION: APPLICANT: Roberts, David D APPLICANT: Krutzsch, Henry C TITLE OF INVENTION: USE OF SEMENOGELIN IN FILE REFERENCE: 224329 CURRENT APPLICATION NUMBER: US/10/474,213 CURRENT FILING DATE: 2002-04-03 PRIOR FILING DATE: 2002-04-05 PRIOR FILING DATE: 2002-04-05 PRIOR FILING DATE: 2001-04 SEQ ID NO 28 LENGTHA: 12 TYPE: PAT GRANIAN: Artificial FEATURE: COTHER INFORMATION: Synthetic peptide	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Q

N

```
US-11-043-806-462
US-11-043-806-462

Sequence 462, Application US/11043806

Sequence 462, Application Wo. US20060051774A1

Sequence 462, Application Wo. US20060051774A1

GENERAL INFORMATION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer FILE REFERENCE: 1847.1003

FILE REFERENCE: 1847.1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOOL499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1022
LENGTH: 432
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                         Gaps
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 6; Length 459;
Pred. No. 0.074;
0; Mismatches 1; Indels
                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
Pred. No. 0.069;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 5;
Pred. No. 0.069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCATION: (1)...(432)
CTHER INFORMATION: Xaa = Any Amino Acid
US-10-741-600-1022
                                                                                                                                                                                                                 ; Sequence 1022, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1047, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.3%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.7'
                                                                                                            208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FOGVLONVRFVF 219
Best Local Similarity 91.7
Matches 11; Conservative
                                                                  1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-925-301-1047
                                                                                                                                                                                                 US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-043-806-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 462
LENGTH: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                     à
                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                             Sequence 40, Application US/10782968

Sequence 40, Application US/2050065324A1

Publication No. US20050065324A1

GENERAL INFORMATION:

APPLICANT: Kevin J. Williams, Kevin J.

TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents

FILE REFERENCE: WILO7-2008 US/10/782,968

CURRENT APPLICATION NUMBER: US/10/782,968

CURRENT FILING DATE: 2004-02-20

PRIOR FILING DATE: 2003-04-21

NUMBER OF SEQ ID NOS: 53

SOFFWARE: Patentin version 3.2

SEQ ID NO 40

LENGTH: 240

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4

US-10-741-600-1020

Sequence 1020, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CL001499

FURENT APPLICATION NUMBER: US/10/741,600

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SEQ ID NO 1020

LENGTH A132
                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                     ; OTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-419-462-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Thrombospondin Region plus N-terminal domain
                                                                                                                                                     Score 56; DB 4; Length 240;
Pred. No. 0.036;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.3%; Score 56; DB 5; Length 240; 91.7%; Pred. No. 0.036; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.3%; Score 56; DB 5; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
LOCATION: (1)...(432)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                          90.3%;
                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                   Query Match 90.3
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                        190 FOGVLONVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 FOGVLONVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                               1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGULNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                US-10-782-968-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-782-968-40
  LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
Sequence 452, Application US/11043806

Sequence 452, Application US/11043806

PUblication No. US20060051774A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods

TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: Lhereof for Diagnosis of Prostate Cancer

FILE REFERENCE: 1847-1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

LENGTH: 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 455, Application US/11043806
; Sequence 455, Application US/11043806
; Publication No. US20660051774A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
; TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
; FILE REFERENCE: 1847.1003
; CURRENT APPLICATION NUMBER: US/11/043,806
; CURRENT PRILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 575
; SEQ ID NO 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 453, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
APPLICANT: Compuge Ltd
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: UNMER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB 6; Length 685; Pred. No. 0.11; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.3%; Score 56; DB 6; Length 804; 91.7%; Pred. No. 0.14; rive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                       208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FOGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                          1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGULNINVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 804
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                         RESULT 10
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                          8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 454, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
FILE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methode
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION UNMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 454
LENGTH: 555
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 456, Application US/11043806

Publication No. US20060051774A1

GENERAL INFORMATION:

APPLICANT: COMPUGEN Ltd

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: UNMARER: US/11/043,806

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

LENGTH: 578

LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 3; Length 466;
Pred. No. 0.075;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.3%; Score 56; DB 6; Length 578; Best Local Similarity 91.7%; Pred. No. 0.095; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 6; Length 555;
Pred. No. 0.091;
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                      CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SEQ ID NO 1047
                                                                                                                                                                                                                                                                                                                                                                          Query Match 90.3%;
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 FOGVLONVREVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 FOGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.3
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGULNNVRFVF 12
                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-11-043-806-456
                          FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-043-806-454
                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
```

셤

ઠે

```
90.3%;
                                                                                                                                                                                                                           208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.3
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                               1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: June
Job time: 79.6207 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 97, Application US/09939853A

Publication No. US2004003163A1

GENERAL INFORMATION:
APPLICANT Burgess et al.
TITLE OF INVENTION: No. US20040039163A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-099
CURRENT FILING DATE: 2001-08-27
FRIOR FILING DATE: 2000-08-25
FRIOR FILING DATE: 2000-08-25
FRIOR FILING DATE: 2000-08-26
FRIOR FILING DATE: 2001-02-08
FRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
UG-09-339-863A-98

Sequence 98, Application US/09939853A

Publication No. US20040039163A1

GENERAL INFORMATION:

TITLE OF INVENTION: No. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same

TITLE OF INVENTION: No. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same

TITLE OF INVENTION: No. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same

TITLE OF INVENTION: No. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same

TITLE OF INVENTION: No. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21010-08-27

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOFTWARE: PATENTION OF 98

LENGTH: 831

TYPE: PRT

TYPE: PRT

TYPE: PRT

TYPE: PRT
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
                                                                                                                                                90.3%; Score 56; DB 6; Length 828; 91.7%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 3; Length 831; Pred. No. 0.14;
                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.3%;
                                                                                                                                       Ouery Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                          208 FÓGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                           1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLNINVRFVF 12
; LENGTH: 828
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
Sequence 461, Application US/11043806
; Publication No. US20060051774A1
; General Information No. US20060051774A1
; General Information No. US20060051774A1
; APPLICANT: Compugen Ltd
: TITLE OF INVENTION: Unvel Nucleotide and Amino Acid Sequences, and Assays and Methods
: TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT PAPLICATION NUMBER: S2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NOS: 575
                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                      Gaps
                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                  Score 56; DB 3; Length 831;
Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.3%; Score 56; DB 6; Length 855; 91.7%; Pred. No. 0.15;
                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6, 2006, 00:00:09
US-09-939-853A-98
```

us-10-030-735-24.rapbn

```
TYPE: PRT
ORGANISM: Homo sapiens
US-11-293-697-3087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39312, A Sequence 662, App Sequence 662, App Sequence 1158, App Sequence 1158, App Sequence 24926, A Sequence 24926, A Sequence 34674, A Sequence 34674, A Sequence 9203, App Sequence 15526, A Sequence 2569, App Sequence 21136, A Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-953-349-39312
US-11-293-697-3087
US-110-505-928-662
US-10-953-349-1158
US-10-953-349-1158
US-10-953-349-1158
US-10-953-349-24926
US-10-953-349-24926
US-10-953-349-24926
US-10-953-349-24926
US-10-953-349-34674
US-10-953-349-34673
US-10-953-349-16527
US-10-953-349-16526
US-10-953-349-13318
                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                        58871 seqs, 11565156 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                                                                                                                                                             1 FQGVLNNVRFVF 12
                                                                                                                                                                                                           US-10-030-735-24
62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249
250
262
310
315
331
358
381
400
401
843
962
                                                                                                                                                                                                                                                                                                           BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      June
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
```

Sequence 21827, A	Seguence 21826, A	Seguence 20148, A	Sequence 26200, A	Sequence 20147, A	Sequence 20146, A	Sequence 3442, Ap	Sequence 36, Appl	Seguence 23556, A	Sequence 32, Appl	Sequence 1348, Ap	Sequence 31207, A	Sequence 23555, A	Sequence 13004, A	Sequence 13003, A	Sequence 23554, A	Sequence 13002, A	Sequence 31206, A	Sequence 88, Appl	Sequence 4588, Ap
US-10-953-349-21827	US-10-953-349-21826	US-10-953-349-20148	US-10-953-349-26200	US-10-953-349-20147	US-10-953-349-20146	US-11-293-697-3442	US-11-242-505A-36	US-10-953-349-23556	US-10-504-120-32	US-10-953-349-1348	US-10-953-349-31207	US-10-953-349-23555	US-10-953-349-13004	US-10-953-349-13003	US-10-953-349-23554	US-10-953-349-13002	US-10-953-349-31206	US-11-249-111-88	US-11-293-697-4588
223 6	273 6	368 6	407 6	437 6	444 6	524 7	980 7	397 6	437 6	440 6	525 6	528 6	531 6	538 6	543 6	546 6	9 095	627 7	108 7
20.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	48.4	48.4	48.4	48.4	48.4	48.4	48.4	48.4	48.4	48.4	48.4	46.8
31	31	31	31	31	31	31	31	30	30	30	30	30	30	30	30	30	30	30	53
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE REPERENCE: 2750-17919023
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ ID NO 39312
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 58.1%; Score 36; DB 6;
54.5%; Pred. No. 3.1;
iive 3; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOHNSTON INCOME.

TITLE OF INVENTION: Novel full length CDNA
FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT FILING DATE: 2005-12-05

PRIOR FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SERVIN 387
                                      Sequence 39312, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3087, Application US/11293697 Publication No. US20060105376Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39312
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.5
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLNNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|:|||
FEGILNNNVFI 76
RESULT 1
US-10-953-349-39312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-293-697-3087
```

```
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEOUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
KURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                            Score 33; DB 6; Length 249;
Pred. No. 24;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 6; Length 262;
Pred. No. 25;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 6
Pred. No. 24;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SEQUENCE-DETERMINED DNA TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579FUS2 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: Patentin version 3.3 LENGTH: 262
TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PUS2 CURRENT PERLICATION NUMBER: US/10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: Patentin version 3.3 SEQ ID NO 1158 LENGTH: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 24927, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1157, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                       TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.2%;
                                                                                                                                                                                                                                  53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: |:: || ||
168 FEAVVDRVRLVF 179
                                                                                                                                                                                                                                                                                                                                             167 FEAVVDRVRLVF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                   Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                        1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QGVLNNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRGANISM: Glycine max US-10-953-349-24927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-953-349-24927
                                                                                                                                                                                             US-10-953-349-1158
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-10-953-349-1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-953-349-1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1157
LENGTH: 250
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1159, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPRERENCE: 2750-1579PUS.
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 1159
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 6; Length 1504;
Pred. No. 1.1e+02;
   Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.2%; Score 33; DB 6; Length 164; 50.0%; Pred. No. 15;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                          Sequence 662, Application US/10505928
| Publication No. US2006008853ZA1
| GENERAL INFORMATION:
| APPLICANT: Ludwig Institute for Cancer Research et TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES | TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES | CURRENT APPLICATION NUMBER: US/10/505,928 | CURRENT FILING DATE: 2004-08-27 | PRIOR APPLICATION NUMBER: US 60/363,019 | PRIOR FILING DATE: 2002-03-07 | NUMBER OF SEQ ID NOS: 866 | SOFTWARE: Patentin 3.2 | SOFTWARE: Patentin 3.2 | LENGTH: 1504
       7;
     Score 34; DB 7
Pred. No. 25;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis thaliana
       54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|:::||||
751 QHILSSLRFVF 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEAVVDRVRLVF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QGVLNNVRFVF 12
                                                                                 1 FOGVLNNVRF 10
                                                                                                       : |:|| |||
69 YPGLLNGVRF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
US-10-505-928-662
       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-10-953-349-1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-1159
                                                                                                                                                                                             US-10-505-928-662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                    g
```

ò

```
APPLICANT: ALEXANIROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ ID NO 34673
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24925, Application US/10953349
Publication No. US20060107345A1
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: 2004-09-30
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ ID NO 24925
LENGTH: 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                              Score 33; DB 6; Length 331;
Pred. No. 32;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.2%; Score 33; DB 6; Length 381; 50.0%; Pred. No. 38; 2; Indels tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                        US-10-953-349-34673
Sequence 34673, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
; SEQ ID NO 34674
; LENGTH: 331
; TYPE: PRT
; CRGANISM: Zea mays subsp. mays
US-10-953-349-34674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; CRGANISM: Zea mays subsp. mays US-10-953-349-34673
                                                                                                                                53.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.2%;
                                                                                                        Query Match
Best Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0
الماسية وفي Conservative في Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                             225 OGVLFNIOYV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 ÓGVLFNIQYV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|| | :||:
252 EGVSNKIRFI 261
                                                                                                                                                                                                                  2 QGVLNNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QGVLNNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QGVLNNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Glycine max US-10-953-349-24925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-953-349-24925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-10-953-349-34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9204, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: UNMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9204
LENGTH: 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34674, Application US/10953349
Publication No. US20060107345A1
Publication No. US20060107345A1
REBERRAL INFORMATION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                      APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE OF INVENTION: ENCONDED THERBY
FILE REFRERNCE: 2750-1579FUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ ID NO 34926
LENGTH: 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.2%; Score 33; DB 6; Length 310; 50.0%; Pred. No. 30; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.2%; Score 33; DB 6; Length 315; 50.0%; Pred. No. 31; tive 3; Mismatches 3; Indels
                                                                                                                              ; Sequence 24926, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FQGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: |:: || ||
82 FEAVVDRVRLVF 93
  : | | : | |:
133 EGVSNKIRFI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|| | :||:
181 EGVSNKIRFI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QGVLNNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max US-10-953-349-24926
                                                                                                            US-10-953-349-24926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-953-349-34674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-953-349-9204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-953-349-9204
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
```

ò

ઠે

```
ઠે
                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Publication No. US20060107345A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: ENCONDED THERBY
TITLE OF INVERTION: ENCONDED THERBY
TITLE OF INVERTION: US/10/953,349
CURRENT PPLICATION
CURRENT PLING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATEMENT VERION 3.3
SEQ ID NO 9203
LENGTH: 400
                  PUBLICATION NO. USZOGOTOT345A1
GENERAL INFORMATION:
TYPLICANT: ALEXANDROV, NICKOLAI et al.
TYPLICANT: ALEXANDROV, NICKOLAI et al.
TYPLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TYPLE OF INVENTION: ENCONDED THERBY
FILE PEPTICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER: OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 34672
LENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9202, Application US/10953349
Publication No. US20060107345A1
Publication No. US20060107345A1
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION OF 15799020
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9202
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 6; Length 400;
Pred. No. 40;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 6; Length 382;
Pred. No. 38;
3; Mismatches 1; Indels
Sequence 34672, Application US/10953349
Publication No. US20060107345A1
                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Zea mays subsp. mays US-10-953-349-34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Arabidopsis thaliana US-10-953-349-9203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Arabidopsis thaliana US-10-953-349-9202
                                                                                                                                                                                                                                                                                                                                                                                      53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: |:: || ||
167 FEAVVDRVRLVF 178
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLNNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 QGVLFNIQYV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QGVLNNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-953-349-9203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-953-349-9202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
```

```
5, 2006, 22:08:53 ; Search time 91.1379 Seconds (without alignments) 60.201 Million cell updates/sec
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                      2589679
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              2589679 seqs, 457216429 residues
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                               1 AQGVLQNVRFVF 12
                                                                                                                                                                                    US-10-030-735-25
59
                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                               June
                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                               Run on:
                                                                                                                                                                                          Title:
```

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003bs:* geneseqp2003as:* geneseqp2006s: geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* geneseqp2005s:* geneseqp1980s:* A_Geneseq_8:* 1: qeneseqp19 .. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Re

Description	Aab35370 Alpha3bet	Aab35357 Alpha3bet	Aab35352 Alpha3bet	Aab35378 Alpha3bet	-	Adl70641 Human thr	Adq39359 Human myo	Adq39357 Human myo	Aau02916 Angiotens	Aab43602 Human can	Aau02915 Angiotens	Adn02474 TSF polyp	Aau02914 Angiotens	Aau02913 Angiotens	Human	Aau74771 Human thr	Abb82285 Human thr	Aab74450 Human var	Aab90800 Human she	Aae25030 Human thr	Aau75315 Human thr	Abp96780 Human COP	Abu03474 Angiogene
ID	AAB35370	AAB35357	AAB35352	AAB35378	ABG72834	ADL70641	ADQ39359	ADQ39357	AAU02916	AAB43602	AAU02915	ADN02474	AAU02914	AAU02913	AAB00042	AAU74771	ABB82285	AAB74450	AAB90800	AAE25030	AAU75315	ABP96780	ABU03474
DB	4	4	4	4	ø	æ	8	8	4	m	4	7	4	4	m	S	ഹ	4	4	ß	ß	φ	9
% Query Match Length DB	12	11	12	12	12	240	432	432	459	466	546	548	555	731	1152	1152	1152	1170	1170	1170	1170	1170	1170
Query Match	100.0	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	•	93.2	93.2
Score	59		55		55	55	55		55		55	55	52	55			52			55	55	55	22
esult No.	-	7	m	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

	Human Human Thromb Human Human	968446	Aabisidi Aiphaiber Aabisida Aiphaiber Aabisi74 Alphaiber Aabisi71 Alphaiber Aabisi68 Alphaiber
ABG74673 AAE36228 ABR62059 ADJ76124 ADJ75296	ADL70639 ADL35874 ADQ26070 ADP54179 ADQ39358	ADQ39356 ADQ3168 ADZ1688 AEB9781 AEB46751 AAB35373	AAB35381 AAB35364 AAB35371 AAB35371 AAB35368
997788	~~~~~	@ @ Q Q Q 4	य य य य य
1170 1170 1170 1170 1170	1170 1170 1170 1170	1170 1170 1170 1170	77777
		,,,,,,,,,	٠. 4. 4. ٢. ٢.
000000	8 8 8 8 8	0 0 0 0 0 0 0 0 0 0 0 0	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
ស ល ល ល ល ល ល ល ល ល ល ល ល	ស ស ស ស ស ស ស ស ស ស	ស ស ស ស ស ស ស ស ស ស ស ស វ ស ស ស ស ស ស	20 20 20 20 20
4 2 2 2 2 2 2 4 4 5 5 5 5 6 5 6 5 6 5 6 5 6 6 6 6 6 6	333 335 435 435	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 4 4 6 6 4 7

ALIGNMENTS

Alpha3betal integrin binding peptide #35. AAB35370 standard; peptide; 12 AA. (first entry) 08-MAY-2001 AAB35370; RESULT 1

Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.

Synthetic.

WO200105812-A2.

12-JUL-2000; 2000WO-US018986. 25-JAN-2001.

99US-0144549P. 15-JUL-1999; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Krutzsch HC; Roberts DD,

WPI; 2001-182656/18.

New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and cancer.

Claim 4; Page 34; 84pp; English.

The present invention provides a number of peptides which bind to alphaibetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention

Sequence 12 AA;

```
(first entry)
                                                                                                                                                                                                                                                                                                                                     Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGVLQNVRFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGVLQNVRFVF
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 AA;
                                                                                                                                       WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200105812-A2
                                                                                                                                                                                                                                                        15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                     Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999;
                                                                                                                                                                             25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2001
                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB35378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB35378
    SOX CCCCCXXXXX FFFF FX BX FX BX FX FX BX F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                       Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
100.0%; Score 59; DB 4; Length 12; 100.0%; Pred. No. 0.00015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.2%; Score 55; DB 4; Le 100.0%; Pred. No. 0.00083;
                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 0.0 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                   Alpha3betal integrin binding peptide #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha3betal integrin binding peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                  AAB35357 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB35352 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                               (first entry
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krutzsch HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                              1 AQGVLQNVRFVF 12
                                                                                                                   AQGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGVLQNVRFVF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-182656/18.
                    Best Local Similarity
Matches 12, Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999;
                                                                                                                                                                                                                                                                                               08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                        AAB35357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB35352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB35352
                                                                                                                                                                                                                                      EXEXEXE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of peptides which bind to alphalbetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid archritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
Alpha3beta1 integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.2%; Score 55; DB 4; Lv
100.0%; Pred. No. 0.00092;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha3betal integrin binding peptide #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB35378 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0144549P.
                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0144549P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUL-2000; 2000WO-US018986
```

```
ö
                                                                                                                                                                          The present invention provides a number of peptides which bind to alphaiberal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid archritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to diagnosing cancer other than prostate cancer in a male mammal, comprising assaying a test sample for increased level of semenogelin, or cancer in a female by assaying for the presence of semenogelin. Administering a semenogelin protein or polypeptide fragment or a semenogelin-specific antibody or active fragment, or a recombinant or expressing the protein or antibody, is useful for inducing an immune response to a cancer in a mammal, where the cancer is not prostate cancer and semenogelin is a marker. The invention is used to diagnose cancer, particularly of epithelial origin such as lung cancer, papillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A new diagnosis for cancer other than prostate cancer in a mammal useful to detect cancer including lung cancer, particularly small cell lung cancer and melanoma comprises detecting semenogelin in a sample.
                                              New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; thrombospondin-1; cytostatic; immunostimulant; cancer; epithelial cancer; lung cancer; papillary renal cell carcinoma; colon cancer; small-cell lung cancer; SCLC; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                              93.2%; Score 55; DB 4; Length 12; 100.0%; Pred. No. 0.00092;
                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombospondin-1 sequence containing synthetic peptide.
                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. ww.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                            Example 2; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG72834 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 14; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-2002; 2002WO-US010535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-2001; 2001US-0281994P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                     2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||||||||||||||||||QGVLQNVRFVF 12
                WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-103329/09.
                                                                                                                                                                                                                                                                       the invention
                                                                                                                                                                                                                                                                                                            Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40200281630-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG72834;
                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                           cancer.
                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
용
                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of the N-terminal domain of human thrombospondin-1 (TSP) ADL/10639. The invention relates to TSP fragments (80-100, 40-55 or 20-35 kDa mol.wt.) found in plasma, and their use in clinical assays for cancer and for generation of antibodies and other binding agents. A method that distinguishes TSP from a TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion as a target for a binding molecule, e.g. an antibody, to obtain a quantitation of TSP plus TSP fragment or portion, (2) using an epitope present in TSP but not in the fragment or portion to obtain a quantitation of TSP only; and (3) using the difference between (1) and (2) as a quantitation of the amount of TSP fragment or portion. Suitable epitopes are provided ADL/1063-ADL/10639. Detection or quantification of the TSP fragment or portion as performed in order to detect the presence, or monitor the course, of a disease or condition selected from cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nsefnl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes.
renal cell carcinoma, colon cancer, especially small-cell lung cancer (SCLC), or a melanoma. The present sequence represents the amino acid sequence of the thrombospondin-1 sequence containing synthetic peptide which binds to alpha-3-beta-1 integrin
                                                                                                                                                                        Gaps
                                                                                                                                                                        ö
                                                                                                                                93.2%; Score 55; DB 6; Length 12; 100.0%; Pred. No. 0.00092; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23. .32
/note= "Heparin binding region"
77. .82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Heparin binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human thrombospondin-1 N-terminal domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 40; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                ADL70641 standard; protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-2003; 2003WO-US026023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2002; 2002US-0405494P.
21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                             2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                 2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WILL/) WILLIAMS K J
                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-226901/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004018995-A2
                                                                                                Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams KJ;
                                                                                                                                                                                                                                                                                                                                                                                     ADL70641;
                                                                                                                                  Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                            RESULT 6
                                                                                                                                                                                                                                                                                                                                  ADL7064
   8886666
                                                                                                                                                                                                                                                 g
```

```
cremal failure, remal disease, atopic dermatitis, vasculitis, acute vasculitis, renal allograft, asthma, diabetes mellitus, myocardial informations renal allograft, asthma, diabetes mellitus, myocardial informations, renal allograft, asthma, diabetes mellitus, myocardial nodosa, systemic lupus erythematosus, lupus erythematosus, Kawasaki condosa, systemic lupus erythematosus, lupus erythematosus, Kawasaki chrom-Schoenlein purpura, rhematoria arthritis, vasculitis syndrome, Hench-Schoenlein purpura, chrometer purpura, an inflammatory condition, a condition associated with platelet activation, a condition associated with intravascular coagulation, a condition associated with intravascular coagulation, extravascular coagulation, a condition associated with endothelial activation, a condition associated with endothelial activation, a condition associated with endothelial activation, a condition and/or release of thrombospondin and/or a thrombospondin cardion, an aspartame reaction, an actopic dermatitis, eczema, programativity, sclarederma, conditions associated with an antiocreacensitivity, sclarederma, conditions associated with an antiocreacensitivity, sclarederma, conditions associated with an antiocreacensitivity, sclarederma, conditions associated with an expection, an aspartame reaction, and a condition associated with a cryofibrinogen, accer, indencer, senter, a cancer a senter all and a condition associated with a cryofibrinogen, a senter of the respiratory system, parcalacory system, intravay system, intravay system, intravay system, indencers, senter (male or female), genitourinary system, kidney, uninary tract, sensory system, merchander a cryofibrior a condition 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human myocardial infarction-associated gene derived protein, SEQ ID 1022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.2%; Score 55; DB 8; Length 240; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Devlin JJ, Iakoubova O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ39359 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-2002; 2002US-0434778P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 OGVLONVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 OGVLONVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004058052-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ39359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention current comprises: an isolated nucleotides of an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification, an isolated polypeptide comprising an amino acid sequence given in the specification, an antibody that specification and which is between about 16 and 1000 nucleotides in capacity; a kit for detecting an SNP in a nucleic acid molecule, a method of detecting an SNP in a nucleic acid molecule; an entryme; a method of detecting an SNP in a nucleic acid molecule; an entryme; and a propertion or transporting an SNP in a nucleic acid molecule; an entryme; and a variant polypopptide; and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-sescoiated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human myocardial infarction-associated gene derived protein, SEQ ID 1020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        decreased risk for developing myocardial infarction and for preparing a
                                                                                                       Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Match 93.2%; Score 55; DB 8; Length 432; Local Similarity 100.0%; Pred. No. 0.053; les 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   Claim 10; SEQ ID NO 1022; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ39357 standard; protein; 432 AA.
                                                                                                                                                                                           the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002US-0434778P.
2003US-0453135P.
2003US-0466412P.
2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 ÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QGVLQNVRFVF 12
WPI; 2004-533949/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 432 AA;
                                   N-PSDB; ADQ38531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004058052-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-2003;
30-APR-2003;
23-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ39357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ39357
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E BERRY LANGE OF THE SERVICE OF THE
```

Bernstein J;

Azar I, Khosravi R,

David A,

Levine Z,

WPI; 2001-336004/35. N-PSDB; AAS06016.

17-NOV-2000; 2000WO-IL000766.

WO200136632-A2. Homo sapiens.

25-MAY-2001

99IL-00133455

17-NOV-1999; 10-DEC-1999; (COMP-) COMPUGEN LTD

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's callered risk for myocardial infarction in the individual. The intention further comprises: an isolated nucleic acid molecule comprising at least sontiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification, an antibody fragment; an amplified polymorleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a veriant polypeptide; and a mucleic acid molecule; a method of detecting a veriant polypeptide; and a mucleic acid molecule; a method of detecting a veriant polypeptide; and comprising the molecule; a method of detecting a veriant polypeptide; and a mucleic acid molecule; a method of detecting a veriant polypeptide; and comprising the molecule; and indentifying an apent useful in treating or preventing method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction, may be used in gene therapy. The commodition for the invention may be used in gene therapy. The commodition for the invention may be used in gene therapy. The commodition for the invention may not may not preparing a commodition for the invention myocardial infarction method be an increased or commodition for the invention myocardial infarction myocardial infarction myocardial infarction method the propertion method the propertio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-sequence containing one or more SNP s of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endochelial cell growth factor; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nonarcoidotto pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                              Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme (ACEV) splice variant protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.2%; Score 55; DB 8; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             core 55,
Pred. No. 0.053;
Pred. ----hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                       Claim 10; SEQ ID NO 1020; 145pp; English.
                                                                            Iakoubova 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU02916 standard; protein; 459 AA.
                                                                                                                                                                                                                                                                       the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QGVLQNVRFVF 12
                                                                            Cargill M, Devlin JJ,
                         (APPL-) APPLERA CORP.
                                                                                                                                  WPI; 2004-533949/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                           N-PSDB; ADQ38529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU02916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of garanlocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders including cardiovascular diseases such as arteriosclerosis, mycoardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy; immune disorders such as immune complex nephritis, multiple sclerosis, cancer, astroidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antishmatic; antishmentic; cantiborateria; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haemacopoietic cell disorder; autoimmune disorder; allegic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.2%; Score 55; DB 4; Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 0.057; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer associated protein sequence SEQ ID NO:1047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB43602 standard; protein; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 16; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 OGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB43602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB43602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 X C C C C C C C C C C C X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

ö

```
N-PSDB; AAS06015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSF polypeptide
                                                                                   WO200136632-A2
                                                                                                                                                                      17-NOV-1999;
                                                                                                                                                                                        LO-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN1401387-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-2003
                                                                                                                25-MAY-2001
                                                                                                                                                                                                                                             Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN02474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN02474
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; coording dermatological; neuroprotective; cardiant; thrombolytic; coagulant; coording and antiangiogenic. The mostropic; vasotropic; antiposoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune rejection, modulate haemostatic or thrombolytic activity, modulate rejection, concers, cardiovascular disorders, neurological disease and inflammation, cancers, cardiovascular disorders, neurological disease and agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumnour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                            Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme (ACEV) splice variant protein #15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.2%; Score 55; DB 3; Length 466; 100.0%; Pred. No. 0.058; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                      Claim 11; Page 1636-1638; 2352pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02915 standard; protein; 546 AA.
                                                                                                  18-MAR-2000; 2000WO-US005882.
                                                                                                                             99US-0124270P
                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 ÓGVLÓNVŘFVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                           Novel isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention
                                                                                                                                                                                      Rosen CA, Ruben SM;
                                                                                                                                                                                                                  WPI; 2000-587533/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                 N-PSDB; AAC77811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 466 AA;
                                         WO200055350-A1.
                                                                                                                             12-MAR-1999;
              Homo sapiens
                                                                      21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adenovirus vector; anti-neoplastic; TSF polypeptide; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 4; Length 546; Pred. No. 0.069; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Preu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Azar I, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADN02474 standard; protein; 548 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 15; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99IL-00132978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 OGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 QGVLQNVRFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-336004/35
```

```
mediated anti-neoplastic composition is prepared through cloning the cDNA sequence from the human peripheral blood cell by specific primer and reverse transcription-polymerase chain reaction (RT-PCR) method for coding TSF polypeptide, construction in human embryonic kidney cell 293 by AdEasy system, and packaging and expressing the recombinant adenovirus vector of TSF. It can suppress the growth and transfer of cancer. The present sequence represents the TSF polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polypeptide receptor 2; arteriosclerosis, cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                   The present invention relates to a novel recombinant adenovirus vector
                                                                                                                                                                                                Tumor suppressing polypeptide TSF and gene therapy vector composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiotensin converting enzyme (ACEV) splice variant protein #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%; Score 55; DB 7; Length 548
100.0%; Pred. No. 0.069;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Levine Z, David A, Azar I, Khosravi R, Bernstein J;
                                                                               (TAID-) TAIDA LIFE SCI TECH RES CENT HEMATOLOGY.
                                                                                                                                                                                                                                Claim 2; SEQ ID NO 1; 13pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU02914 standard; protein; 555 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99IL-00132978.
             21-AUG-2002; 2002CN-00129408
                                              21-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QGVLQNVRFVF 12
                                                                                                                                               WPI; 2003-469302/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-336004/35.
                                                                                                                                                                N-PSDB; ADN02475
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200136632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU02914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                              Han Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ठ
```

ö

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and vasoactive intestinal colypeptides receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various associated infarction and coronary arterial thrombosis, renal diseases cuch as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular thrombosis as asbestosis and vascular thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; multiple sclerosis; immune disorder; sarcoidosis; nultiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiotensin converting enzyme (ACEV) splice variant protein #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.2%; Score 55; DB 4; Length 555; 100.0%; Pred. No. 0.07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU02913 standard; protein; 731 AA
                                                                                                                 Claim 4; Fig 14; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99IL-00132978.
99IL-00133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                David A,
N-PSDB; AAS06014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40200136632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU02913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU02913
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

WPI; 2001-336004/35

us-10-030-735-25.rag

```
ô
                                                                                                                                     The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal apolypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy.
                                                                                                                                                                                                                                                                                                                                                     immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection; glaucoma.
                               Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%; Score 55; DB 4; Length 731; 100.0%; Pred. No. 0.096; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361. .416
/label= Type 1 repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417. .473.
/label= Type 1 repeat region
/label= Type 1 repeat region
/label= Type 1 repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                               abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB00042 standard; protein; 1152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                       Claim 4; Fig 13; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human thrombospondon-1 (TSP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-FEB-2000; 2000WO-US002482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 OGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-514823/46
N-PSDB; AAS06013
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 731 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200044908-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawler JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB00042
ò
```

```
New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TSP (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerase chain caction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. Anti-angiogenic therapy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
               Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.2%; Score 55; DB 3; Length 1152; 100.0%; Pred. No. 0.16; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5, 2006, 22:24:58
                                                                                                                       Disclosure, Fig 1, 40pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           does not induce drug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||||||||||
191 QGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: June
Job time: 91.1379 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
```

```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

Run on:

5, 2006, 22:25:22 ; Search time 13.9655 Seconds (without alignments) 82.675 Million cell updates/sec

US-10-030-735-25 59 1 AQGVLQNVRFVF 12 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	٦.	thrombospondin 1 p	thrombospondin 1 p	tRNA-pseudouridine	thrombospondin 2 p	N	probable pilin, ty	124	cadherin-associate	hypothetical prote	alternative respir		probable transcrip		thrombospondin pre				leukocidin chain l	leukotoxin LukE [i	L-lactate dehydrog	hypothetical prote		Lupus autoantigen	hypothetical prote			문	hypothetical prote
SUMMARIES	ΩI	7	TSHUP1	A40558	C57253	TSHUP2			T08870	B39529					T43110	A39804		C90261		JC5468	C89968	_			A43534		T17230	T05178	.699	875258
	BB	7		7		Н			7	7	•	•	•	~	7	Н	•	N						7			~	~	7	0
	Query Match Length	229	1170	1170	151	1172	1172	186	40	88	102	326	747	783	927	1178	102	106	265	308	311	333	337	417	595	597	993	1308	54	175
عيق	Query Match	93.2	93.2	93.2	62.7	62.7	62.7	61.0	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3		57.6	57.6		57.6			57.6				57.6	55.9	
	Score	55	55	22	37	37	37	36	35	35	35	35	35	35	35	35	34	34	34	34	34	34	34	34	34	34	34	34	33	33
	Result No.	1	73	e	4	Ŋ	9	7	80	0	10	11	12	13	14		16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable imidazole	probable 3-oxoacyl	3-oxoacyl-[acyl-ca	gamma-hemolysin co	FdhD protein (impo	synergohymenotropi	leukocidin chain S	leucocidin chain S	leucocidin R S com	leukocidin chain S	gamma-hemolysin co	hlgC-like protein	repA protein - Bac	rep A protein - Ba	GTP-binding regula	GTP-binding regula
D81929	A64590	B71923	C49238	C87403	S68225	T00160	S32211	A49234	JN0626	E90043	PC4078	S54267	S54263	RGBOT1	RGHUT1
~	н	~	N	N	N	~	7	~	N	~	N	ď	N	ч	н
212	247	247	286	298	310	312	312	315	315	315	315	326	331	350	350
o,	o,	o,	9	6	σ,	٥	0	6	o,	0	0	6	6	ō	o,
55.	55.	55	55	55.	22	55.	55.	55.	55.	55.9	55.	55.9	55.9	55.	55.
33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 SS7957
thrombospondin 1 - bovine (fragment)
 c;species: Bos pirmigenius caurus (carcie) C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
 CyAccession, S57957
Nimateurinade, b.; Feiterin; b.; Ataminada, m.; Limimoda, b.m.; Feige, b.o. submitted to the EMBL Data Library, July 1995
A; Description: Opposite regulation of thrombospondin-1 and CISF/thrombospondin-2 expressi
A.Reterence number: 85/955 A.Accession: S57957
A; Status: preliminary
 A; Molecule type: mRNA
A; Residues: 1-229 < LAF>
A; Cross-references: UNIPROT: Q28194; UNIPARC: UPI000008740A; EMBL: X89511; NID: 9899228; PIDN
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
Query Match 93.2%; Score 55; DB 2; Length 229;
Hest Local Similarity 100.0%; Fred. No. 0.001/; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 QGVIQUVREVF 12
Db 191 QGVLQNVRFVF 201
 RESULT 2

thrombospondin 1 precursor - human

Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo Assis; A4274; A30140; A25812; A05172; A42927
Ciscession: A26155; A4274; A30140; A25812; A05172; A42927
J. Cell Biol. 103, 1635-1648, 1986
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple cs A;Reference number: A26155; MUID:87057617; PMID:2430973
A;Reference number: A26155
A;Molecule type: mRNA
A;References: Universe (minimal properties)
A;Ross-references: Universe (minimal properties)
A;Coss-references: Universe (minimal properties)
A;Title: Characterization of the promoter region of the human thrombospondin gene. DNA se A;Reference number: A34274; MUID:89291870; PMID:2544587

A; Accession: A34274

A;Molecule type: DNA
A;Residues: 1-166 <LAHS
A;Cross-references: UNIPARC:UPI00001742BF; GB:J04835
A;Cross-references: UNIPARC:UF100001742BF; GB:J04835
B;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, F B;Hennessy, S.W.; Frazier, B.A.; Kim, B.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, F J. Cell Biol. 108, 729-736, 1989
A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the

a

```
A; Molecule Lype: DNA
A; Residues: 1-1170 < LLAW>
A; Cross-references: UNIPROT: P35441; UNIPARC: UPI0000028012; GB: M62449; GB: M62450; GB: M62451;
B; GB: M62462; GB: M62463; GB: M62464; GB: M62465; GB: M62466; GB: M62467; GB: M62468; GB: M62465;
B; Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P.
J. Blol. Chem. 265; 16691-16698, 1990
A; Fitle: Characterization of the mouse thrombospondin gene and evaluation of the role of A; Reference number: A37905; MUID: 90375546; PMID: 2398070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-1152, P'. 1154-1170 < LAH>
A;Residues: 1-1152, P'. 1154-1170 < LAH>
A;Cross-references: UNIPARC: UP10000177496; GB:M87276
A;Note: sequence extracted from NOBI backbone (NCBIP:81501)
B;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FRBS Lett. 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar
A;Reference number: S68787; MUID:96234006; PMID:8654563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERNA-pseudouridine synthase (EC 5.4.99.-) - Acinetobacter calcoaceticus (fragment)
NyAlternate names: hypothetical protein lipB 5'-region
C;Species: Acinetobacter calcoaceticus
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 05-Oct-2004
C;Accession: C57253
R;Kok, R.G; van Thor, J.J; Nugteren-Roodzant, I.M.; Vosman, B.; Hellingwerf, K.J.
A;Title: Characterization of lipase-deficient mutants of Acinetobacter calcoaceticus BD41
A;Reference number: A57253; MUID: 95286514; PMID:7768830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI000016D076; GB:J05605; GB:J05606; NID:g201991; PIDN:AAA404 R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M. J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell c A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: B42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55, DB 2, Length 1170,
Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 1-151 <KOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                         A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI000017879A; GB:X80800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
    587-600, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-490 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A37905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: C57253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allote: the list of introns may be incomplete
C;Complex: homotrimer, disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;19-1170/Product: thrombospondin type 1 repeat homology <WWC>
F;317-375/Domain: thrombospondin type 1 repeat homology <THR1>
F;314-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;51-586/Domain: EGF homology <EGF1>
F;551-586/Domain: EGF homology <EGF2>
F;551-586/Domain: EGF2>
F;551-586/Domain: 
                                                                          A; Molecule type: mRNA
A; Residues: 1-83, 'A', 85-52, 'A', 524-1170 cHEN>
B; Robayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
B; Robayashi, S.; 8418-8425, 1986
A; Richerty 25, 8418-8425, 1986
A; Richert amino acid sequence of human thrombospondin as determined by analysis of A; Reference number: A25812; MUD:87157592; PMID:303036
A; Recension: A25812
A; Molecule type: mRNA
A; Residues: 1-83, 'A', 85-397 cKOB>
A; Cross-references: UNIPARC:UPI00001680CA; GB:M25631; NID:9538353; PIDN:AAA36741.1; PID: R; Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rottwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A; Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: A05172
A, Molecule type: mRNA
A, Mosher. D.F.
A, Note: parts of this sequence, including the amino end of the mature protein, were dete
B, Sun, X, S, Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A, Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A, Reference number: A42927
A, Molecule type: protein
A, Residuce type: protein
A, Molecule type: protein
A, Note: Cys-992 is shown to have a free sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Dacies: Mus musculus (house mouse)
C;Dacession: A90558; A37905; B42587; S68787
R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
Reference number: A30140; MUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.2%; Score 55; DB 1;
100.0%; Pred. No. 0.01;
iive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: GDB:THBS1; TSP1; TSP
A;Cross-references: GDB:120438; OMIM:188060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 15q15-15q15
A;Introns: 23/1
                                              Accession: A30140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
A40558
```

ô

셤

ò 셤

```
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell callecence number: A42587; MUID:92147683; PMID:1371115
A;Reference number: A42587
                                                                                                                                                                                 A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Status: 1-112 - 4.AH-
A;Readidus: 1-112 - 4.AH-
A;Cross-references: UNIPROT: Q03350; UNIPARC: UPI0000029847; GB:L07803; GB:R87275; NID:g34(
A;Cross-references: UNIPROT: Q03350; UNIPARC: UPI0000029847; GB:L07803; GB:R87275; NID:g34(
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
R;Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
J; Biol. Chem. 266, 12821-12824, 1991
A;Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
A;Reference number: A39851; MUID:91302287; PMID:1712771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UP100016D077; GB:M64866; NID:9201994; PIDN:AAA40432.1; PID:s
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J.D.; Dodson, R.J.; F
T.; Zalewski, C.; Mab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:09RUZ7; UNIPARC:UPI0000003E03; GB:AE001971; GB:AE000513; NID:
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Delnococcus radiodurans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

    soybean (fragment)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: calcium binding; glycoprotein
F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>
F;380-431/Domain: thrombospondin type 1 repeat homology <THRI>
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;435-549/Domain: thrombospondin type 1 repeat homology <THR2>
F;553-588/Domain: EGF homology <EGFI>
F;552-691/Domain: EGF homology <EGFI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: B75421
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson,
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback,
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable pilin, type IV - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alternative respiratory pathway oxidase (EC 1.-.-.) 3 C;Species: Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 2;
Pred. No. 50;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2;
Pred. No. 10;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|:|||| ||
203 RGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 QGVLQNVRFVF 12
   C; Accession: A42587; A39851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OGVLENVR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGVLQNVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-873 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-186 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: A39851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B75421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: DR1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  perceiption: participates in cell migration and adhesion, and in platelet aggregation Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc. fixewords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer; 1-18/Domain: signal sequence #status predicted <IGS.
19-1172/Product: thrombospondin 2 #status predicted <MAT>
13-93-74/Domain: von Willebrand factor type C repeat homology <VWC>
13-1172/Domain: thrombospondin type 1 repeat homology <THR2>
136-431/Domain: thrombospondin type 1 repeat homology <THR2>
1553-588/Domain: EGF homology <EGF>
1553-588/Domain: EGF homology <EGF>
1552-691/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1928-930/Region: cell attachment (R-G-D) motif
1511,316,330,497,584,710,1069/Banding site: carbohydrate (Asn) (covalent) #status predi
1.167-226/Disulfide bonds: #status predicted
1.66,270/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Actes 1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Actession: A47379; A42173
R;LaBell, T.L.; Byers, P.H.
R;LaBell, T.L.; Sequence P.H.
A;Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: pote A;Title: Sequence and characterization of the Complete human thrombospondin 2 cDNA: pote A;Reference number: A47379; MUID:94010892; PMID:8406456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1172 <LAB>
A;Residues: 1-1172 <LAB>
A;Coss.references: UNIPROT:P35442; UNIPARC:UPI0000046680; GB:L12350; NID:g307505; PIDN:R;LaBell, T.L.; Milewicz, D.J.; Disteche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992
A;Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression cA;Reference number: A42173; MUID:92217961; PMID:1559694
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Species: Mus musculus (house mouse)
C,Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
                                  C; Keywords: intramolecular transferase; isomerase; tRNA modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1172
                                                                                                  Length 151;
                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Molecule type: mRNA
, Residues: 560-1172 c.LA2>
, Cross-references: UNIPARC:UP100001742C1; GB:M81339
, Experimental source: fibroblast
                                                                                            Score 37; DB 2;
Pred. No. 5.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.7%; Score 37; DB 63.6%; Pred. No. 50; ive 2; Mismatches
C; Superfamily: tRNA pseudouridine synthase B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GDB:128789; OMIM:188061
Map position: 6q27-6q27
Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombospondin 2 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombospondin 2 precursor - mouse
                                                                                               62.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.68;
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.7
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AQGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                           SNGVLOKVRWLF 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGVLQNVRFVF 12
                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: GDB:THBS2; TSP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A47379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: A42173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
```

В.

셤 ठ

ઠ 셤

```
diternative respiratory pathway oxidase (EC 1.-.-.) Aox3 - soybean C; Species: Glycine max (soybean)
C; Accession: T08849
R; Finnegan, P.M.; Whelan, J.; Millar, A.H.; Zhang, Q.; Smith, M.K.; Wiskich, J.T.; Day, I Plant Physiol. 118, 675-682, 1998
A; Fille: Differential expression of the multigene family encoding the soybean mitochondri A; Reference number: Z16494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A98353 probable transcription regulator PA1760 [imported] - Agrobacterium tumefaciens (strain C: probable transcription tumefaciens (Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              two component response regulator Atu3035 [imported] - Agrobacterium tumefaciens (strain (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-326 cFIIN>
A;Cross-references: UNIPROT:003376; UNIPARC:UPI0000125BB2; EMBL:U87907; NID:g1946337; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cjaccession: AE2929
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClells; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-223, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AE2929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan_2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 2;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 31;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: Aox3
C,Superfamily: alternative oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.3%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Genetics:
A,Gene: Atu3035
A,Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.77
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 ÁQGVFFNAFFVF 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 66.7
Les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AQGULQNVRFVF 12
                                   1 AQGVLQNVRF 10
                                                                                               53 AQAVMQQVRF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|::||||
42 GILESVRFV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: T08849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                         T08849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                               8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q41267; UNIPARC:UPI00000A7E2A; EMBL:S81471; NID:g1478346; PI
C;Superfamily: alternative oxidase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species Neisesta meningitidis
C;Species Neisesta meningitidis
C;Decies Neisesta meningitidis
C;Decies Neisesta meningitidis
C;Decession: D81910
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morells, Policy S, S. Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, S02-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Accession: D81910
A;Access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:09JUB1, UNIPARC:UPI00000C4BB6; GB:AL162755, GB:AL157959, NID
A,Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPARC:UP1000017753A
C,Superfamily: alpha-catenin; vinculin amino-terminal homology; vinculin carboxyl-termin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aypothetical protein NMA1411 [imported] - Neisseria meningitidis (strain 22491 serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                 C,Accession: T08870
R;Whelan, J.; Millar, A.H.; Day, D.A.
Planta 198, 197-201, 1996
A;Tile: The alternative oxidase is encoded in a multigene family in soybean.
A;Reference number: Z16502; MUID:96165778; PMID:8580775
20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 14-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: NWA1411
Superfamily: Neisseria meningitidis hypothetical protein NWB1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 2; Length 102; Pred. No. 8.6; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cadherin-associated protein, 102K - rat (fragments)
N;Alternate names: catenin alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 2;
Pred. No. 7.4;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB;
Pred. No. 3.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                              A, Accession: T08870
A, Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:|||| ::
31 ARGILQNVPILY 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AQGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AQGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AQGVFFNAFFVF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-89 <NAG>
                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-40 <WHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: B39529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
```

ò

Gaps

ö

Length 1178;

```
59.3%; Score 35; DB 1; 1
45.5%; Pred. No. 1.3e+02;
tive 4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5, 2006, 22:44:59
F;658-697/Domain: EGF homology < EGF>
                                                                           Query Match 59.3
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                   :|:|||: :|
209 RGLLQNIHLIF 219
                                                                                                                                                                                                                                                       2 OGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: June
Job time: 14.9655 secs
                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                  g
                          Rigodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Tiel: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:2160853; PMID:11743194
A; Accession: A98353
A; Ascession: A98353
A; Ascession: A98353
A; Consecule type: DMA
A; Ascession: Ascordance A; Ascordance A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule rype: mRNA
A; Residues: 1-178 «LANA
A; Cross-references: UNIPROT: P35440; UNIPARC: UPI000013776D; GB:M60853; NID: G212763; PIDN:
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type i repeat homology; vd
F; 325-383/Domain: von Willebrand factor type C repeat homology «VWC»
F; 386-437/Domain: thrombospondin type 1 repeat homology «THR1»
F; 442-498/Domain: thrombospondin type 1 repeat homology «THR2»
F; 499-555/Domain: thrombospondin type 1 repeat homology «THR3»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lacticin 481/lactococcin biosynthesis protein LCNDR2 - Lactococcus lactis plasmid pMRC01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:O87240; UNIPARC:UP100000B9A11; EMBL:AE001272; PIDN:AAC56013. A;Experimental source: strain DPC3147 C;Genetics: A;Genome: Dlasmid runca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T43110
R;Dougherty, B.A.; Hill, C.; Weidman, J.F.; Richardson, D.R.; Venter, J.C.; Ross, R.P. Mol. Microbiol. 29, 1029-1038, 1998
A;Title: Sequence and analysis of the 60 kb conjugative, bacteriocin-producing plasmid A;Reference number: Z22314
A;Accession: T43110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Lactococcus lactis
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A39804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.3%; Score 35; DB 2; Length 927; 58.3%; Pred. No. 1e+02; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A39804
R;Lawler, J.; Duquette, M.; Perro, P.
Biol. Chem. 266, 8039-8043, 1991
A;Title: Cloning and sequencing of chicken thrombospondin.
A;Reference number: A39804; MUID:91217026; PMID:2022631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.3%; Score 35; DB 2; 66.7%; Pred. No. 83; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-927 <DOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombospondin precursor - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: AGR L 3540
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.3
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | |||| : ||:
821 ASGVLQTLLFVY 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AOGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|::||||
GILESVRFV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Genome: plasmid pMRC01
A;Note: ORF00039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A39804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
```

THIS PAGE BLANK (USPTO)

```
Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 QGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AA;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                            Feige J.J.;
  00000000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSU903
ID QS
AC QS
DT 07
DT 07
  RESULT
                                                                                                                                                                                                                             028194
                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xenopus lae
homo sapien
brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tetraodon n
tetraodon n
tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q28194 bos taurus (28194 bos taurus (28198 bos taurus (28178 bos t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rattus norv
mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ustilago ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thermoanaer
burkholderi
                                                                           5, 2006, 22:09:41 ; Search time 108.931 Seconds
(without alignments)
101.901 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                       2849598 seqs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q28194_BOVIN
Q5U903_PIG
Q7SY84_XENLA
TSP1_BOVIN
TSP1_HUMAN
TSP1_MOUSE
Q3TR40_MOUSE
Q3TR40_MOUSE
Q11SA3_RAT
Q8CQ1_MOUSE
Q8CG2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4RQ74_TETNG
Q4P665_USTMA
Q3CJK9_THEET
Q3F1U8_9BURK
Q44XL2_9BURK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q4LLM8 9BURK
Q563V1 XENLA
Q563S6 9PIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XENLA
99 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      056389 9PIPI
0563T0 9PIPI
0563T1 9PIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TETING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q563T2_9PIPI
Q563T3_9PIPI
Q563T4_9PIPI
                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q56387_9PIPI
Q56388_9PIPI
                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                          Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        059E99 1
                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q4RLR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q4S758
                                                                                                                                                                                                                                                                                                                                             1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                               1 AQGVLQNVRFVF 12
                                                                                                                         US-10-030-735-25
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                  UniProt_7.2:*
                                                                                                                                                                                                                                                                                                                                                                                                                                      %
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                  Database
                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
```

```
ö
Q563t5 xenopus ami
Q563u6 xenopus pyg
Q563u1 xenopus cli
Q563u3 xenopus fra
Q563u3 xenopus fra
Q563u4 xenopus ves
Q563u7 xenopus ves
Q563u9 xenopus wit
Q563u9 xenopus gil
Q563v2 xenopus gil
Q563v2 xenopus gil
Q563v2 xenopus gil
Q563v2 xenopus qil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Opposite regulation of thrombospondin-1 and corticotropin-induced secreted protein/thrombospondin-2 expression by adrenocorticotropic hormone in adrenocortical cells."; J. Cell. Physiol. 167:164-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDLINE=96331130; PubMed=8698834;
DOI=10.1002/(SICI)1097-4652(199604)167:1<164::AID-JCP19>3.3.CO;2-0;
Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chambaz E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARENTIN PRELIMINARY; PRT; 229 AA. (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (228194). (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25015 MW; 90D9EBCE4E6B669C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X89511; CAA61682.1; -; mRNA.
PIR, S57957; S57957.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR031320; ConA like_subgrp.
InterPro; IPR03129; Laminin_G_TSP_N.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 2
03 PIG
05 PIG
06 PIG
07 PIG
08 PIG
08 PIG
08 PIG
07 PIG-2004, integrated into UniProtKB/TrEMBL.
07 PIG-2004, sequence version 1.
07 PIG-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 55; DB 100.0%; Pred. No. 0.0 ive 0; Mismatches
     0563T5_9PIPI
0563U0_XENCL
0563U1_9PIPI
0563U3_9PIPI
0563U4_9PIPI
0563U4_9PIPI
0563U5_9PIPI
0563U5_9PIPI
0563U2_9PIPI
0563U2_9PIPI
0563U2_9PIPI
0563U2_9PIPI
0563U2_9PIPI
0563U2_9PIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
```

```
Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO1705; TSPIREPEAT.
SMART; SM00209; TSP1; 2.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 ÓGVLÓNVRFVF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QGVLQNVRFVF 12
                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                rissum=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
TSP1 BOVIN
  SOR REPLACE SOR REPLACED REPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-2238257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-2238257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A pischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Browstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Tucchman J.W., Grenn E.D., Dickson M.C.,

Blakesley R.W., Tucchman J.W., Grenn E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
               Name=Thbs1;
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Namelia: Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , DB 2; Lenson o. 0.022; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 249;
                                                                                                                                                                                                 Zhang K., Mauco G., Hauet T.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 AA; 27560 MW; 465D664BE0329C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003, integrated into UniProtKB/TrEMBL 01-0CT-2003, sequence version 1. 07-FEB-2006, entry version 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.2%; Score 55; DB 100.0%; Pred. No. 0.0 cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                           EMBL, AY773342; AAV38110.1; -; mRNA.
InterPro; IPR000884; TSP1.
InterPro; IPR018085; TSP_1.
InterPro; IPR011007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1705; TSPIREPEAT.
SMART; SM0209; TSP1; 1.
SMART; SM00204; VWF; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS501208; VWFC_1; 1.
PROSITE; PS50184; VWFC_1; 1.
NON_TER 1 1
NON_TER 249 249
SEQÜENCE 249 AA; 27560 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus; Xenopus
Thrombospondin 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00090; TSP 1; 2. Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QGVLQNVRFVF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGC64438 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                 NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7SY84_XENLA
Q7SY84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA].
STRAIN=HOLStein; TISSUB=TOOth;
MEDLINE=98173773; PubMed=9507064; DOI=10.1016/S0167-4838(97)00188-X;
WEDLINE=98173773; PubMed=9507064; DOI=10.1016/S0167-4838(97)00188-X;
WEDLINE=98173773; PubMed=9507064; DOI=10.1016/S0167-4838(97)00188-X;
WEDLINE=98173773; PubMed=9507064; DOI=10.1016/S0167-4838(97)00188-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=THBŠ1; Synonyms=TSP-1, TSP1;
Bos taurus (Bovine).
Bus taurus (Bovine).
Bus taurus (Bovine).
Busaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                    Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                            "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inoue H.;
"CDNA cloning of bovine thrombospondin 1 and its expression in
odontoblasts and predentin.";
Biochim. Biophys. Acta 1382:17-22(1998).
                                                                                                                                                                                                                       TISSUE=whole;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.2%; Score 55; DB 2; Length 496; 100.0%; Pred. No. 0.047; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50092; TSP1; 2.
PROSITE; PS01208; VWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_2; 1.
SEQUENCE 496 AA; 54843 MW; E4FD2F07CB7EF51B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC054970; AAH54970.1; -; mRNA.
G0; G0:0005198; F:structural molecule activity; IEA.
G0; G0:0007155; P:cell adhesion; IEA.
InterPro; IPR013320; ConA like subgrp.
InterPro; IPR003129; Laminin.G_TSP_N.
InterPro; IPR008085; TSP_1.
InterPro; IPR008085; TSP_1.
InterPro; IPR008085; TSP_1.
Figh: PF00090; TSP_1; 2.
Pfam; PF00099; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSP1 BOVIN STANDARD; PRT; 1170 AA. 028178; 028179; 021779; 021779; 01-NOV-1997, integrated into UniProtKB/Swiss-Prot. 01-DEC-2000, sequence version 2. 07-MAR-2006, entry version 56. Thrombospondin-1 precursor.
                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
```

```
NUCLEOTIDE SEQUENCE.
TISSUE=Endothelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo.
NCBI_TaxID=9606;
                                        DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
REGION
REGION
RATIF
REGION
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT S
TSP1 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઢ
                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                        TISSUB=Aortic endothelium;
Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin stimulatory effect of
TGF-beta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
TSP-like 1.
EGF-like 2; calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPROPIED 1 PROUBLID EGF 3.

INTERPROPIO 1 PROUBLID EGF 3.

INTERPROPIO 1 PROUBLID EGF Ca bd.

INTERPROPIO 1 PROUBLID EGF Ca bd.

INTERPROPIO 1 PROUBLID EGF Ca bd.

INTERPROPIO 1 PROUBLID EGF 1 LAWININ G TSP N.

INTERPROPIO 1 PROUBLID 1 TSP 1.

INTERPROPIED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
Thrombospondin-1.
/FTIG=PRO_0000035841.
TSP N-terminal.
[2]
NUCLEOTIDE SEQUENCE [MRNA] OF 1-18 AND 710-1170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AB005287; BAA21115.1; -; mRNA.
EMBL, X87618; CAA60950.1; -; mRNA.
FMBL, X87619; CAA60951.1; -; mRNA.
FTR, SS5501; S55501.
HSSP; P07996; 1LSL.
SNR; Q28178; 549-1169.
GlycosuitedB, Q28178; -.
InterPro; IPR013320; CONA_like_subgrp.
InterPro; IPR013320; CONA_like_subgrp.
InterPro; IPR013320; CONA_like_subgrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heparin-binding;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIMMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
```

4

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-like 2; calcium-binding (Potential).
                 domain.
                              domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=PRO 0000035842.
TSP N-terminal.
-!- SIMILARITY: Contains 3 EGF-like domains.
-!- SIMILARITY: Contains 1 TSP C-terminal (TSPC)
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN)
-!- SIMILARITY: Contains 3 TSP type-1 domains.
-!- SIMILARITY: Contains 1 VMFC domains.
-!- SIMILARITY: Contains 1 VMFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombospondin-1
                                                                                                                                  EMBL; M25631; AAA36741.1; .; mRNA.
EMBL; X04665; CAA28370.1; -; mRNA.
EMBL; X14787; CAA32893.1; -; mRNA.
EMBL; X14787; CAA32893.1; -; mRNA.
EMBL; J04835; AAA61277.1; -j mRNA.
EMBL; J04835; AAA61178.1; -j Genomic_DNA.
EMBL; M99425; AA859366.1; -; mRNA.
PDB; LLSL; X-ray; A=434-546.
PDB; LLSL; X-ray; A=434-1170.
PDB; LZR; X-ray; A=10-233.
PDB; LZA; X-ray; A=10-257.
PDB; ZERF; X-ray; A=10-257.
PDB; ZERF; X-ray; A=169.
Glycosuitche; P07996; -.
GGP; P07996; -.
GGP; P07996; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heparin-binding; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221
3373
429
4490
547
587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
316
316
435
549
588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
  Lawler J., Hynes R.O.; "The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
                                                                                                                                                                                                                                                                                                                                    MEDLINE-86287276; PubMed-3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
"Characterization of a cDNA encoding the heparin and collagen binding
                                                                                                                                                                                                                      MEDINE-2115. Pubmed-1930396;
Kobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.;
"Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 1-166.
MEDLINE-89291870; PubMed-2544587;
Laherty C.D., Gierman T.M., Dixit V.M.;
"Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.";
J. Biol. Chem. 264:11222-11227(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human plasma N-91ycoprotecome analysis by immunoaffinity subtraction, hydrazide chemistry, and mass spectrometry.";
J. Protecome Res. 4:2070-2080(2005).
-1- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type V collagen and integrins alpha-V/beta-1, alpha-luk/beta-3 and alpha-IIb/beta-3.
-1- SUBUNIT: Homotrimer; disulfide-linked.
-1- SIMILARITY: Belongs to the thrombospondin family.
                                                                                                           MEDLINE=89139590; PubMed=2918029; DOI=10.1083/jcb.108.2.729; Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L., Baumgartel D.M., Rotwein P., Frazier W.A.; Equalgate thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES.

MEDLINE=22338361; PubMed=12450399; DOI=10.1021/bi026463u;

Huwiler K.G., VeeFling M.M., Annis D.S., Mosher D.F.;

"Biophysical characterization, including disulfide bond assignments, of the anti-anglogenic type 1 domains of human thrombospondin-1.";

Biochemistry 41:14329-14339(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               la Fleur M., Jobin C., Gauthier J., Kreis C.G.;
"Expression of thrombospondin in chronic inflammation: neutrophils
from synovial fluids synthesize a novel 3.9 kb TSP mRNA.";
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'C-mannosylation and O-fucosylation of the thrombospondin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYDRATE-LINKAGE SITES ASN-248 AND ASN-1067.
PubMed=16335952; DOI=10.1021/pr0502065;
Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
Moore R.J., Smith R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21125860; PubMed=11067851; DOI=10.1074/jbc.M008073200;
Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J.,
Mosher D.F., Peter-Katalinic J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441;
THR-450; TRP-498 AND THR-507.
TISSUE-Platelet;
  MEDLINE=87057617; Pubmed=2430973; DOI=10.1083/jcb.103.5.1635;
                                                                                                                                                                                                                                                                                                                                                                              domains of human thrombospondin."; Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 276:6485-6498(2001).
                                                                      Cell Biol. 103:1635-1648(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 1028-1170.
                                                                                                                                                                     J. Cell Biol. 108:729-736(1989)
[3]
                                                                                                                                                                                                                                                                                             Biochemistry 25:8418-8425(1986)
                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE OF 1-397
                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE OF 1-374
                                                                                                 NUCLEOTIDE SEQUENCE
```

S

```
C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF 3.
EGF Ca bd.
EGF like.
EGF like reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA53063.1;
AAA53063.1;
AAA40431.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006210;
InterPro; IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006209;
InterPro; IPR013032;
InterPro; IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M87276;
EMBL; J05606;
   Laherty C.
Dixit V.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; P
EMBL; P
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metaroa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                               /FTIG=CAR 000208.
O-linked FPuc. .).
/FTIG=CAR 000209.
C-linked TMan).
/FTIG=CAR 000210.
O-linked TGLC. .).
/FTIG=CAR 000211.
N-linked GGCNAC. .) (Potential).
EGF-like 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 3.
TSP type-3 4.
TSP type-3 5.
TSP type-3 6.
TSP type-3 7.
TSP type-3 7.
TSP type-3 7.
TSP type-3 7.
TSP C-terminal.
Heparin-binding (Potential).
Cell attachment site (Potential).
N-linked (GlonAc. . .).
N-linked (GlonAc. . .).
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
NUCLECTIDE SEQUENCE.MEDLINE=92128941; PubMed=1774063;Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
                                                                                                                                                                                                                                                                                                                                                                     93.2%; Score 55; DB 1; Length 1170; 100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jenkins N.A.; "Characterization of the murine thrombospondin gene.";
                                                                                                                                    /FTId=CAR_000206.
C-linked [Wan]
/FIId=CAR_000207.
/FIId=CAR_000207.
                                                                                                                                                                                                                                                                   Interchain (Probable)
Interchain (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994, integrated into UniProtKB/Swiss-Prot. 01-JUN-1994, sequence version 1. 07-MAR-2006, entry version 57. Hrombospondin-1 precursor. Name-Fibbs; Synonyms-Tspl; Mus musculus (Mouse).
                                                                                                                             /FTId=CAR 000205.
O-linked [Fuc.
                                                                                                                      (Man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1170 AA
                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
                                                                                                                      C-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
MEDLINE=92147683; PubMed=1371115;
                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 11:587-600(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                    |||||||||||||||||||QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         2 QGVLQNVRFVF 12
 690
758
781
817
840
878
878
914
950
11170
232
232
232
360
360
                                                                                                                                                                                           450
                                                                                                                                                                                                              498
                                                                                                                                       394
                                                                                                                                                         438
                                                                                                                                                                           441
                                                                                                                                                                                                                               507
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                           441
                                                                                                                                                                                            450
                                                                                                                                                                                                              498
                                                                                                                                                                                                                                                                                     394
                                                                                                                                                                                                                               507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSP1 MOUSE
                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                   DISULFID
                                                                                                   CARBOHYD
                                                                                                                                      CARBOHYD
                                                                                                                                                        CARBOHYD
                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                        DOMAIN
REGION
 DOMAIN
DOMAIN
DOMAIN
                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P35441;
                                     DOMAIN
                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
TSP1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
```

셤 δ

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 1-490.
MEDLINE=50375546; PubMed=2398070;
BOTINE=50375546; PubMed=2398070;
BOTINE=50375546; PubMed=2398070;
BOTINESTEIN ALF ID., DEVATAGIN S., Framson P., Li P.;
"Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";
J. Biol. Chem. 265:16691-16698(1990).
"Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development."; J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; JOSGOS; AAA40431.1; JOINED; Genomic_DNA.
PIR; A40558; A40558.

BRSP; P07996; 1LS.
SMR; P35441; 549-1169.
Ensembl; ENSWUSGO000040152; Mus musculus.
MGI; MGI:98737; Thbs1.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0016525; P:negative regulation of angiogenesis; IDA.
InterPro; IPR013320; ConA_like_subgrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, M62470; AAA50611.1; -; Genomic DNA.

EMBL, M62451; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62451; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62453; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62454; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62454; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62456; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62457; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62457; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62467; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62467; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62461; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62462; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62463; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62463; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62464; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62464; AAA50611.1; JOINED; Genomic DNA.

EMBL, M62466; DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -; Genomic_DNA.
JOINED; Genomic_DNA
```

```
OJTR40 MOUSE
ID QJTR40 MOUSE PRELIMINARY; PRT; 1170 AA.
AC QJTR40;
                                                                                                                 93.2%; Score 55; DB 100.0%; Pred. No. 0.1 ive 0; Mismatches
                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                     OGVLONVRFVF 219
                                                                                                                                                                                     QGVLQNVRFVF 12
            874 89
910 93
946 116
1025 102
1170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Thbs1;
                                               DISULFID
CONFLICT
SEQUENCE
                                                                                                                                                                                                                       209
              DISULFID
                                                                                                                     Query Match
Best Local
                                                                                                                                                       Matches
SHHHHS
                                                                                                                                                                                        ð
                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                                                                                              DR InterPro; IPR003367; tsp_3.

DR InterPro; IPR003367; tsp_3.

DR InterPro; IPR0030859; TSP_C.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00009; TSP_1; 3.

DR Pfam; PF00393; VWC; 1.

DR PRINTS; SM00210; TSP1; 3.

DR SWART; SM00214; VWC; 1.

DR PROSITE; PS00126; EGF 2; 1.

DR PROSITE; PS00126; EGF 2; 1.

DR PROSITE; PS00126; EGF 2; 1.

DR PROSITE; PS001208; VWFC_1; 1.

DR PROSITE; PS01208; VWFC_1; 1.

DR PROSITE; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2.
EGF-like 3.
TSP type-3 1.
TSP type-3 1.
TSP type-3 2.
TSP type-3 4.
TSP type-3 4.
TSP type-3 7.
TSP type
                                                                                                                                                                                                                                                                                                                                                                                                            Thrombospondin-1.
/FTId=PRO_000035843.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
360
708
1067
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274
391
395
406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551
556
575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
```

```
NCLEOTIBE SEQUENCE.

RA CTRAIN=CS/BL/60; TISSUE-Aborta and vein;

RA CATHINE-CS/BL/60; TISSUE-Aborta and vein;

RA CATHINE IP. Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,

CATHING IP., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,

RA Oyama R., Ravael T., Lehhard B., Wells C., Kodzius R., Shimokawa K.,

RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,

RA Ambeel-Impionbato A., Apweiler R., Alturaliya R.M., Bailey T.L.,

RA Ambeel-Impionbato A., Apweiler R., Atturaliya R.M., Baisel K.W.,

RA Ghiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA Bensal M., Bayter L., Engetrom P., Fagololini M., Faulkhar G.,

RA Bensal M., Harbers M., Hayashi Y., Hensch T.K., Hirokawa T.,

RA Crowe M.L., Latore M., Rayashi Y., Hensch T.K., Hirokawa T.,

RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

RA Milson A., Madan Babu M., Madera M., Marchionni D.,

RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

RA Milson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,

RA Milson R., Nishiguchi S., Nishikawa S., Nori P., Randachi C.,

RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Senbelder C.,

RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,

Ramoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,

Ramonja K., Tan S.L., Tang S., Zaylor M.S., Tegner J., Teichmann S.A.,

Ramonja K., Tan S.L., Tang S., Zhume P.A., Hide W., Bult C.,

Ramanshi H., Zabarovsky E., Zhu E., Sasaki D., Todmaru Y.,

Ramanshi H., Zabarovsky E., Zhu E., Sasaki D., Todmaru Y.,

Ramanshi H., Zabarovsky E., Hume D.A., Kai C., Sasaki D., Tomaru Y.,

Raimmond S.M., Teasdale R.D., Liu E.T., Hard C., Sasaki D., Tomaru Y.,

Raimen S., Waller R.D., Sasaki D., Hume D.A., Rai C., Sasaki D., Tomaru Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CC7BL/65; TISSUB=Aorta and vein; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
Adult male aorta and vein cDNA, RIXEN full-length enriched library, clone: A530055N06 product:thrombospondin 1, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                      DB 1; Length 1170;
956 By similarity.
994 By similarity.
930 By similarity.
167 By similarity.
157 F -> L (in Ref. 2).
129647 MW; 0443E493615E7F06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
```

```
WEDLINE-2136463; PubMed=12466851; DOI=10.1038/nature01266; MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature012. Kiyocawa H., Nadado I., Gaato N., Gato N., Chockenbuach C., Gojobori T., Radafuelli R., Hill D.P., Bult C., Hume D.A., Quackenbuach J., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Akwaji H., Kawasawa Y., Kedziereki R.A., Kawaji H., Kawaji H., Merchionni L., McKenzie L., Miki H., Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescole G., Petroveky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Radelin A., Schneider C., Semple C.A., Setcu M., Shimada K., Sandelin A., Schneider C., Semple C.A., Setcu M., Shimada K., Wangi Y., Wangi Y., Watanabe Y., Wangi Y., Himing L.G., Wynnbaw-Boris A., Yanaqisawa M., Yang I., Yang I., Wan Z., Zavolan M., Zhu Y., Zimmer A., Arakawa T., Fukuda S., Kavani H., Nakamura M., Sakazume N., Sakazume N., Shimada A., Yashaki A., Sasaki A., Sasaki Y., Endre Y., Lander E.S., Rogers J., Hirrar A., Hara A., Haraki Y., Shibata K., Shinagawa A., Hara A., Hara A., Haraki Y., Shibata K., Lander E.S., Rogers J., Hara A., Haraki Y., Shibata K., Shinagawa H., Nakami Y., Lander E.S., Rogers J., Hara A., Haraki Y., Wangi Y., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Azawa T., Tawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Relischmann M., Gassterland T., Gissi C., King B., Kochiwa H., Kell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomite M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Gariboldi M., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havashi Zaki, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iidh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kodo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;

"The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                               RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANYOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/60; TISSUE=Aorta and vein;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE-Aorta and vein;
PubMed=16141073; DOI=10.1126/science.1112009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birney E., Hayashizaki Y.;
                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
```

Nature 409:685-690(2001).

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                              STRAIN=C57BL/6J; TISSUE=Aorta and vein; MEDILIB=2049374; PubMed=11042159; DOI=10.1101/gr.145100; MEDILIB=2049374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Publariation and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/61; TISSUE-Aorta and vein;

STRAIN=C99913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=2030913; PubMed=11076861; DOI=10.1101/gr.152600;

A MEDLINE-2030913; PubMed=11076861; DOI=10.1101/gr.152600;

A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Makamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A Yoneda Y., Ishikawa T., Ozawa Y., Izawa M., Ohara E., Matshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system=384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Aorta and vein;
Arakawa T., Carninci P., Pukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Immune K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI; MGI:98737; Thbsl.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0016525; P:negative regulation of anglogenesis; IDA.
InterPro; IPR006210; EGF.
InterPro; IPR000742; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.2%; Score 55; DB 2; Length 1170; 100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS50092; TSPI, 3.
PROSITE; PS01208; WWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
SEQUENCE 1170 AA; 129619 MW; 55BF04A20D91B194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000742; EGF 3.
InterPro; IPR001881; EGF 7.
InterPro; IPR001881; EGF Ca bd.
InterPro; IPR006209; EGF like reg.
InterPro; IPR0013029; LamInin G TSP N.
InterPro; IPR000884; TSP 1.
InterPro; IPR003367; tsp 3.
InterPro; IPR003367; tsp 3.
InterPro; IPR008859; TSP C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AK163092; BAE37190.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.4",
100.0%; Pru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSPIREPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001007; VWF_C.
Pfam; PF001009; BGF; 2.
Pfam; PF00109; TSP_1; 3.
Pfam; PF02412; TSP_2; 12.
Pfam; PF005735; TSP_C; 1.
Pfam; PF000093; VWC; 1.
PRINTS; PR01705; TSPL13.
SWART; SM00181; EGF; 3.
SWART; SM00210; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
```

```
QBOYQ1 MOUSE
QBOYQ1;
          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
RESULT 9
          Q80YQ1
                   ö
                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                        Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                  STRAIN=Sprague-Dawley;
Iwabu A., Hirohata S., Kusachi S., Nakamura K., Murakami T.,
Ninomiya Y., Tsuji T.;
Submitted (SEP-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129671 MW; 6F38D3DCE733060F CRC64;
                                                                                                                                                                                                                                                                                        SMR; Q718A3; 834-1169.
G0; G0:0005576; c:extracellular region; IEA.
G0; G0:0005509; F:calcium ion binding; IEA.
G0; G0:0005198; F:structural molecule activity; IEA.
G0; G0:0007155; P:call adhesion; IEA.
InterPro; IPR013320; ConA_like_subgrp.
InterPro; IPR006210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%; Score 55; DB 2; 100.0%; Pred. No. 0.12;
                                                                                   UniProtKB/TrEMBL
                                                                 PRELIMINARY; PRT; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR000742; EGF 3.
InterPro, IPR001881; EGF Ca bd.
InterPro, IPR006209; EGF Like reg.
InterPro, IPR013032; EGF Like reg.
InterPro, IPR003129; LamInin G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50092; TSPT; 3.
PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
SEQUENCE 1170 AA; 129671 MW; 6F31
                                                                                                                                                                                                                                                                               EMBL; AF309630; AAQ14549.1; -; mRNA.
                                                                        0715A3;
05-JUL-2004, integrated into Unii
05-JUL-2004, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003367; tSp_3.
InterPro; IPR008059; TSP_C.
InterPro; IPR001007; VWF_C.
Pfam; PF00008; BGF; 2.
Pfam; PF00409; TSP_1; 3.
Pfam; PF05735; TSP_2; 1.
Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1705; TSPIREPEAT.
SWART; SMO0181; EGF; 3.
SWART; SMO0209; TSP1; 3.
SWART; SMO0210; TSP1; 1.
SWART; SMO0210; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  TSP 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                 209 ÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 QGVLQNVRFVF 12
                                                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR013032; E
InterPro; IPR003129; L
InterPro; IPR000884; T
InterPro; IPR008085; T
InterPro; IPR003367; C
                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                Thrombospondin 1.
                                                                                                                                                                       NCBI_TaxID=10116;
                                                    Q71SA3_RAT
ID Q71SA3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                  셤
                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

```
STATELESTBLE STATE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R SWR; Q80YQ1, 335-1170.

R DARRY, Q80YQ1, 335-1170.

R Ensembl; ENSUNGG0000040152; Mus musculus.

R MG1; MG1:9873; Thbs1.

R GO; GO:0005615; C:extracellular space; RCA.

GO; GO:0005615; C:extracellular space; RCA.

GO; GO:0016525; P:negative regulation of angiogenesis; IDA.

R InterPro; IPRO01320; COAA like_subgrp.

R InterPro; IPRO06210; EGF.

R InterPro; IPRO06209; EGF.

R InterPro; IPRO06209; EGF.

R InterPro; IPRO01303; EGF. Like reg.

R InterPro; IPRO01303; EGF. Like reg.

R InterPro; IPRO01809; EGF. Like reg.

R InterPro; IPRO018094; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
STRAIN-ESTBL/6; TISSUB-Brain;
Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                01-JUN-2003, integrated into UniProtKB/TrEMBL. 01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC050917; AAH50917.1; -; mRNA.
HSSP; P07996; 1LSL.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003367; tsp. 3.
InterPro; IPR008859; TSP_C.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00093; VWC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                              Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6;
```

σ

us-10-030-735-25.rup

```
The Structure Structure of the Cartesian Structure of Structure of the Cartesian Structure of the Cartesian Structure of the Cartesian Structure of the Cartesian Structure of the Cart
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 22.
Thrombospondin 1 (Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-
length enriched library, clone:G930018021 product:thrombospondin 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                 Length 1171;
            SMART; SM00181; EGF; 3.
SMART; SM00209; TSP1; 3.
SMART; SM00209; TSP1; 3.
SMART; SM00210; TSPN; 1.
FMOSITE; PS00204; VWC, 1.
FROSITE; PS50026; EGF, 3; 2.
FMOSITE; PS50092; TSPI; 3.
FMOSITE; PS01089; VWFC, 1; UNKNOWN, 1.
FMOSITE; PS01089; VWFC, 2; 1.
SEQUENCE 1171 AA; 129690 MW; 12E077B50C64E2D3 CRC64;
                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                              93.2%; Score 55; DB 2;
100.0%; Pred. No. 0.12;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY; PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci P., Hayashizaki Y.;
PRINTS; PR01705; TSP1REPEAT
                                                                                                                                                                                                                 Local Similarity 100.
Les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse cDNA sequences.
                                                                                                                                                                                                                                                                                    209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                   2 OGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                  QBCGB2_MOUSE
QBCGB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Thbs1;
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                datches
                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
```

```
Pubmedia1641072; DOI=10.1126/Science.1121014;

Ray Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Ray Bajic V.B., Bernard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidnis V., Allen J.E.,

Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,

Ra Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,

Ra Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,

Ray Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

Ray Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

Ray Stetcher C.F., Rukushima T., Fragatom P., Fagiolini M., Faulkner G.,

Ray Crowe M.L., Davn T., Engstrom P., Fagiolini M., Faulkner G.,

Ray Crowe M.L., Davn T., Engstrom P., Fagiolini M., Faulkner G.,

Ray Crowe M.L., Iacono M., Rawasawa Y., Kelso J., Kitamura H.,

Ray Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,

Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa T.,

Ray Att M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

Ray Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

Ray Kitano H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

Misson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,

Ray Ratura S., Mulder N., Nakano N., Nakauchi H., Ng P.,

Rott B., Ruan Y., Salzberg S.L., Sandelin A., Schonsder C.,

Rottobach C., Sekiguchi K., Seenple C.A., Seno S., Sessa L., Shong Y.,

Ray Sherling S., Stupka E., Sugiura K., Salena Y., Ringe S., Stupka E.,

Ray Sperling S., Stupka E., Sugiura K., Salena Y., Ride W., Bult C.,

Ramoja K., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,

Ramonja K., Varandale R.D., Liu E.T. Brusic V., Guckenbush J.,

Ramonja K., Ranshima M., Salo T., Rawaii H., Kawadashira N., Itah M., Rato T., Rawaii H., Zabarowaka M., Salo T., Rawaii H., Zabarowaka M., Salo T., Rawaii H., Rayadashira N., Itah M., Itah M., Itah M., Itah M., Rato T., Rawaii H., Rayadashira N., Itah M., Itah M., Ita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Mammary gland;

MEDLINE-22154683; PubMed=12466851; DOI=10.1038/nature01266;

Mikaido I., Osatto N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Mikaido I., Osatto N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Gasterland T.A., Fletcher C.F., Forrest A., Guagh J.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

Konadaya A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konadaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Pontius J.U., Qi D., Ramachandran S.,

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ilda J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Mishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Mammary gland;
PubMed=16141073; DOI=10.1126/science.1112009;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKBN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).
                                                                                                                                                              NUCLEOTIDE SEQUENCE.
TISSUE-Mammary gland;
PubMed=16141072; DOI=10.1126/science.1112014;
"High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
```

```
TSP1 XENLA
 2888
                                                                                                                                                                  ò
                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                               Arakawa T., Shingawa A., Shibara K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibara K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komoo H., Adachi J., Fukuda S., Aizawa M., Nishii K., Kisosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Riel P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackehbush J., Schriml L., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackehbush J., Schriml L., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Winnhaw-Boxis M., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming I., Winnhaw-Boxis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
         Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Walming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishirkawa T., Komo H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Saski D., Shibata K., Shinagawa A., Hayashizaki Y., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length comes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Mammary gland;
MEDLINE=20499374; Dubed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; Dubed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Mammary gland;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunnoto H., Sakaguchi S., Inegami T., Rashiiwaji K., Fujiwas S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiiwaji K., Fujiwas S., Inoue K., Tozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Mammary gland;
Arakwa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakarume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.,
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
Tomita M.
                                                                                                                                                                                                                                                                           TISSUE=Mammary gland;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 Taylor M.S., Teasdale R.D.,
 R., Takenaka Y.,
                                                                                                                                                                                                                       Nature 420:563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Name=thbs1; Synonyms=tsp1;
Renopus lacvis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Urry L.A., Ramos J., Duquette M., Desimone D.W., Lawler J.; "Cloning, characterization and expression of thrombospondin-1 in Xenopus laevis embryos.";
                                                                                                           ö
                                                                    Score 55; DB 2; Length 1171;
Pred. No. 0.12;
                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                  01-JUN-1994, integrated into UniProtKB/Swiss-Prot
                                                         PRT; 1173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L04278; -; NOT_ANNOTATED_CDS; mRNA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF 3.
EGF 7.
EGF Ca bd.
EGF like.
EGF like reg.
Lamlin G TSP N.
TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P07996; 1LSL.
SMR; P35448; 552-117.
InterPro; IPR013320; ConA_like_subgrp.
InterPro; IPR006210; EGF.
EMBL; BC042422; AAH42422.1; -; mRNA.
EMBL; AX145202; BAE26293.1; -; mRNA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                 01-JUN-1994, sequence version 1. 07-MAR-2006, entry version 54. Thrombospondin-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003367; tsp_3.
InterPro; IPR008869; TSP_C.
InterPro; IPR001007; VWP_C.
Pfam; PF00008; EGF; 1.
Pfam; PF00412; TSP_1; 3.
Pfam; PF05735; TSP_C; 1.
Pfam; PF00535; TSP_C; 1.
Pfam; PF00535; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRNA].
                                               Query Match
Best Local Similarity 100.
Thes 11; Conservative
                                                                                                                                                                                209 OGVLONVREVE 219
                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00181; EGF; 2.
SMART; SM00209; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000742; E
InterPro; IPR001881; E
InterPro; IPR006209; E
InterPro; IPR013032; E
InterPro; IPR003129; InterPro; IPR00884; T
InterPro; IPR008884; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                             TSP1 XENLA
P35448;
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
TISSUE-Aorta endochelial cell;
TOCKNY Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 2; Length 1225;
Pred. No. 0.12;
0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Existing Series | Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                     26-APR-2005, integrated into UniProtKB/TrEMBL 26-APR-2005, sequence version 1. 21-FEB-2006, entry version 10. Thrombospondin 1 variant (Fragment).
                                                                                                                          QS9E99 HUMAN PRELIMINARY; PRT; 1225 AA.
QS9E99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.2%; Scor
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
The 11; Conservative
          212 QGVLQNVRFVF 222
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                     HUMAN
                                                                                                           Q59E99
                                                                                                                                  TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 2; calcium-binding (Potential).
EGF-like 3.
TSP type-3 1.
TSP type-3 3.
TSP type-3 4.
TSP type-3 4.
TSP type-3 5.
TSP type-3 5.
TSP type-3 7.
TSP type-3 1.
TSP type-3 7.
TSP type-3 7.
TSP type-3 7.
TSP type-3 7.
TSP t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%; Score 55; DB 1; Length 1173; 100.0%; Pred. No. 0.12;
SMART; SM00210; TSPN, 1.

SMART; SM00214; VWC, 1.

PROSITE; PS0022; BGF_2; 1.

PROSITE; PS0026; BGF_2; 2.

PROSITE; PS50026; BGF_3; 2.

PROSITE; PS50026; TSP1; 3.

PROSITE; PS00184; VWFC_1; 1.

PROSITE; PS0184; VWFC_2; 1.

Calcium; Cell adhesion; EGF-1ike domain; Glycoprotein; Heparin-binding; Repeat; Signal.

SIGNAL

23 Thrombospondin-1.
                                                                                                                                                                                                                                                                           Thrombospondin-1.
/FIId=PRO_000035844.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.1
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.2.;
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1173 AA; 130020 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
Les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGION
                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
            ODRARA SETT TO SET TO S
```

QGVLQNVRFVF 12 ò

ö

Gaps

ö

Indels

ö

Gaps

; 0

264 QGVLQNVRFVF 274

유

```
ö
                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                       Barker D., Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collagen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                          21-DEC-2004, integrated into UniProtKB/TrEMBL.
21-DEC-2004, sequence version 1.
21-DEC-2006, entry version 12.
Novel protein similar to vertebrate thrombospondin 1.\n\ (Fragment).
ORFNames=DKEY-11E23.1-001;
                                                                                                                        Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordaca, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell adhesion; EGF-like domain.
NON TER
SEQUENCE 1090 AA; 120978 MW; 5A9320504A22D836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL928866; CAI20599.1; -; Genomic_DNA.
SMR; Q5SPG5; 751-804, 754-1089.
Ensembl; ENSDARGO00001010785; Danio rerio.
G0; G0:0005509; F:calcium ion binding; IEA.
G0; G0:0008201; F:heparin binding; IEA.
G0; G0:000515; F:protein binding; IEA.
G0; G0:000515; F:protein binding; IEA.
G0; G0:000515; P:cpl adhesion; IEA.
InterPro; IPR002048; F: Frhand_Ca.
InterPro; IPR002048; F: Fhand_Ca.bd.
InterPro; IPR002048; F: Fhand_Ca.bd.
InterPro; IPR002048; F: Fhand_Ca.bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.7%; Score 50; DB 2; 100.0%; Pred. No. 1.1;
               PRT; 1090 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRULIVOS, CELS SMART; SMOOLB1; EGF; 2.
SMART; SMOOLB1; EGF; 2.
SMART; SMOOLB1; ESP1; 2.
SMART; SMOOLB1; TSP1; 1.
RPOSITE; PSOOLB1; EF HAND 1; UNKNOWN 1.
R PROSITE; PSOOLB1; EGF 2; 1.
R PROSITE; PSSOOB2; TSP1; 2.
RR PROSITE; PSSOOB2; TSP1; 2.
RR PROSITE; PSOOLB3; WWFC 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000742; EGF_3.
InterPro; IPR001881; EGF_Ca bd.
InterPro; IPR06209; EGF_like.
InterPro; IPR013032; EGF_like reg.
InterPro; IPR013129; LamInin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003129; Laminin G
InterPro; IPR000884; TSP1.
InterPro; IPR008086; TSP 1.
InterPro; IPR003867; tsp 3.
InterPro; IPR008859; TSP C.
Pfam; PF00008; EGF; 1.
Pfam; PF00009; TSP 1; 2.
Pfam; PF00090; TSP 1; 2.
Pfam; PF005735; TSP 2; 12.
Pfam; PF005735; TSP C; 1.
             QSSPGS BRARE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                [1]NUCLEOTIDE SEQUENCE.
                                                                                                                                                                       Cyprinidae; Dani
NCBI_TaxID=7955;
BRARE
```

```
Wheel-15496914; DOI=10.1038/nature03025;

Whomed-15496914; DOI=10.1038/nature03025;

Advanceli E. Bouneau L. Fischer C., Ozouf-Costaz C., Bernot A.,

Mucaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,

Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Rarra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"The early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                      19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2006, sequence version 1.
19-JUL-2006, entry version 8.
Chromosome 10 SCAF15019, whole genome shotgun sequence. (Fragment).
ORFNames-GSTENG00032374001;
                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Schinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetraodontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R EMBLY, CAREAULDS, CALLOBO, 1, -; Genomic_DNA.

R SNR; Q4RLRS; 834-887, 837-1171.

GQ; GQ:0005576; C:extracellular region; IEA.

GQ; GQ:0005509; F:calcium ion binding; IEA.

GQ; GQ:000519; F:epearin binding; IEA.

GQ; GQ:000515; F:protein binding; IEA.

GQ; GQ:000515; F:protein binding; IEA.

GQ; GQ:000515; F:protein binding; IEA.

GQ; GQ:000715; P:protein binding; IEA.

GQ; GQ:000715; F:protein binding; IEA.

GQ; GQ:000715; F:protein binding; IEA.

R GG; GQ:000715; F:protein binding; IEA.

GQ; GQ:000715; F:protein binding; IEA.

InterPro; IPR006104; EGF_3.

InterPro; IPR001302; EGF_1ike_reg.

InterPro; IPR001302; EGF_1ike_reg.

InterPro; IPR001302; EGF_1ike_reg.

InterPro; IPR001804; TSP_1.

InterPro; IPR0010084; TSP_1.

InterPro; IPR001008; TSP_1.

InterPro; IPR001008; TSP_1.

Pfam; PF00008; EGF; 1.

Pfam; PF00019; TSP_1; 3.

Pfam; PF00191; TSP_1; 12.

Pfam; PF00191; WWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; CAAE01015019; CAG10667.1; -; Genomic_DNA
                                                                                                                                       OARLES TETNG PRELIMINARY; PRT; 1171 AA.
QARLES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; 1.
TSPIREPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 431:946-957(2004).
                                        187 GVLONVRFVF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01705; TSP1RE
SMART; SM00181; EGF; 2.
3 GVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=99883;
                                                                                                                            ઠે
                                      유
```

```
ON THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The pubmed-15496914; DOI=10.1038/nature03025;

A Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Muccell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,

Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

A Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., De Berardinis V.,

Relis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindbtad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindbtad-Toh K., Schachter F., Saurin W., Scarpelli C.,

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

He Garil, Morten Determent Fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
19-JUL-2006, entry version 8.
Chromosome 14 SCAF1473, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENG00022976001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 84.7%; Score 50; DB 2; Length 1171; Best Local Similarity 100.0%; Pred. No. 1.2; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          1171 AA; 129304 MW; 865F3749693F7FCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0005576; Crextracellular region; IEA.
GO:0005509; F:calcium ion binding; IEA.
GO:0008201; F:heparin binding; IEA.
GO:0005515; F:protein binding; IEA.
GO:000519; F:structural molecule activity; IEA.
GO:0007155; F:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; CAAE01014723; CAG03524.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q4S758 TETNG PRELIMINARY; PRT; 1193 AA. Q4S758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the early vertebrate proto-karyotype.";
SMART; SM00209; TSP1; 3.
SMART; SM00210; TSPN; 1.
SMART; SM00214; WC; 1.
PROSITE; PS00186; EGF 2; UNKNOWN_1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50026; TSPI; 3.
PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS0184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 GVLQNVRFVF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                  1171 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                              Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

8758

             셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 2; Length 1193;
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                1193 AA; 133256 MW; 6E8781648FCEC7F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
EGF 3.
EGF Ca bd.
EGF like reg.
Laminin G TSP N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 5, 2006, 22:42:39 Job time : 109.931 secs
                                                                                                                                                                                                                                                                                                           PROSITE; PS01186; EGF 2; UNKNOWN 1. PROSITE; PS50026; EGF 3; 2. PROSITE; PS50092; TSPI 3. PROSITE; PS01208; VWFC 1; 1. PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.7%; Scc.
100.0%; Pred
0; F
                                                                                                                       Pfam; PF00009; BGF; 2.
Pfam; PF00009; TSP_1; 3.
Pfam; PF0012; TSP_3; 12.
Pfam; PF05735; TSP_C; 1.
Pfam; PF05735; TSP_C; 1.
PRINTS; PR01705; TSPIREPEAT.
SNART; SM00209; TSPI; 3.
SNART; SM00209; TSPI; 3.
SNART; SM00210; TSPI; 3.
                              InterPro; IPR013032; EGF_11Ke
InterPro; IPR003129; Laminin_
InterPro; IPR00884; TSP1.
InterPro; IPR008085; TSP 1.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 GVLQNVRFVF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GVLQNVRFVF 12
                     InterPro; IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                               Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

THIS PAGE BLANK (USPTO)

```
US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 482, Appl Sequence 97, Appl Sequence 20, Appl Sequence 20, Appl Sequence 2150, Appl Sequence 11112, A Sequence 19, Appl Sequence 19, Appl Sequence 46041, A Sequence 44, Appl Sequence 47, Appl Sequence 47, Appl Sequence 7, Appl Sequence 6, Appli Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6333, Ap
18826, A
44, Appl, A
42, Appl
6, Appli
6, Appli
7, Appli
6, Appli
67, Appli
67, Appli
67, Appli
67, Appli
                                                                           5, 2006, 22:43:07; Search time 23.8966 Seconds (without alignments) 43.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                        lesued Patents AA:*
l: /EMC Celerra SIDS3/ptodata/2/iaa/6_COMB.pep:*
c: /EMC Celerra SIDS3/ptodata/2/iaa/6_COMB.pep:*
l: /EMC Celerra SIDS3/ptodata/2/iaa/T_COMB.pep:*
l: /EMC Celerra SIDS3/ptodata/2/iaa/H_COMB.pep:*
l: /EMC Celerra SIDS3/ptodata/2/iaa/FCTUS COMB.pep:*
l: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6
Sequence 4
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Sequence Sequence S
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-939-853A-98
US-08-313-288B-20
US-09-949-002-350
US-09-199-637A-267
US-09-199-637A-267
US-09-949-016-11112
US-09-949-016-6333
US-09-949-016-6333
US-09-252-991A-18826
US-09-270-767-46041
US-09-605-703B-44
US-09-605-703B-42
US-09-605-703B-42
US-09-605-703B-42
US-09-605-703B-42
US-09-605-703B-42
US-09-605-703B-42
US-09-605-703B-42
US-09-605-703B-42
US-09-805-703B-42
US-09-805-703B-42
US-09-922-635-6
                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-922-635-22
                                                                                                                                                                                                                           650591 segs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                  Listing first 45 summaries
                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                              US-10-030-735-25
59
1 AQGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                             Run on:
                                                                                                                                 Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
No.
```

```
US-09-99-002-48.

US-09-99-002-48.

US-09-99-002-48.

Patent No. 690016

FALENT NO. 690016

FALENT NO. 690016

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH IRPLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WITH IRPLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WITH IRPLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WITH IRPLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WITH IRPLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

FILE REFERENCE: C1000-10-8

CURRENT APPLICATION NUMBER: 60/231,401

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 482

LENGTH: 825

LENGTH: 825

TYPE: PRT

CREANISM: Human

US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 97, Application US/09939853A
; Patent No. 6989232
; GENERAL INFORMATION:
    APPLICANT: Burgess et al.
    TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same
    TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same
    TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same
    TITLE OF INVENTION: NO. 6989232el Proteins and Nucleic Acids Encoding Same
    TITLE OF INVENTION: NO. 6989232el PROSE PRIOR APPLICATION NUMBER: 60/228,191
    PRIOR PILING DATE: 2001-08-25
    PRIOR PILING DATE: 2001-02-08
    PRIOR PILING DATE: 2001-02-08
    PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                           Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 33170, A
Sequence 48387, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                         Sequence
              Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.2%; Score 55; DB 2; Length 825; 100.0%; Pred. No. 0.024; ive 0; Mismatches 0; Indels
                          US-07-868-353A-3
US-08-407-804-3
US-09-124-807-3
US-09-270-767-48387
US-09-270-767-48387
US-09-134-001C-3732
US-09-134-001C-3732
US-09-134-807-23
US-09-124-807-23
US-09-124-807-23
US-07-868-353A-13
US-07-868-353A-15
US-07-868-353A-15
US-07-868-353A-15
US-07-868-353A-15
US-07-868-353A-15
US-08-407-804-22
US-08-407-804-22
US-08-407-804-24
                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 QGVLQNVRFVF 319
                                             2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 11; Conserv
```

us-10-030-735-25.rai

```
GENERALL IN CARACTURE EXIC S.
APPLICANT: Cargill, Michele
APPLICANT: Lander, Bric S.
APPLICANT: Encland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, George Q.
APPLICANT: Bolk, George Q.
APPLICANT: MCCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 282: 1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/123,357
PRIOR PELLING DATE: 1999-09-10
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 55; DB 1; Length 1170; 100.0%; Pred. No. 0.036; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55; DB 2;
Pred. No. 0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                   FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-949-002-350

; Sequence 350, Application US/09949002

; Patent No. 6900016

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
                                                                                                                                                                                                                                            20:
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                          TELEFAX: (212) 391-0526
TELEX:
                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 ÇGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                           Sequence 98. Application US/09939853A

Sequence 98. Application US/09939853A

Patent No. 6989232

GENERAL INFORMATION:

APPLICANT: Burgess et al.

TITLE OF INVENTION: No. 6989232e1 Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099

CURRENT APPLICATION NUMBER: US/09/39,853A

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR APPLICATION NUMBER: 60/269,961

PRIOR APPLICATION NUMBER: 60/269,961

PRIOR FILING DATE: 2001-03-20

PRIOR PRIOR APPLICATION NUMBER: 60/277,337

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 98

LENGTH: 831
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  °;
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                           93.2%; Score 55; DB 2; Length 831;
100.0%; Pred. No. 0.024;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 831; 0.024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20. 20 Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: L185 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.2%; Score 55; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WT-
NUMBER OF SEQ ID NOS: 159
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 97
LENGTH: 831
                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                   209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                            2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QGVLQNVRFVF 12
                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mus musculus
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-313-288B-20
                                                                                                                       US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

ö

Gaps

ö

ö

Gaps

ö

```
62.7%; Score 37; DB 2; 163.6%; Pred. No. 1.1e+02; ive 2; Mismatches 2.
    PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SSCTVARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267
LENGTH: 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                               TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                           Query Match 62.7%;
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.0.
T. Conservative
                                                                                                                                                                                                                                                                                                                                329 AČGALENVRKV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|:|||| ||
282 RGLLQNVHLVF 292
                                                                                                                                                                                                                                                                                          1 AQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-11112
                                                                                                                                                                     US-09-199-637A-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-313-288B-19
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT PILING DATE: 2000-01-28
PRIOR RPELICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 350
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42057, Application US/09270767

Fatent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburse et al.
TITLE OF INVENTION:
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42057

LENGTH: 731
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                 93.2%; Score 55; DB 2; Length 1170;
100.0%; Pred. No. 0.036;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPERENCE: 00786/361002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 2;
Pred. No. 30;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/199,637A CURRENT FILING DATE: 1998-11-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 267, Application US/09199637A; Sequence 267, Application US/09199637A; Patent No. 6355411; GENERAL INFORMATION: APPLICANT: Ausubel, Frederick; APPLICANT: GOOGMan, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rahme, Laurence G.
Mahajan-Miklos, Shalina
Tan, Man-Wah
Cao, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.1%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 QGVLQNVDFM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                        ; ORGANISM: Human
US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-270-767-42057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
US-09-949-016-11112

US-09-949-016-11112

Sequence 1112. Application US/09949016

Sequence 1112. Application US/09949016

Sequence 1112. Application US/09949016

Heart No. 6812339

GENERAL INFORMATION:
TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PELLING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

TEMPORAL IN O 11112
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                               Gaps
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1045;
Score 37; DB 2; Length 446;
Pred. No. 44;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
```

```
; Sequence 44, Application US/09605703B; Patent No. 6962989; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Drosophila melanogaster
US-09-270-767-46041
                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                             59.3%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.6%;
      FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                         Query Match 59.3
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.6
Best Local Similarity 97.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                           41 ÓGVLDAVQFLF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LONVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 LONVRLVF 85
                                                                                                                                                                                                                                                                     US-09-252-991A-18826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-605-703B-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6333, Application US/09949016

Sequence 6333, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WIMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/02/10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ 1D NO 6333
LENTH: 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.7%; Score 37; DB 1; Length 1172; Best Local Similarity 63.6%; Pred. No. 1.3e+02; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: Unanuary 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 2;
Pred. No. 1.3e+02;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-252-991A-18826
'Sequence 18826, Application US/09252991A
'Patent No. 6551795
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1172 amino acids
TYPE: amino acid
STRANDEDNESS: aingle
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.7
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 RGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|:||| ||
203 RGLLONVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-313-288B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                     TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-270-767-46041

Sequence 46041, Application US/09270767

Sequence 46041, Application US/09270767

Sequence 46041, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 46041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Oskar
TITLE OF INVENTION: CORNNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: CORNNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: UNMBER: US/09/605,703B
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR PILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
IENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·.
                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2; Length 175;
Pred. No. 38;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 2; Length 89;
Pred. No. 28;
0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PRILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 175
```

Search completed: June 5, 2006, 22:48:53 Job time: 23.8966 secs

189 AMGGLGSIRFVF 200

1 AQGVLQNVRFVF 12

ઠે



us-10-030-735-25.rapbm

```
Sequence 28, Appl
Sequence 40, Appl
Sequence 1020, Appl
Sequence 1022, Appl
Sequence 462, Appl
Sequence 462, Appl
Sequence 452, Appl
Sequence 454, Appl
Sequence 456, Appl
Sequence 455, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 98, Appl
Sequence 451, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1, Appli
1, Appli
7, Appli
12, Appli
2, Appli
114, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             App1:
                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA Main:*
.: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
.: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
.: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
.: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
.: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
.: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                                                                               5, 2006, 23:46:43 ; Search time 78.6207 Seconds (without alignments) 70.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
5.1.9
Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-474-213-28

US-10-419-462-40

US-110-782-968-40

US-110-741-600-1020

US-110-741-600-1020

US-110-743-806-462

US-110-043-806-454

US-111-043-806-454

US-110-043-806-455

US-110-043-806-453

US-110-043-806-453

US-110-043-806-453

US-110-043-806-453

US-110-043-806-453

US-110-043-806-451

US-110-043-806-451

US-110-043-806-451

US-110-043-806-451

US-110-043-806-451

US-110-043-806-451

US-110-043-806-451

US-110-043-806-451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-211-462-38
US-10-231-956A-482
                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-020-141-12
US-10-017-721-2
                                                                                                                                                                                                                                     2097797 seqs, 463214858 residues
GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                              Listing first 45 summaries
                                                       OM protein - protein search, using sw model
                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
                                                                                                                                                                1 AQGVLQNVRFVF 12
                                                                                                                                     US-10-030-735-25
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                855
1000
11005
11150
11169
11170
11170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
                                                                                                                                                                                                                                                                                          Minimum DB seq
Maximum DB seq
                                                                                                                                                     Perfect score:
                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
No.
```

```
US-10-474-213-28

US-10-474-213-28

Sequence 28. Application US/10474213

Publication No. US20040214248A1

GENERAL INFORMATION:

APPLICANT: Roberts David D

APPLICANT: RCULETS DAVID USE OF SEMENOGELIN IN THE DIAGNOSIS, PROGNOSIS AND TREATMENT OF

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: CANCER

TITLE OF INVENTION UNDBER: US/10/474,213

CURRENT FILING DATE: 2003-10-06

PRIOR APPLICATION NUMBER: 60/281,994

PRIOR PLING DATE: 2002-04-03

PRIOR PLING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.2

SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-419-462-40

US-10-419-462-40

Sequence 40, Application US/10419462

Publication No. US20040053392A1

SEQUENCE ATTILE OF UNIVENTION:

TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents FILE REFERENCE: W1107-20005

CURRENT APPLICATION NUMBER: US/10/419,462

CURRENT PILING DATE: 2003-04-17

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn version 3.2

SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                 38, Appl
44, Appl
548, App
1376, Ap
                                                                                                                                                                                           13287, A
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                       Sequence
Sequence
Sequence
                                                                                                         Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
  Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
US-10-419-462-38
US-10-741-600-1019
US-10-741-600-1019
US-10-741-600-1021
US-10-782-968-34
US-10-831-967-3
US-10-631-467-548
US-10-631-467-1376
US-10-631-467-1376
US-10-995-561-594
US-10-995-561-595
US-11-046-644-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 4;
Pred. No. 0.001;
0; Mismatches (
                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic peptide US-10-474-213-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.2%; Scur.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
  11170
11170
11170
11170
11170
11170
11170
11170
11170
11170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Similarity
11; Conserv
  Query Match
Best Local S:
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
   g
```

~

```
MS-11-043-806-462

| Sequence 462, Application US/11043806
| Sequence 462, Application No. US20060051774A1
| Publication No. US20060051774A1
| GENERAL INFORMATION:
| APPLICANT: Compugen Ltd
| TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
| TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
| TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer
| TITLE OF INVENTION: WHORER: US/11/043,806
| CURRENT PAPLICATION UNMERR: US/11/043,806
| CURRENT PAPLICATION UNMERR: US/11/043,806
| NUMBER OF SEQ ID NOS: 575
| LENGTH: 459
| TYPE: RRT
                                                                                                                                                                                                                                      Sequence 10.22, Application US/10741600
Sequence 10.22, Application US/10741600
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                             Gaps
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 93.2%; Score 55; DB 5; Length 432 Best Local Similarity 100.0%; Pred. No. 0.053; Matches 11; Conservative 0; Mismatches 0; Indels
  100.0%; Pred. No. 0.053;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.2%; Score 55; DB 6; Le
100.0%; Pred. No. 0.057;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i LOCATION: (1)...(432)
i OTHER INFORMATION: Xaa = Any Amino Acid
US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1047, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100
les 11; Conservative
                                                                                                                            209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 OGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 QGVLQNVRFVF 12
                                                                               2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
Best Local Similarity
Matches 11; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
                                                                                                                                                                                                         RESULT 5
US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-043-806-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40, Application US/10782968

Sequence 40, Application US/10782968

Publication No. US20050065324A1

GENERAL INPORMATION:
APPLICANT: Williams, Kevin J. TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
FILE REFERENCE: WI107-20005
FILE REFERENCE: WI107-20005
CURRENT APPLICATION NUMBER: US/10/782,968
CURRENT APPLICATION NUMBER: US/10/419,462
PRIOR FILING DATE: 2003-04-21
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.2

LENGTHAR: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1020, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 1020
SEQ ID NO 1020
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                       CTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-419-462-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Thrombospondin Region plus N-terminal domain
                                                                                                                                                                           Query Match
93.2%; Score 55; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.2%; Score 55; DB 5; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.2%; Score 55; DB 100.0%; Pred. No. 0.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1) ... (432)
OTHER INFORMATION: Xaa = Any Amino Acid
                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                  191 ÓGVLÓNVRFVF 201
                                                                                                                                                                                                                                                                                     2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-782-968-40
     LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
Sequence 452, Application US/11043806
| Publication No. US20060051774A1
| Publication No. US20060051774A1
| Publication No. US20060051774A1
| Publication No. US2006005177AA1
| APPLICANT: Compugen Ltd | APPLICANT: Compugen Ltd | APPLICANT: Compugen Ltd | TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer | FILE REFERENCE: 1847.1003 | CURRENT APPLICATION NUMBER: US/11/043,806 | CURRENT FILING DATE: 2005-01-27 | NUMBER OF SEQ ID NOS: 575 | LENGTH: 685 | LENGTH: 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 453, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: UNMBER: US/11/043,806
CURRENT APPLICATION UNMBER: US/11/043,806
UNMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-043-806-455

Sequence 455, Application US/11043806

Sequence 455, Application US/11043806

Sequence 455, Application OS USO060051774A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

FILE REFERENCE: 1847.1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 6; Length 685;
Pred. No. 0.088;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.2%; Score 55; DB 6; Length 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; bcc.
100.0%; Pred. No. c.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.2%; Score 55; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                      209 ÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 QGVLQNVRFVF 219
                             2 OGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                       RESULT 10
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                               8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 454, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
TITLE OF INVENTION: Load Nucleotide and Amino Acid Sequences, and Assays and Methode TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT PILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 454
LENGTH: 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 456, Application US/11043806

Publication No. US2066051774A1

Publication No. US2066051774A1

GENERAL INFORMATION:
TITLE OF INVENTION: Lhereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 456
LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                     , DB 3; Leas
0. 0.058;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.2%; Score 55; DB 6; Length 578; 100.0%; Pred. No. 0.073; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          Length 466;
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR PLING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PATENTIN Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 6;
Pred. No. 0.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%; Scc...
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                     Query Match 93.2%; Score 55; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 QGVLQNVRFVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 OGVLONVREVE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-11-043-806-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-11-043-806-454
                                                                                                                                                                                                                                             LENGTH: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

ઠે

ઠ

```
Query Match 93.2
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                   209 OGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 ÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QGVLQNVRFVF 12
                                                                                                                                                                                                                             2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
   US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-043-806-461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search cor
Job time
                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Squence 98, Application US/09939853A

Squence 98, Application US/09939853A

Publication No. US20040039163A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: No. US20040039163A1el Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-099

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR APPLICATION NUMBER: 60/28,191

PRIOR FILING DATE: 2001-08-25

PRIOR PELING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR PRIOR PRIOR OWNER: 60/277,337

PRIOR PRIOR PRIOR OWNER: 60/277,337

PRIOR PRIOR SACILING DATE: 201-02-08

PRIOR PRIOR PRIOR DATE: 201-02-08

PRIOR PRIOR PRIOR DATE: 201-02-08

PRIOR PRIOR PRIOR DATE: 201-02-08

PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Squence 97, Application US/09939853A

Fublication No. US20040039163A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVERTION:

CURRENT ELLIGO ATE: 2001-09-9

CURRENT FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: 60/28,191

PRIOR FILING DATE: 2001-08-25

PRIOR PRILING DATE: 2001-08-25

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

SOFTWARE:

SOFTWARE:

SOFTWARE:

LENGTH:

SEQ ID NO 97

LENGTH:

LENGTH: 831
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.2%; Score 55; DB 3; Length 831; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      Query Match 93.2%; Score 55; DB 6; Length 828; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            209 QGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 GGVLONVREVE 219
                                                                                                                                                                                                                                                                                                                                          2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 QGVLQNVRFVF 12
; LENGTH: 828
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: 1047,1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 461
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
             Score 55; DB 3; Length 831; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.2%; Score 55; DB 6; Length 855; 100.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                         0; Indels
93.2%; Scor.
100.0%; Pred. No. v...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: June 6, 2006, 00:00:10
ne: 79.6207 secs
                                                                                                                                                                                                                                   US-11-043-806-461

; Sequence 461, Application US/11043806

; Publication No. US20060051774A1

; GENERAL INFORMATION:
```

```
Sequence 15318, A Sequence 65, Appli Sequence 642, Appli Sequence 9347, A P Sequence 34673, A Sequence 3672, A P Sequence 5024, A P Sequence 5024, A P Sequence 5023, A P Sequence 1348, A P Sequence 13583, A P Sequence 15583, A P Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15282,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30699,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31888,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA New:*

1. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

4. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

8. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                            6, 2006, 00:00:38; Search time 3.72414 Seconds (without alignments) 37.266 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-953-349-15318

US-11-203-828-5

US-10-953-349-9347

US-10-953-349-34674

US-10-953-349-34674

US-10-953-349-34672

US-10-953-349-5023

US-10-953-349-5023

US-10-953-349-5023

US-10-953-349-26582

US-11-294-697-4132

US-11-294-697-4132

US-11-294-697-497-2

US-11-953-349-1995

US-11-953-349-15283

US-10-953-349-1699

US-10-953-349-1699

US-10-953-349-11888

US-10-953-349-11888

US-10-953-349-31888

US-10-953-349-31888

US-10-953-349-31888

US-10-953-349-31828

US-10-953-349-31828

US-10-953-349-31828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58871 seqs, 11565156 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                 1 AQGVLQNVRFVF 12
                                                                                                                                                                                                                                                                      US-10-030-735-25
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                  June
                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
No.
```

Sequence 21826, A Sequence 31698, A Sequence 31698, A Sequence 31687, A Sequence 26200, A Sequence 26300, A Sequence 2988, Ap Sequence 2988, Ap Sequence 31323, Ap Sequence 2388, Ap Sequence 2388, Ap Sequence 2387, Ap Sequence 31898, A Sequence 31207, A Sequence 1717, Ap	S AND CORRESPONDING POLYPEPTIDES	Length 182; ; Indels 0; Gaps 0;	FOR CARDIOVASCULAR
US-10-953-349-21826 US-10-953-349-39136 US-10-953-349-39136 US-10-953-349-26200 US-10-953-349-7070 US-10-953-349-7069 US-11-293-697-2998 US-11-293-697-2998 US-11-293-697-3938 US-11-293-697-3938 US-11-293-697-3323 US-10-953-349-5461 US-10-953-349-288 US-10-953-349-288 US-10-953-349-288 US-10-953-349-288 US-10-953-349-2861 US-10-953-349-31207 US-10-953-349-31207 US-10-953-349-31206 US-10-953-349-31207	RESULT 1 US-10-953-349-15318 Sequence 15318, Application US/10953349 Publication No. US2060107345A1 Sequence 15318, Application US/10953349 Publication No. US2060107345A1 TOTILE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND FITTLE OF INVENTION: ENCONDED THERBY FILLE REFERENCE: 2750-1579PUS2 CURRENT FELING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: PatentIn version 3.3 SEQ ID NO 15318 LENGTH: 182 LENGTH: 182 CURRENTSM: Glycine max US-10-953-349-15318	Score 34; DB 6; Len Pred. No. 7.1; 2; Mismatches 2;	8 KU AS A TREATMENT /203,828
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Dlication US 20060107345A N: N: REOV, Nickol N: ENCONDED N: ENCONDED N: NUMBER: UF: N: 5004-09 VS: 40252 1 version 3.	larity 60.0%; Conservative 60.0%; CONVREVE 12 12 13 13 13 13 13 14 15 15 15 15 15 15 15	ation US/112 20060110390A W, LESLIE ROV, CARMEN W: INHIBITIO W: INHIBITIO W: INHIBITIO W: NUMBER: U DN NUMBER: U DN NUMBER: 00/ COS: 7 1 Ver. 2.1
20000000000000000000000000000000000000	RESULT 1 35-10-953-349-15318 Sequence 15318, Application US/1 Sequence 15318, Application US/1 GENERAL INFORMATION: APPLICANT: ALEXANDROV, Nickolai TITLE OF INVENTION: SEQUENCE-DE TITLE OF INVENTION: ENCONDED TITLE OF INVENTION: ENCONDED TITLE OF INVENTION: ENCONDED TITLE OF INVENTION: ENCONDED TITLE OF SEQUENCE-DE CURRENT FILING DATE: 2004-09-33 SOFTWARE: PATENTING DATE: 2004-09-35 SOFTWARE: PATENTING MAX TYPE: PATENTING MAX	imi ' ' GVI GLL	US-11-203-828-5 Sequence 5, Application US/11203828 Publication No. US20060110390A1 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: INHIBITION OF KU J. TITLE OF INVENTION: INHIBITION OF KU J. TITLE OF INVENTION: UNBERSES FILE REFERENCE: MYOG:58US CURRENT APPLICATION NUMBER: US/11/203 CURRENT APPLICATION NUMBER: 60/604,435 PRIOR FILING DATE: 2004-08-24 NUMBER: OF SEQ ID NOS: 7 SOFTWARE: Patentin Ver: 2.1 SEQ ID NO 5 LENGTH: 608 TYPE: PRT CREATH: 608
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-10-95; Sequence is	Query Match Best Local S Matches 6 Qy 3	RESULT 2 US-11-203-828 Sequence 5, Sequence 5, Publication GENERAL INI APPLICANT TITLE OF TITLE OF TITLE OF TITLE OF FILE REFER CURRENT AR CURR

Gaps

g

```
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILE REPRENENT SEPRENENT SEQUENCE: 2750-15799082

CURRENT APPLICATION NUMBER: US.10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 34674

LENGTH: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-953-349-34673

Sequence 34673, Application US/10953349

Publication No. US20060107345A1

SEQUENCE 34673, Application US/10953349

Publication No. US20060107345A1

SERENTAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

APPLICANT: ALEXANDROV, Nickolai et al.

APPLICANT: ALEXANDROV, Nickolai et al.

APPLICANTON WORTHON: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

CURRENT APPLICATION WOMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PATENTIN VETSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34672, Application US/10953349

Bublication No. US20060107345A1

GENERAL INFORMATION:
THILE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN Version 3.3
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.9%; Score 33; DB 6; Length 382; 60.0%; Pred. No. 25; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.9%; Score 33; DB 6; Length 358; 60.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                    Length 331;
                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                  Score 33; DB 6;
Pred. No. 21;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
APPLICANT: ALEXANDROV, Nickolai et al
                                                                                                                                                                                                                                     ; ORGANISM: Zea mays subsp. mays US-10-953-349-34674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                       55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     225 QGVLFNIQYV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 QGVLFNIQYV 261
                                                                                                                                                                                                                                                                                                                                                                                        2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-953-349-34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-953-349-34673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-953-349-34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 34672
LENGTH: 382
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 34673
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALEXANDO, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579P012
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ THARE: Patentin version 3.3
SEQ ID NO 9347
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 6; Length 1504;
Pred. No. 69;
                                      Score 34; DB 7; Length 608; Pred. No. 26; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.9%; Score 33; DB 6; Length 298; 40.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
FRIOR PEDLICATION NUMBER: US 60/363,019
FRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE PARENTIN 3.2
LENGTH: 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-953-349-34674
; Sequence 34674, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9347, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                       US-10-505-928-662
; Sequence 662, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Arabidopsis thaliana
US-10-953-349-9347
                                        57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Overy Match
Best Local Similarity 40.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACGVLQNVRFVF 12
                                                                                                                                                                      461 KAIVÓNVRFTY 471
                                                                                                                              2 QGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|::| |:|:
87 EGIIQGVKFI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens
US-10-505-928-662
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-953-349-9347
US-11-203-828-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
```

ઠે

ö

Gaps

ö

Gaps

g ઠે

```
Sequence 26582, Application US/10953349
Publication No. US20060107345A1
Publication No. US20060107345A1
GENERAL INPORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN Version 3.3
SEQ ID NO 26582
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                         Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                       Score 32; DB 6;
Pred. No. 27;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 6;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.2%; Score 32; DB 7; 70.0%; Pred. No. 30; iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-11-293-697-4132
Sequence 4132, Application US/11293697
Sequence 4132, Application US/11293697
PUBLICATION NO. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT APPLICATION NUMBER: US/10/108,260
FRIOR APPLICATION NUMBER: US/10/108,260
FRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOUTHWARE: PARENTIN VEY. 2.1
SEQ ID NO 4132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                           ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5022
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 5022
LENGTH: 273
                                                                                                                                                         54.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.2%;
                                                                                                                                                                                                                                                              |:|| | |:| |
111 AKGVIYLSNIRMVF 124
                                                                                                                                                                                                                                     1 AQGV--LONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26582
                                                                                                                                         Query Match
Best Local Similarity 57.14
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 58.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AQGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 ADGERONMDFVF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 GVVFNVRVVF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-10-953-349-26582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-293-697-4132
                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                          쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5023, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARKE: PATENTION version 3.3
SOFTWARKE: Patentin version 3.3
                                                                                                                                               Sequence 5024, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
PUBLICALL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 5224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5022, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL TINORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 6;
Pred. No. 20;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.2%; Score 32; 57.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5023
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Arabidopsis thaliana
US-10-953-349-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AQGV--LQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 AKGVIYLSNIRMVF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AOGV--LONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 AKGVIYLSNIRMVF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.11
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                             276 QGVLFNIQYV 285
                      2 QGVLQNVRFV 11
                                                                                                                                       US-10-953-349-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-953-349-5022
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
```

ð g ઠે

Gaps

. 0

Score 31; DB 6; Length 1234; Pred. No. 2.2e+02; 3; Mismatches 1; Indels

```
6, 2006, 00:12:55
                                                                 TYPE: PRT
ORGANISM: Arabidopsis thaliana
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3997
LENGTH: 1234
                                                                                                                                                    Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                  :|||| |:
1122 ILENVRLVY 1130
                                                                                                                                                                                                                                       4 VLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                 Search completed: June
Job time : 3.82414 secs
                                                                                                            US-10-953-349-3997
                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                  g
                                                   Sequence 1348. Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-15799022
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 1348
INDICATION OF SEQ ID NOS: 40250
SOFTWARE: A400
MANUEL NO 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3997, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: SEQUENCE-BETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPRENCE: 2750-15799US2
CURRENT APPLICATION VMDER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Genzyme Corporation
APPLICANT: Roberts, Bruce
TITLE OF INVENTION: METHODS TO DIAGNOSE AND TREAT LUNG CANCER
FILE REFERENCE: 5257C
CURRENT APPLICATION NUMBER: US/11/247,437
CURRENT APPLICATION NUMBER: PCT/US2004/011193
PRIOR PILING DATE: 2004-04-12
PRIOR PILING DATE: 2004-04-12
PRIOR FILING DATE: 2004-04-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                54.2%; Score 32; DB 6; Length 440; 60.0%; Pred. No. 45; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 7; I
Pred. No. 1.5e+02;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/11247437; Publication No. US20060110753A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Arabidopsis thaliana US-10-953-349-1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 GVLENVSAIF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | : | | : | 445 RGVYENVKYV 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-11-247-437-2
                                          US-10-953-349-1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-953-349-3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-247-437-2
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
Tue
```

```
Aab35369 Alpha3bet
Aab3532 Alpha3bet
Aab35378 Alpha3bet
Abg72834 Thrombosp
Ad170641 Human thr
Ad39357 Human myo
Aau02916 Angiotens
Aab43602 Human can
Aau02916 Angiotens
Aau02915 Angiotens
Aau02914 TSF polyp
Aau02914 Angiotens
Aau02914 Angiotens
Aau02914 Human thr
Aau14771 Human thr
Abb82285 Human thr
Abb82285 Human thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human var
Human she
Human thr
Human COP
Angiogene
Human THB
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      5, 2006, 22:08:53 ; Search time 91.1379 Seconds (without alignments) 60.201 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aau75315 R
Abp96780 R
Abu03474 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aab90800 1
Aae25030 1
5.1.9
Biocceleration Ltd.
                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                               2589679 seqs, 457216429 residues
                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB35369
AAB35352
AAB35378
ABG72834
ADL70641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ39359
ADQ39357
AAU02916
AAB43602
AAU02915
ADN02474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB00042
AAU74771
ABB82285
AAB74450
AAB90800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP96780
ABU03474
ABG74673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE25030
                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                      geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
                                                                                                                                                                                                                                                                                         geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
                                                                                                                                                                                                                                                                                                                                                                      geneseqp2006s:
                                                                                                                                                                                                                                                                                                                                                             geneseqp2005s:*
                                                                                                                                                                                                                                                                                geneseqp1980s:*
                                                                                                                1 FAGVLQNVRFVF 12
                                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                                                         US-10-030-735-26
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                        Geneseq_8:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length
                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10:
                                                                                                                                  Scoring table:
                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0B
0B
                                      OM protein
                                                                                                                  Sequence:
                                                                                                                                                                Searched:
                                                                                                                                                                                                      Minimum Maximum
                                                                                                                                                                                                                                                                        Database
                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š.
```

27 55 91.7 1170 8 ADJ76124 Adj75296 Adj752124 Marker ge 28 55 91.7 1170 8 ADJ70639 Adj76296 Adj76299 Adj76299 Adj76299 Adj76299 Adj76299 Adj76297 Human thr Human thr Human thr Adj26070 Thrombosp Adj26070 Thrombosp Adj29358 Human myo Adj29358 Human myo Adj39358 Human myo Adj39369 Adj39369
--

ALIGNMENTS

Alpha3betal integrin binding peptide #34 AAB35369 standard; peptide; 12 AA (first entry) 08-MAY-2001 AAB35369; RESULT 1 AAB35369

Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.

Synthetic.

WO200105812-A2.

25-JAN-2001.

12-JUL-2000; 2000WO-US018986.

99US-0144549P. 15-JUL-1999; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Krutzsch HC; Roberts DD,

WPI; 2001-182656/18.

New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and cancer

Claim 4; Page 34; 84pp; English.

The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention

Sequence 12 AA;

```
Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                    1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                    FOGVLONVRFVF 12
                                                                                                                                                                            WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                            the invention
                                                                                                                                                                                                                                                                                                                              Sequence 12 AA;
                                                                WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VO200281630-A2
                                                                                                                       15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-FEB-2003
                                                                                                                                                           Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2002.
                                                                                  25-JAN-2001
                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG72834;
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                            cancer.
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention
                                                                                                                                                                         Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                 New peptides that bind to or are recognized by alphal-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
100.0%; Score 60; DB 4; Length 12; 100.0%; Pred. No. 7e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 4; Length 12;
Pred. No. 0.0007;
0; Mismatches 1; Indels
                                                                                                                                                          Alpha3betal integrin binding peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha3betal integrin binding peptide #43.
                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                   AAB35352 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB35378 standard; peptide; 12
                                                                                                                                                                                                                                                                       12-JUL-2000; 2000WO-US018986.
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                               Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 91.7
1; Conservative
                   Conservative
                                               1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FAGVLONVRFVF
                                                                                                                                                                                                                                                                                                                                                WPI; 2001-182656/18.
         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 AA;
                                                                                                                                                                                                                                   WO200105812-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi:
Matches 11;
                                                                                                                                                                                                                                                                                          15-JUL-1999;
                  12;
                                                                                                                                        08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2001
                                                                                                                                                                                                                                                      25-JAN-2001
                                                                                                                                                                                                                  Synthetic
                                                                                                                       AAB35352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB35378;
Query Match
         Best_Local
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                               cancer.
                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB35376
                                     à
                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, thrombospondin-1, cytostatic; immunostimulant; cancer; epithelial cancer; lung cancer; papillary renal cell carcinoma; colon cancer; small-cell lung cancer; SCLC; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 4; Length 12;
Pred. No. 0.0007;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombospondin-1 sequence containing synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG72834 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2001; 2001US-0281994P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-2002; 2002WO-US010535
                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0144549P
```

```
The invention relates to diagnosing cancer other than prostate cancer in a male mammal, comprising assaying a test sample for increased level of semenogalin, or cancer in a female by assaying for the presence of semenogalin, or cancer in a female by assaying for the presence of semenogalin. Administering a semenogalin protein or polypeptide fragment or a semenogalin-specific antibody or active fragment, or a recombinant vector expressing the protein or antibody, is useful for inducing an immune response to a cancer in a mammal, where the cancer is not prostate cancer, particularly of epithelial origin such as lung cancer, papillary renal cell carcinoma, colon cancer, sepecially small-cell lung cancer (SCLC), or a melanoma. The present sequence represents the amino acid sequence of the thrombospondin-1 sequence containing synthetic peptide which binds to alpha-3-beta-1 integrin
                                                                           A new diagnosis for cancer other than prostate cancer in a mammal useful to detect cancer including lung cancer, particularly small cell lung cancer and melanoma comprises detecting semenogelin in a sample.
                                                                                                                                                                                     Example 1; Page 14; 32pp; English.
                         WPI; 2003-103329/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12 AA;
```

91.7%; Score 55; DB 6; Length 12; 91.7%; Pred. No. 0.0007; ive 0; Mismatches 1; Indels Query Match Best Local Similarity 91.7 Matches 11; Conservative 1 FAGVLQNVRFVF 12 1 FOGVLONVRFVF 12 셤 8

ö

Gaps ö

> Human; thrombospondin-1; epitope; cancer; diagnosis. Human thrombospondin-1 N-terminal domain. ADL70641 standard; protein; 240 AA. 20-MAY-2004 (first entry) Homo sapiens ADL70641; Region ADL/70641
>
> ID ADL/70641
>
> XX AC ADL/
> XX ADL/XX Hum
> XX Hum
> XX Hum
> XX Hom
> X

/note= "Fibrinogen binding region" .82 .e= "Heparin binding region" "Heparin binding region" Location/Qualifiers 23. .32 /note= " /note= Region Region

WO2004018995-A2

20-AUG-2003; 2003WO-US026023 23-AUG-2002; 2002US-0405494P 04-MAR-2004.

(WILL/) WILLIAMS K J.

21-APR-2003; 2003US-00419462.

Williams KJ;

WPI; 2004-226901/21.

New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma

cardiant; gene therapy; human.

The present sequence is that of the N-terminal domain of human thromospoponian-1 (TSP) ADL70639. The invention relates to TSP fragments (B0-100, 40-55 or 20-35 MB mol.wt.) found in plasma, and their use in (thromospoponian-1 (TSP) ADL70639. The invention relates to TSP fragments (B0-100, 40-55 or 20-35 MB mol.wt.) found in plasma, and their use in continuing agents. A method that distinguishes TSP from a TSP fragment or portion involves: (I) using an epitope shared by TSP and antibody, to obtain a quantitation of TSP plus of TSP fragment or portion in the fragment or portion; (2) using an quantitation of the amount of TSP fragment or portion in the control of the amount of TSP fragment or portion of the amount of TSP fragment or or portion of the amount of TSP fragment or portion of the amount of TSP fragment or portion or portion of a disease or condition selected from cancer, or monitor the course, of a disease or condition selected from cancer, creat failure, renal disease, appendently dermaticmy myosacial infarction, liver disease, splenectomy dermaticmy oscillate, polyarterities or monitor architic ascollate, syndrome, henoche Schemich plantelet or activation, a condition associated with intravascular platelet activation, a condition associated with intravascular platelet cartivation, a condition associated with intravascular openity on the condition associated with platelets or cartivation, a condition associated with pluging of reactivation, a condition associated with pluging of cardivation, an apparame read and dissembners of thrombospondin and/or release of thrombospondin and/or releaded with activa ö gland, prostate gland, endometrial tissue, mesodermal tissue, ectodermal tissue, entodermal tissue, a teratoma, a poorly-differentiated cancer, a well-differentiated cancer or a moderately differentiated cancer. Gaps or leukemia or as calibrators, indicators, immunogens and analytes. ö Score 55; DB 8; Length 240; Pred. No. 0.019; 0; Mismatches 1; Indels Disclosure; SEQ ID NO 40; 76pp; English Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative 190 FOGVLONVRFVF 201 1 FAGVLONVRFVF 12 Sequence 240 AA; ð g

Human myocardial infarction-associated gene derived protein, SEQ ID 1022. Myocardial infarction; detection; single nucleotide polymorphism; SNP; ADQ39359 standard; protein; 432 AA. 18-NOV-2004 (first entry) ADQ39359; RESULT 6 ADQ39359 **必然なまなおななな** Human myocardial infarction-associated gene derived protein, SEQ ID 1020.

Myocardial infarction; detection; single nucleotide polymorphism; SNP;

cardiant; gene therapy; human

WO2004058052-A2 Homo sapiens

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

10-MAR-2003; 2003US-0453135P. 30-APR-2003; 2003US-0466412P. 23-SEP-2003; 2003US-0504955P. 20-DEC-2002; 2002US-0434778P.

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least current sequences given in the specification or its complement and encoding any one of the amino acid sequences given in the specification, an antibody that specificatly binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid, comprising the matched of a variant polypeptide; and a min and a variant polypeptide; and a min and a containing and and a series.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 method is useful in identifying an individual who was and for preparing a decreased risk for developing myocardial infarction. This composition for treating or preventing myocardial infarction-sequence represents the protein of a human myocardial infarction-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%; Score 55; DB 8; Length 432; 91.7%; Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; SEQ ID NO 1022; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                lakoubova 0;
                                                                                                                                                                                                   20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-ABR-2003; 2003US-046612P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                      22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                              Devlin JJ,
                                                                                                                                                                                                                                                                                                                 (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-533949/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADQ38531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 432 AA;
                                                                 WO2004058052-A2
                       Homo sapiens.
                                                                                                              15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                              Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
ð
```

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Iakoubova 0;

Cargill M, Devlin JJ, (APPL-) APPLERA CORP

WPI; 2004-533949/51. N-PSDB; ADQ38529.

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises an isolated nucleic acid molecule comprising at least of contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino the specification or its complement and encoding any one of the amino comprising an amino acid sequence given in the specification; an antibody that specification and unforted polymorphide or its antigen-binding that specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a myocardial infarction. The novel detection method has cardiant activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The nucleic acids of the invention may be used in gene therapy. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction. This sequence containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; SEQ ID NO 1020; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ39357 standard; protein; 432 AA.
```

```
Gaps
                                             ö
ch 91.7%; Score 55; DB 8; Length 432; 1 Similarity 91.7%; Pred. No. 0.037; 11; Conservative 0; Mismatches 1; Indels
```

ö

RESULT 8 AAU02916

18-NOV-2004 (first entry)

ADQ39357;

exaxe.

ADQ39357

S

```
granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                     Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                            Angiotensin converting enzyme (ACEV) splice variant protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                       Khosravi R, Bernstein J;
AAU02916 standard; protein; 459 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 16; 519pp; English.
                                                                                                                                                                                                                                                                                                                           17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                       Levine Z, David A, Azar I,
                                                                                                                                                                                                                                                                                                                                                       99IL-00132978
                                                                                                                                                                                                                                                                                                                                                                     99IL-00133455
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS06016.
                                                                                                                                                                                                                                                                          WO200136632-A2
                                                  12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                      17-NOV-1999;
                                                                                                                                                                                                                                                   Ното варіепв
                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1999;
                                                                                                                                                                                                                                                                                                    25-MAY-2001
                         AAU02916;
```

The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated mucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as shpertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis

Sequence 459 AA;

```
Gaps
                                  ö
      Score 55; DB 4; Length 459;
Pred. No. 0.04;
0; Mismatches 1; Indels
          91.78;
Query Match
Best Local Similarity 91.79
These 11; Conservative
```

1 PAGVLQNVRFVF 12

ö

Gaps

ö

RESULT 9 AAB43602

```
AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immnomodulator; antidiabetic; antiabthematic; antiathritic; antidiabetic; antithrounatic; antianthritic; antifilammatory; antithrounatic; antiabtertarial; antithral; caracological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; autipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agoniers and antagoniers from the present invention may be used to treat immune disorders by activating crimibiting the proliferation, differentiation or mobilisation of cimumne cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, differentiation or mobilisation of cimumne cells, to treat disorders of haematopoietic cells, modulate haemostatic or thrombolytic activity, modulate criection, modulate haemostatic or thrombolytic activity, modulate corrections or antipodies, adonists and antagonists may be also be used in drug screens. AAC78449 to AAC78473 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                     diagnosis, cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antidiametic; antidarthritic; antiviral; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; haematopoletic cell disorder; autoimmune disorder; haemostatic; cardiovascular disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                       Human; cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.7%; Score 55; DB 3; Length 466; 91.7%; Pred. No. 0.04; ive 0; Mismatches 1; Indels
                                                                                                                            Human cancer associated protein sequence SEQ ID NO:1047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 1636-1638; 2352pp; English.
AAB43602 standard; protein; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000; 2000WO-US005882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1999; 99US-0124270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 FQGVLQNVRFVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAC77811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000.
                                                                                   08-FEB-2001
                                           AAB43602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
```

ADN02474 standard; protein; 549 AA.

ADN02474;

```
RESULT 11
                        ADN02474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated mucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy,
                                                                                                                                                                                                          Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; ranal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                   nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                      Angiotensin converting enzyme (ACEV) splice variant protein #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%; Score 55; DB 4; Length 546; 91.7%; Pred. No. 0.048; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               such as deep vein thrombosis
                                          AAU02915 standard; protein; 546 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Fig 15; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levine Z, David A, Azar I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99IL-00132978
99IL-00133455
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS06015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200136632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                            12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abnormality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001
                                                                                  AAU02915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
  RESULT 10
                        AAU02915
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a novel recombinant adenovirus vector mediated anti-neoplastic composition is prepared through cloning the cDNA sequence from the human peripheral blood cell by specific primer and reverse transcription-polymerase chain reaction (RT-PCR) method for coding TSF polypeptide, construction in human embryonic kidney cell 293 by AdBasy system, and packaging and expressing the recombinant adenovirus vector of TSF. It can suppress the growth and transfer of cancer. The present sequence represents the TSF polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nonarcoidotic pulmonary granulômatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor suppressing polypeptide TSF and gene therapy vector composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angiotensin converting enzyme (ACEV) splice variant protein #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                 adenovirus vector; anti-neoplastic; TSF polypeptide; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 7; Length 548;
Pred. No. 0.048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                      (TAID-) TAIDA LIFE SCI TECH RES CENT HEMATOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 1; 13pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU02914 standard; protein; 555 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                     21-AUG-2002; 2002CN-00129408.
                                                                                                                                                                                                                                                                                     21-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                        2003-469302/45
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-469302/
N-PSDB; ADN02475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 548 AA;
                                                                                 TSF polypeptide
                                                                                                                                                                                                                                                                                                                                                        Liu P;
                                                                                                                                                    Homo sapiens
                                               17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2001
                                                                                                                                                                                    CN1401387-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU02914;
                                                                                                                                                                                                                                                                                                                                                        Han Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02914
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

ö

Gaps

ö

208 FOGVLONVRFVF 219

음 ð

Local Similarity 91.7 Les 11, Conservative 1 FAGVLQNVRFVF 12

Best Loca Matches

```
vascular disorder; asbestosis.
                              Homo sapiens.
                                                                                                                                     17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                 25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB00042
 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various cidsorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; mycoardial infarction; coronary arterial thrombosis; rand disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                          Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme (ACEV) splice variant protein #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 4; Length 555;
Pred. No. 0.049;
0; Mismatches 1; Indels
                                                                                                                                                                                                        Levine Z, David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU02913 standard; protein; 731 AA.
                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 14; 519pp; English
vascular disorder; asbestosis.
                                                                                                                                     99IL-00132978.
                                                                                                           17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vuery Match 91.7%;
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FAGVLQNVRFVF 12
                                                                                                                                                                             (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                   2001-336004/35.
                                                                                                                                                                                                                                              N-PSDB; AAS06014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 555 AA;
                                                      WO200136632-A2
                              Homo sapiens.
                                                                                                                                   17-NOV-1999;
10-DEC-1999;
                                                                                25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU02913
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
```

```
The sequence represents an angiotensin converting enzyme splice variant

(ACEV) polypeptide. The polypeptides of the invention include variants of
granulocyte colony stimulating factor receptor, glucapon, interleukin 6,
platelet-derived endothelial cell growth factor, cyclin-dependent kinase
inhibitor IC, cellular tumour antigen P53, and vasoactive intestinal
colypeptide receptor 2. The polypeptides and their associated nucleic
acids are useful for identification of variant sequences and detection of
candidate compounds capable of binding the molecules. The sequences of
the invention can be used in the treatment and diagnosis of various
disorders including cardiovascular diseases such as attrioral-colerosis,
myocardial infarction and coronary arterial thrombosis, renal diseases
such as diabetic nephropathy, muscular diseases such as hypertrophy,
immune disorders such as immune complex nephritis, multiple sclerosis,
cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such
as asbestosis and vascular pathologies involving an endothelial
abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection; glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 4; Length 731;
Pred. No. 0.067;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Levine Z, David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361. .416
/label= Type 1 repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB00042 standard; protein; 1152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 13; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human thrombospondon-1 (TSP-1).
                                                                                                                                                                 17-NOV-2000; 2000WO-IL000766
                                                                                                                                                                                                                                             99IL-00132978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                         (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS06013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 731 AA;
40200136632-A2
```

ö

ω

.309

```
/label= Type 3_repeat_domain
/note= "This region contains 7 type 3 repeats, from
/residues 698-733, residues 734-756, residues 757-792,
residues 793-815, residues 816-853, residues 854-889 and
residues 890-925"
                                                                                                                                                                                                                                                                                                                                                                                                                                531. .673
/labol= Type_2 repeat domain
/note= "This region contains 3 type 2 repeats, from
residues 531-571, residues 572-629 and residues 630-673"
                                                                                                                             /note= "This region contains 3 type 1 repeats, from
residues 361-416, residues 417-473 and residues 474-530"
                                                                                                                                                                                     413. 415
/label= RFK_motif
/note= "Necessary and sufficient for activation of transforming growth factor beta (TGF beta)"
                                                                                                                                                                                                                                            118. .423
/label= TGF-beta_and_fibronectin_binding_domain
/note= "Transforming growth factor"
                                                                    /label= Procollagen homology_domain
/note= "Required in_inhibition of angiogenesis"
                                                                                               361. .530 1
|label= Type 1 repeat domain
|note= "This region contains 3 type 1
                             163. .360
'label= Procollagen_homology_region
                                                                                                                                                                                                                                                                                                                                                                         81. .499 -
label= Anti-angiogenesis_domain
                                                                                                                                                                                                                                                                                      120. .426
'label= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                             177. .483
|abel= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          570. .601
/label= Calcium_binding_domain
                                                                                                                                                                        'label= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                 186. .491
/label= Cell_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2001; 2001WO-US017250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2000US-0207994P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200191781-A2
                Key
Region
                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                        Domain
                                                                                                   Domain
                                                                                                                                                            Domain
                                                                                                                                                                                       Region
                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
 New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TCP (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerase chain reaction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful of or treating angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. Anti-angiogenic therapy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                        Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%; Score 55; DB 3; Length 1152; 91.7%; Pred. No. 0.11; ive 0; Mismatches 1; Indels
417. .473
/label= Type 1 repeat region
474. .530
                                         /label= Type 1 repeat region
                                                                                                                                                                                       (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              does not induce drug resistance
                                                                                                                               31-FEB-2000; 2000WO-US002482.
                                                                                                                                                            99US-0118053P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 91.7
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOGVLONVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                               WPI; 2000-514823/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1152 AA;
                                                                        40200044908-A2
                                                                                                                                                            01-FEB-1999;
                                                                                                   33-AUG-2000
                                                                                                                                                                                                                   lawler JW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
```

. 925

```
The invention describes a composition comprising cDNA encoding fragments of human thrombospondin-1 (TSP -1), a type 1 repeat polypeptide and potent inhibitor of tumour growth and angiogenesis. The composition is useful for killing cancerous cells (preferably tumour); for reducting volume or inhibiting growth of a tumour (inhibiting neovascularisation the tumour); for decreasing proliferation of tumour cells; in the treatment of diseases and conditions associated with angiogenic activity or misregulated growth and angiogenesis-mediated diseases such as cancer, solid tumour, tumour metastasis, benign tumour, (e.g. haemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas),
                                                                                                                                                                                                             Composition useful for treatment of cancer comprises cDNA encoding amino acids of human thrombospondin-1 or its conservative variant and a
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 7; 54pp; English.
                                                                                                         WPI; 2002-106273/14.
Lawler JW;
                                                                                                                                                                                                                                                                                                                                               carrier.
```

Thrombospondin-1; TSP-1; cytostatic; angiogenesis; vasotropic; vulnerary; neovascularisation; cell proliferation inhibitor; cancer; solid tumour; haemangioma; acoustic neuromas; neurofibroma; trachoma; acoustic neuromas; are trachoma; trachoma; pyogenic granulomas; rheumatoid arthritis; ocular angiogenic disease; retinopathy; psoriasis; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rebeosis; angiofibroma; Osler-Webber syndrome; myocardial angiogenesis; haemophilac joints; plaque neovascularisation; telangiectasia; wound granulation; apoptosis.

Homo sapiens

AAU74771 standard; protein; 1152 AA

ठ g Human thrombospondin-1 (TSP-1).

(first entry)

09-APR-2002

AAU74771;

```
rheumatoid arthritis, psoriasis, ocular angiogenic diseases (e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascullar glaucoma, retrolental fibroplasias, rebensis), Osler-Webber syndrome, myocardial angiogenesis, telangisctasia, plaque neovascularisation, haemophiliac joints, angiofibroma or wound granulation. The composition induces apoptosis and inhibits neovascularisation in the tumour cells. This amino acid sequence represents human thrombospondin-1 (TSP-1), on which the recombinant proteins of the invention are based
                                                                                                                                                                                                                                                                                               Sequence 1152 AA;
           8888888888888
```

ö Gaps ö Query Match 91.7%; Score 55; DB 5; Length 1152; Best Local Similarity 91.7%; Pred. No. 0.11; Matches 11; Conservative 0; Mismatches 1; Indels

| ||||||||||| 190 FQGVLQNVRFVF 201 1 FAGVLONVRFVF 12 કે g

Search completed: June 5, 2006, 22:25:00 Job time: 91.1379 secs

THIS PAGE BLANK (USPTO)

Sequence:

Run on:

Searched:

```
thrombospondin 1 -
thrombospondin 1 p
thrombospondin 1 p
thrombospondin 2 p
thrombospondin 2 p
two component resp
probable transcrip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical prote
protein F15D4.3 [i
hypothetical prote
FRNA-pseudouridine
malate dehydrogena
G protein alpha ch
IAA-Ala hydrolase
probable protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical prote
hypothetical prote
hypothetical prote
probable proteinas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombospondin pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                    5, 2006, 22:25:22 ; Search time 13.9655 Seconds (without alignments) 82.675 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                    283416 segs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSHUP1
A40558
A40558
A42872
A5287
A58353
A38804
T20385
T50315
C57253
D81399
F56556
AE0774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H64974
A98990
D85835
AG0347
D84938
S32491
                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                1 PAGVLQNVRFVF 12
                                                                                                                                                                                                                             US-10-030-735-26
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 4 4 5 5 3 3 4 4 6 5 4 4 6 5 3 3 4 4 6 5 4 4 6 5 7 4 6 5 7 5 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 2 8 7 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
3: pir4:*
                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             991.7
992.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
993.7
                                                                                                                                         June
                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
```

Database

Result

Š.

	30	35	58.3	338	~	G91264	
	31	35	58.3 58.3	417	~ ~	H83708 H96556	
	0. 6. 6. 4.	992	58.3	465	0 0	S76464 S45068	4 hypothetical prote 53% glycoprotein -
-	32	32.	58.3	3587	(1)	140486	
	37	. G	56.7	167	4 (4	AD1526	
	8 6 6 6	9 9 4 4	56.7 56.7	199 308	ч 0	G64070 JC5468) imidazoleglycerol- leukocidin chain l
	40	34	56.7	311	00 0	C89968	
	4 4	υ ω 4 4	56.7	459	4 (7	D86669	
	64.4	34	56.7	460	α α	G64066	collagenase prtC h
	45	34	56.7	541	10	543061	
						ALI	ALIGNMENTS
	RESULT 1						
	S57957 thrombospondin 1	նումյո 1	- bovine		E C	(fragment)	
	C; Species: Bos primigenius taurus (catt	Вов р	rimigen	ius ta	Ę,	B (cattl	le)
	C; Accessi	3-0an-1	957 #se	duence	ו נו	TOTETA	ב כזומוואם
	R; Lafeuil	lade, B	., Pell	erin,	S.;	Kerami	idas, M.; Chambaz, E.M.; Feige, J.J.
	submitted	to the	EMBL D	ata Li	bra	ry, Jul	ly 1995 - Prombognondin-1 and CTSD/thrombognondin-2 expressi
	A; Descrip	ce numb	pposite er: 8579	1 egu 1	arı	5	מוות כוצל כוודסיייסספססייסדוו
	A, Accessi	on: \$57	957				A, Accession: 557957
	A; Status:	prelim	inary				
	A:Residue	e Lype: 8: 1-22	METAF>		•		
	A;Cross-r C;Superfa	eferenc milv: t	es: UNI	PROT:Q	281	94; UNI EGF ho	A; CTOSTANDES TEFETENCES: UNIPROT: Q28194; UNIPARC: UPI000008740A; EMBL: X89511; NID: 9899228; PID: A; CTOSTANDES TEFETENCES: UNIPROT: Q2819228; PID: C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
	, S	, 4 0	•	5	7.	0,000	
	Wheny march Best Local	al le	Similarity	91.78		Pre	0.0037;
	Matches	-	Conservative	vative		;	зпас
	ò	1 FA	FAGVLONVRFVF	FVF 12			
	g	190 FQ		 FVF 201	-		
		!					
-	RESULT 2						
	TSHUP1				1	5	
	C.Species: Homo	Homo	precursor sapiens (m	(man)	יוחוושיו	T	
	C;Date: 2	3-Aug-1	987 #se	quence	re.	vision	03-Aug-1995 #text_change 09-Jul-2004
	C, Accessi	on: A26	155; A3	4274;	A30	140; A2	25812; A05172; A42927
	K;Lawler,	iol.; HY	3, 1635	-1648,	19	96	K;Lawler, J.; Hynes, K.O. J. Cell Biol. 103, 1635-1648, 1986
	A;Title:	The str	ucture (of hum	an	thrombo	ospondin, an adhesive glycoprotein with multiple
	A;Referen	ice numb	er: A26.	155; M	E E	:870576	A;Reference number: A26155; MUID:87057617; PMID:2430973 A:Accesian: A26155
	A; Molecule type: mRNA	e type:	mRNA				
	A; Residue	8: 1-11	70 < LAW		- 1		
	A; Cross-r	eferenc	es: UNI	PROT: P	079	96; UNI	IPARC:UPI0000046821; GB:X04665; NID:g37137; FIDN:C
	A; Note: F R; Laherty	, C.D.;	Gierman	a, T.M	. · ·	Dixit,	
	J. Biol.	Chem. 2	64, 112;	22-112	27,	1989	
	A;Title:	Charact	erizatio	on of	the	promot.	cer region of the human thrombospondin gene. DNA 270. DMID:2544587
	A:Accession: A34274	on: A34	274 A34	E	1	076760:	CONTROL OF THE COLOR
	A, Molecul	e type:	DNA				
	A;Residue	B: 1-16	6 < LAH>	נוי טמעם	DIO	1001742	A;Residues: 1-166 <lah> A.fras-rafarances: INIPARC:UPIONO01742BP: GB:104835</lah>

A, Cross-references: UNIPARC:UP100001742BF; GB:J04835
R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, f J. Cell Biol. 108, 739-736, 1989
J. Cell Biol. 108, 739-736, 1989
A, Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the

probable cytochrom hypothetical 527K hypothetical prote probable membrane

S57908 AI1167 860950

H+-transporting tw testosterone 7alph

binding protein co carbon-phosphorus hypothetical prote

```
A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUD:92128941; PMID:1774063
A;Recession: A40558
A;Status: DNA
A;Residues: 1-1170 <-LAW
A;Residues: 1-1170 <-LAW
A;Residues: 1-1170 <-LAW
A;Cross-references: UNIPROT:P35441; UNIPARC:UP10000028012; GB:M62449; GB:M62450; GB:M62465; B:M62462; GB:M62463; GB:M62463; GB:M62463; GB:M62465; GB:M62465; GB:M62465; B:Bornstein, P.; A1fi, D.; Devarayalu, S.; Framson, P.; Li, P.
J; Biol. Characterization of the mouse thrombospondin gene and evaluation of the role of A;Reference number: A37905; MUID:90375546; PMID:2198070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI000016D076; GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40; R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M. J. Biol. Chem. 267, 3274-3281, 1992
A;Tile: Chem. 267, 3274-3281, 1992
A;Tile: Chem. 267, 3274-3281, 1992
A;Tile: Chem. 267, 3274-3281, 1992
A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: B42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-1152, P', 1154-1170 < LAH>
A;Residues: 1-1152, P', 1154-1170 < LAH>
A;Cross-references: UNIPARC:UPI0000177496; GB:M87276
A;Note: sequence extracted from NOB1 backbone (NCBIP:81501)
R;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar
A;Reference number: S68787; MUID:96234006; PMID:8654563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 19-26, 'X', 28-37 cCHE>
A; Residues: 19-26, 'X', 28-37 cCHE>
A; Cross-references: UNIPARC; UPIO000177A97
A; Cross-references: UNIPARC; UPIO000177A97
C; Complex: homotrimer, disultide linked
C; Complex: homotrimer, disultide linked
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor C; Reywords: calcium binding; glycoprotein; homotrimer
F; 1-18/Domain: signal sequence #status predicted <SIG>F; 1-9-1170/Product: thrombospondin 1 #status predicted <SIG>F; 1-1370/Domain: thrombospondin type 1 repeat homology <THR1>
F; 317-349/Domain: thrombospondin type 1 repeat homology <THR2>
F; 318-439/Domain: thrombospondin type 1 repeat homology <THR3>
F; 51-586/Domain: EGF homology <EGF>
F; 51-586/Domain: EGF homology <EGF
F; 51-586/Domain: EGF homology <EGF
F; 51-586/Domain: EGF
F; 51-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;ACCCESSIA.....A...A;MNA
A;MOJECULE LYPE: mRNA
A;Residues: 1-1172 <LAB>
A;Residues: 1-1172 <LAB>
A;Cross-references: UNIPROT:P35442; UNIPARC:UPI0000046680; GB:L12350; NID:g307505; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A47379; A42173
R;LaBell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A;Titles: Sequence and characterization of the complete human thrombospondin 2 cDNA: 1, R*Reference number: A47379; MUID:94010892; PMID:8406456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 2; Length 1170;
Pred. No. 0.021;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombospondin 2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-490 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <BOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A37905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISHUP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer induction:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc
C;Superfamily: thrombospondin 1; EGF homology; vc
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;1378-429/Domain: von Willebrand factor type C repeat homology <VWC>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-497/Domain: thrombospondin type 1 repeat homology <THR2>
F;51-586/Domain: EGF homology <EGFI>
F;51-586/Domain: EGF homology <EGFI>
F;51-586/BRegion cell attachment (R-G)D motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA

A; Residues: 1-83, 'A', AS-374,'RC' < DIX>

A; Cross-references: UNIPARC: UPI000016B140; GB:M14326; NID:g340005; PIDN:AAA61237.1; PID:

A; Note: parts of this sequence, including the amino end of the mature protein, were dete

A; Note: parts of this sequence, including the amino end of the mature protein, were dete

B; Sun, X:, Skorstengaard, K.; Mosher, D.F.

J; Cell Biol. 118, 693-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 193-701, 19
                                                                                                                                                                            A, Residues: 1-83, 'A', 85-522, 'A', 524-1170 <HEN>, ALACOSS-TETERENCES: UNIVERNAC:UPIO000033898.1; PIL A,/Cross-Tereferences: UNIVERAC:UPIO000033881.1; BMBL:XI4787; NID:g37464; PIDN:CAA32889.1; PIL A,/Cross-Teferences: UNIVERNAC:UPIO000033881; BMBL: A,/NOTE: parts of this sequence, including the amino end of the mature protein, were deter R; Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P. B. Eden-McCutchan, F.; Framson, P.; Bornstein, P. Bater 425, 1986 ; A,/Title: Partial amino acid sequence of human thrombospondin as determined by analysis of A,/Reference number: A25812; MUID:87157592; PMID:303305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: A25812

A;Moldcule type: mRNA

A;Residues: 1-83, 47, 85-397 <KOB>

A;Cross-references: UNIPARC:UPI000016B0CA, GB:M25631; NID:G538353; PIDN:AAA36741.1; PID:

A;Cross-references: UNIPARC:UPI000016B0CA, GB:M25631; NID:G538353; PIDN:AAA36741.1; PID:

B;Coss-references: UNIS, S. W. Grant, G.A.; Rotwein, P.; Frazier, W.A.

B;Coss. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986

A;Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787
*Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;926-928/Region: cell attachment (R-G-D) motif
F;171-232/Disulfide bonds: #status predicted
F;171-232/Disulfide bonds: #status predicted
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;270,274/Disulfide bonds: interchain #status predicted
F;610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;1051/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.7%; Score 55; DB 1; Length 1170;
91.7%; Pred. No. 0.021;
ive 0; Mismatches 1; Indels
number: A30140; MUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: protein
A,Residues: 987-1003 <SUNA
A,Cross-references: UNIPARC:UPI00001742C0
A,Notes Cys-992 is shown to have a free sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Note: the list of introns may be incomplete C, Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: GDB:THBS1; TSP1; TSP
A,Cross-references: GDB:120438; OMIM:188060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 91.7 ses 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 15q15-15q15
A;Introns: 23/1
                                                                                                                             A; Molecule type: mRNA
                                                           A; Accession: A30140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A42927
```

poter

ö

Query Match

Best Loca Matches

RESULT 3

```
65.0%;
milarity 70.0%;
Conservative 3
                                         68.3%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: AGR_L_3540
A;Map position: linear chromosome
   Query Match
Best Local Similarity 66.7-
8; Conservative
                                                                                                                                                                                                                                | |:|||| ||
202 FRGLLQNVHLVF 213
                                                                                                                                                                                       1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AGILESVRFV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 AGILESVRFV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
ses 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-747 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-783 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: AE2929
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: AE2929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: Atu3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: participates in cell migration and adhesion, and in platelet aggregation c; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc c; Superfamily: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer c; 1-18/Domain: signal sequence #status predicted <EGC <MAT>
F;1-18/Domain: von Willebrand factor type C repeat homology <WWC>
F;319-317/Domain: von Willebrand factor type C repeat homology <FHRI>F;319-317/Domain: thrombospondin type 1 repeat homology <FHRI>F;32-598/Domain: thrombospondin type 1 repeat homology <FHRI>F;53-598/Domain: thrombospondin type 1 repeat homology <FHRI>F;52-591/Domain: EGF homology <EGFP>
F;52-591/Domain: EGF homology <EGFP>
F;52-691/Domain: EGF homology <EGFP>
F;52-651/Domain: EGF homology <EGFP>
F;52-65/Disulfide bonds: interchain #status predicted
F;66,270/Disulfide bonds: interchain #status predicted
F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ); Cross-references: UNIPARC:UP1000016D077; GB:M64866; NID:g201994; PIDN:AAA40432.1; PID: Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc. f.keywords calcium binding; glycoprotein
7; S19-377/Domain: von Willebrand factor type C repeat homology <VWC>
7; S19-377/Domain: thrombospondin type 1 repeat homology <THR1>
7; S19-377/Domain: thrombospondin type 1 repeat homology <THR2>
7; S53-588/Domain: thrombospondin type 1 repeat homology <THR3>
7; S53-588/Domain: EGF homology <EGF>
7; S53-691/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A42587; A39851
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3381, 1992
J. Biol. Chem. 267, 3274-3381, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell A;Reference number: A42587; MUID:92147683; PMID:1371115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Rostaluse: 1-1172 cLAH>
A;Cross-references: UNIPROT;Q03350; UNIPARC:UP10000029847; GB:L07803; GB:M87275; NID:G34
A;Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression A;Reference number: A42173; MUID:92217961; PMID:1559694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: sequence extracted from NCBI backbone (NCBIP:81502)
(Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
Biol. Chem. 266, 12821-12824, 1991
(Filte: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
(Reference number: A39851; MUID:91302287; PMID:1712771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lirombospondin 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                               A;Cross-references: UNIPARC:UP100001742C1; GB:M81339
A;Experimental source: fibroblast
A;Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.3%; Score 41; DB 1; Length 1172;
66.7%; Pred. No. 12;
iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                  A/Gene: GDB:THBS2; TSP2
A/Cross-references: GDB:128789; OMIM:188061
A/Map position: 6427-6427
C/Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66...
Best Local 8. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 FRGLLONVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FAGVLQNVRFVF 12
                                                                                                                Molecule type: mRNA
Residues: 560-1172 <LA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-873 < BOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: A39851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
probable transcription regulator PA1760 [imported] - Agrobacterium tumefaciens (strain Cf c) Species: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens (spacession: Agriculation Agricu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2223, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       two component response regulator Atu3035 [imported] - Agrobacterium tumefaciens (strain (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:QBUBI1; UNIPARC:UPI0000164787; GB:AE008689; PIDN:AAL43851.1; A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q8UBI1; UNIPARC:UPI00000D2059; GB:AE007870; PIDN:AAK90347.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; WUID:21608550; PMID:11743193
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Agrobacterium tumefaciens
C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Score 41; DB 2; Length 1172;
pred. No. 12;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.0%; Score 39; DB 2; Length 783; Best Local Similarity 70.0%; Pred. No. 19; Matches 7; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 2;
Pred. No. 18;
3; Mismatches (
```

```
61.7%;
50.0%;
                                                                                                                                                                                                                                                                                                          | | | | :|::|
90 FMGVAQGLRYIF 101
                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                             1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 63.6 toes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 AGILONVYFKY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||| ||::|
29 GVLQKVRWLF 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GVLQNVRFVF 12
                                                                                                                                                                                                   Best Local Similarity
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: C57253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 38/2
                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein F15D4.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B88349
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleA;Note: published errata appeared in Science 283, 15, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPROT:P35440; UNIPARC:UP1000013776D; GB:M60853; NID:g212763; PIDN: C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology vor F;386-437/Domain: von Willebrand factor type C repeat homology <VWC> F;386-437/Domain: thrombospondin type 1 repeat homology <THRI> F;440-498/Domain: thrombospondin type 1 repeat homology <THRI> F;499-555/Domain: thrombospondin type 1 repeat homology <THR2> F;658-697/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q93511; UNIPARC:UPI000007BE33; EMBL:Z80344; PIDN:CAB02486.2;
A;Experimental source: clone F15D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                     C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.0%; Score 39; DB 1; Length 1178;
50.0%; Pred. No. 30;
tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                      R;Lawler, J.; Duquette, M.; Ferro, P.
J. Biol. Chem. 266, 8039-8043, 1991
A;Title: Cloning and sequencing of chicken thrombospondin.
A;Reference number: A39804; MUID:91217026; PMID:2022631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F15D4.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-145 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, September 1996
A;Reference number: Z19354
A;Accession: T20985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.7%; Score 37;
50.0%; Pred. No. 7
                          thrombospondin precursor - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRGLLONIHLIF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | || || || || || FMGVAQGLRYIF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1178 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: published err.
A;Accession: B88349
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 2
A; Introns: 21/3; 82/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Gene: CESP:F15D4.3
                                                                                               Accession: A39804
                                                                                                                                                                                                                           A; Accession: A39804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
```

```
TENA-Dseudouridine synthase (EC 5.4.99.-) - Acinetobacter calcoaceticus (fragment)
NyAlternate names: hypothetical protein lipB 5'-region
C;Species: Acinetobacter calcoaceticus
C;Species: Acinetobacter calcoaceticus
C;Date: 19-Jan.1996 #sequence_revision 19-Jan.1996 #text_change 05-Oct-2004
C;Accession: C57253
R;KoK, R.G.; van Thor, J.J.; Nugteren-Roodzant, I.M.; Vosman, B.; Hellingwerf, K.J.
A;Title: Characterization of lipase-deficient mutants of Acinetobacter calcoaceticus BD41
A;Reference number: A57253; MUID:95286514; PMID:7768830
A,Residues: 1-162 <STO>
A,Residues: 1-162 <STO>
A,Cross-references: UNIPROT:Q93511; UNIPARC:UPI0000179EEB; GB:chr_II; PIDN:CAB02486.1; PI C,Genetics:
C,Genetics:
A,Gene: F15D4.3
A,Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9P7W8; UNIPARC:UPI000006A13D; EMBL:AL136536; PIDN:CAB66446.1
A;Experimental source: strain 972h(-); cosmid c1703
C;Genetics:
A;Gene: SPDB:SPBC1703.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C'Species: Schizosaccharomyces pombe
C'Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50315
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert, F. submitted to the EMBL Data Library, January 2000
A;Reference number: Z25061
A;Accession: T50315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SPBC1703.02 with ARID DNA-binding domain [imported] - fission yeast
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Residues: 1-151 <KOK>
A,COSS-references: UNIPARC:UP1000017879A; GB:X80800
A,COSS-references: UNIPARC:UP1000017879A; GB:X80800
C,Superfamily: tRNA pseudouridine synthase B
C,Superfamily: tRNA pseudouridine synthase B
C,Keywords: intramolecular transferase; isomerase; tRNA modification
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 60.0%; Score 36; DB 2; Length 151; Local Similarity 70.0%; Pred. No. 13; hes 7; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 780;
                                                                                                                                                                                                             Length 162;
                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-780 <MCD>
                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                             Score 37; DB :
Pred. No. 8.8;
                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 47;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.7%; Score 37;
63.6%; Pred. No.
```

us-10-030-735-26.rpr

```
Search completed: June
Job time: 13.9655 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                         C;Accession: D81399
F;Parkhilli, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: D81399
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reaidues: 1-300 <PAR>
A;Cross-references: UNIPROT:Q9PHY2; UNIPARC:UPI00000C216B; GB:AL139075; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q05424; UNIPARC:UP1000000D1BE; EMBL:L11452; NID:g168813; PIC
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; P-loop; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAB-Ja hydrolase (IAR3) [imported] - Arabidopsis thaliana C;5pecies: Arabidopsis thaliana (mouse-ear cress)
C;5pecies: Arabidopsis thaliana (mouse-ear cress)
C;5pecies: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C;5Accession: F96556
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hungles, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
malate dehydrogenase (EC 1.1.1.37) Cj0532 [imported] - Campylobacter jejuni (strain NCTC
C,Species: Campylobacter jejuni
C,Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Turner, G.E.; Borkovich, K.A.
J. Biol. Chem. 268, 14805-14811, 1993
A;Title: Identification of a G protein alpha subunit from Neurospora crassa that is a
A;Reference number: Z25084; MUID:93315452; PMID:8325859
A;Accession: T50479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Neurospora crassa
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 2; Length 300; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.0%; Score 36; DB 2; Length 355; llarity 50.0%; Pred. No. 32; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein alpha chain (imported) - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: L-lactate dehydrogenase C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || :||: | :|
75 FANILQSFRLIF 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 AGVLDNARFKY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-355 < BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: mdh; Cj0532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.Reference number: A86141; MUID:21016719; PMID:11130712

A.Accession: F96556
A.Status: preliminary
A.Molecule type: DNA
A.Residus: 1.440 <STO>
A.Gross-references: UNIPROT:081642; UNIPARC:UPI000004837A; GB:AE005173; NID:gl1094766; PJ
A.Genetics: F19624 4
A.Gene: T19624 4
A.Map position: 1
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                     2; Length 440,
                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                   Score 36; DB 2
Pred. No. 40;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        5, 2006, 22:45:04
                                                                                                                                                                                                                                                     60.0%;
63.6%;
                                                                                                                                                                                                                                                     Query Match 60.0
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                            181 AGVLENVSAIF 191
                                                                                                                                                                                                                                                                                                                                      2 AGVLQNVRFVF 12
```

THIS PAGE BLANK (USPT	0)	
		,

```
666.77
666.77
666.77
666.77
666.77
666.77
666.77
                                                                                                                                                                                                                                                    Q4RLR5 TETNG
Q4RLR5;
Q4RLR5
                                                                                                                                                                                                                                                      tetraodon n
ustilago ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xenopus lae
brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rattus norv
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ciona intes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bos taurus
                                                                               5, 2006, 22:09:41; Search time 108.931 Seconds
(without alignments)
101.901 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xenopus s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xenobns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xendous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xenobns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xenobns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0411r5
028134
058134
058178
028178
028178
097396
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
087318
           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  2849598 segs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSP1 XENLA
Q4S758 TRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q4RLR5_TETNG
Q28194_BOVIN
Q7SY84_XENLA
Q5SPGS_BRARE
TSP1_BOVIN
TSP1_HUMAN
TSP1_MOUSE
Q3TR40_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q4RQ74_TETNG
Q4P665_USTWA
QSVH52_CIOIN
TSP2_HUMAN
TSP2_MOUSE
QSRI52_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TETING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q563T0_9PIPI
Q563T1_9PIPI
Q563T2_9PIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7TMT3 MOUSE
Q8CG21 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q80YQ1 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8CG21_MOUSE
Q563V1_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q563S8_9PIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPIP1
                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         protein search, using sw model
                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q59E99
Q5U903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             071SA3
                                                                                                                                                                                                                                                                                                                                                  UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                                                       1 FAGVLQNVRFVF 12
                                                                                                                                US-10-030-735-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1173
1193
1225
249
1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
9911.7
99
                                                                                                                                                                                                                                                               Minimum DB seq
Maximum DB seq
                                                                                                                                             Perfect score:
                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein -
                                                                                                                                                        Sequence:
                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
```

```
PubMed=15496914; DOI=10.1038/nature03025;

PubMed=15496914; DOI=10.1038/nature03025;

PubMed=15496914; DOI=10.1038/nature03025;

Nature Jaillon O. Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,

Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Riemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Goury J.,

Relis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Wincker P., Lander E. S., Weisenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"The early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    xenopus wit
xenopus wit
xenopus gil
                                                                                                                                                                                                                                                                         fra
fra
bou
                                                                                                                                                                                                                                                                                                                                                                                                                   ves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vibrio para
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
xenopus
                                                                                                                                                                                                                          xenopus
                                                                                                                                                                                                                                                                                                                                                                   xenopus
                                                                                                                                    xenopna
                                                                                                                                                                                                                                                                                                                         xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                   xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xendous
                                                                                              xenopus
                                                                                                                                                                                        xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
19-JUL-2006, entry version 8.
Cl-FBB-2006, entry version 8.
CREMAGE-GSTENG00032314001;
Tetradon nigroviridis (Green puffer).
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei; Actinopterygii, Neopterygii; Percomorpha; Tetradoncidea; Tetradontidae; Tetradoncidea; Tetrado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

Genoscope; Whitehead Institute Centre for Genome Research;

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                Q563t6
Q563t6
Q563u0
Q563u1
Q563u1
Q563u4
Q563u5
Q563u5
Q563u9
Q563u9
Q563u9
Q563u9
Q563u9
Q563u9
Q563u9
Q563u9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; CAAE01015019; CAG10667.1; -; Genomic_DNA.
SMR; QARLR5; 834-887, 837-1171.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005501; F:equatium ion binding; IEA.
GO; GO:000511; F:heparin binding; IEA.
GO; GO:000515; F:protein binding; IEA.
GO; GO:000515; F:structural molecule activity; IEA.
GO; GO:000715; P:etal adhesion; IEA.
InterPro; IPR006210; EGF.
InterPro; IPR00742; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1171 AA
                                          056374 9PIPI
056375 9PIPI
056310 XENCL
056310 YENPI
056310 9PIPI
056314 9PIPI
056314 9PIPI
056319 9PIPI
056319 9PIPI
056319 9PIPI
056310 9PIPI
056310 9PIPI
056310 9PIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.
```

2

ö

Gaps

.. 0

DAR XAM DAR A DO BRAN A DO

```
KENDERMILE 22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Seberg B., Wagner L., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., Rahe S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bonask S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones E.D., Dickson M.C., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones E.D., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones E.D., Marra M.A., Schein J.E., Jones E.D., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones J. M. Marra M.A., Schein J.E., Jones E.D., Marra M.A., Schein J.E., Jon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Aenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC054970; AAH54970.1; -; mRNA.

GO; GO:0005194; F:structural molecule activity; IEA.

GO; GO:0007155; P:sell adhesion; IEA.

InterPro; IPR003129; Laminin_G_TSP_N.

InterPro; IPR003109; Laminin_G_TSP_N.

InterPro; IPR008084; TSP_1.

InterPro; IPR008085; TSP_1.

InterPro; IPR0090095; TSP_1.

Pfam; PF00090; TSP_1; 2.

Pfam; PF00090; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003, integrated into UniProtKB/TrEMBL.
   Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                              496 AA.
                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003, sequence version 1. 07-FEB-2006, entry version 12. MGC64438 protein.
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                    Q7SY84_XENLA PRELIMINARY;
Q7SY84;
                                                                                                                                                                          190 FOGVLONVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
                                      11; Conservative
                                                                                                     1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Whole;
Klein S., Stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    initiative."
                                                                                                                                                                                                                                                                                                               27SY84 XENLA
                                         Matches
                                                                                                                                                                                                                                                                        RESULT 3
                                                                                                            ઠ
                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Opposite regulation of thrombospondin-1 and corticotropin-induced secreted protein/thrombospondin-2 expression by adrenocorticotropic hormone in adrenocortical cells.", 0. Cell. Physiol. 167:164-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96331130; PubMed=8698834;
DOI=10.1002/(SICI)1097-4652(199604)167:1<164::AID-JCP19>3.3.CO;2-0;
Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chambaz E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.7%; Score 55; DB 2; Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1171 AA; 129304 MW; 865F3749693F7FCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25015 MW; 90D9EBCE4E6B669C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, S57957, S57957, PIRNA.

PIR, S57957, S79957, S799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 2;
Pred. No. 0.083;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996, integrated into UniProtKB/TrEMBL.
01-NOV-1996, sequence version 1.
07-FEB-2006, entry version 24.
Thrombospondin-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 AA.
                                                                                                                                                                                                                           Pfam; PF00009; TSP 1; 3.
Pfam; PF02412; TSP 1; 3.
Pfam; PF02412; TSP 3; 12.
Pfam; PF05712; TSP 2; 12.
Pfam; PF05703; VWC; 1.
PRINTS; PR01705; TSP1REPEAT.
SWART; SM00210; TSP1; 3.
SWART; SM00210; TSP1; 3.
SWART; SM00210; TSP1; 3.
SWART; SM00210; TSP1; 3.
SWART; SM00214; VWC; 1.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS01208; VWFC 2; 1.
Cell adheaton.
NON TER
                               EGF_like reg.
Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X89511; CAA61682.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.3%;
                                                                                                                                InterPro; IPR008085; TSP 1.
InterPro; IPR001007; VWF C.
Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 FTGVLONVRFVF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FAGVLQNVRFVF 12
                                                                         IPR003129;
IPR000884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q28194_BOVIN
Q28194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige J.J.;
                                                                                                        interPro;
                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
```

RESULT 2

g

DER PER PROPERTY OF THE PROPER

```
Query Match
                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
    SO F W B DR R B B F F S
                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barker D.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collagen (By similarity).
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-2004, integrated into UniProtKB/TrEMBL.
21-DEC-2004, sequence version 1.
21-FEB-2006, entry version 12.
Novel protein similar to vertebrate thrombospondin 1.\n\ (Fragment) Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                             Length 496;
                                                                                                                                                                                                                                      1; Indels
                                                                                PROSITE; PS50092; TSP1; 2.
PROSITE; PS501208; WWFC 1; UNKNOWN 1.
PROSITE; PS50184; WWFC 2; UNKNOWN 2.
SEQUENCE 496 AA; 54843 MW; E4FDZF07CB7EFS1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AL928866; CAI20599.1; -; Genomic_DNA.
SWR; QSSPG5; 751-804, 754-1089.
ENSEMBL: ENSDARG0000010705; Danio rerio.
GO; GO: 0005576; C:extracellular region; IEA.
GO; GO: 0005576; F:calcium ion binding; IEA.
GO; GO: 0005515; F:calcium ion binding; IEA.
GO; GO: 00051515; F:protein binding; IEA.
GO; GO: 0005199; F:structural molecule activity; IEA.
GO; GO: 0007155; P:cell adhesion; IEA.
                                                                                                                                                                                         91.7%; Score 55; DB 2;
91.7%; Pred. No. 0.052;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             OSSPGS_BRARE PRELIMINARY; PRT; 1090 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IRR013320; ConA_like_subgrp.
InterPro; IPR002048; EF hand_Ca_bd.
InterPro; IPR006210; EGF.
InterPro; IPR000142; EGF.
InterPro; IPR000619; EGF.Ca_bd.
InterPro; IPR0006209; EGF.Like_reg.
InterPro; IPR013032; EGF_like_reg.
InterPro; IPR013032; EGF_like_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR003367; tsp_3:
Interpro; IPR008859; TSP_C.
Interpro; IPR001007; VWF_C.
Pfam; PP00008; BGP; 1.
Pfam; PP00412; TSP_1; 2.
Pfam; PP02412; TSP_3; 12.
Pfam; PP05735; TSP_C; 1.
PRINTO: NOTO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1705; TSP1REPEAT.
SMART; SM00181; EGF; 2.
SMART; SM00209; TSP1; 2.
PRINTS; PR01705; TSPIREPEAT.
SMART; SM00210; TSP1; 2.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSP_1.
                                                                                                                                                                                                                                                                                                                          214 FOGVLÓNVRFVF 225
                                                                                                                                                                                                               Local Similarity 91.7
nes 11; Conservative
                                                                                                                                                                                                                                                                                1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003129;
InterPro; IPR000884;
InterPro; IPR008085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               OSSPG5 BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          05SPG5;
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
    8888888888
                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                      11D
DD41D
DD51D
D51D
D
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGF-beta.";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type V collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-IIb/beta-3. May play a role in dentinogenesis and/or maintenance of dentin and dental pulp.

-!- SUBUNIT: Homotrimer; disulfide-linked.

-!- SIMILARITY: Contains 3 BGF-like domains.

-!- SIMILARITY: Contains 1 TSP N-terminal (TSPC) domain.

-!- SIMILARITY: Contains 3 TSP type-1 domains.

-!- SIMILARITY: Contains 7 TSP type-3 domains.

-!- SIMILARITY: Contains 1 TSP V-terminal (TSPN) domain.

-!- SIMILARITY: Contains 1 TSP V-terminal (TSPN) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE (MRNA) OF 1-18 AND 710-1170.
TISSUE=Aortic endothelium;
Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin stimulatory effect of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA].
STRAIN-BADJENEL, TSSUE-TOOCH;
MEDLINE-98173773; PubMed-5507054; DOI=10.1016/S0167-4838(97)00188-X;
Weno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inoue H.; "cDNA cloning of bovine thrombospondin 1 and its expression in adontoblasts and predentin."; Biochim. Biochim. Biochim. Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 91.7%; Score 55; DB 2; Length 1090; Local Similarity 91.7%; Pred. No. 0.12; nes 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                     1090 AA; 120978 MW; 5A9320504A22D836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSP1 BOVIN

ID TSP1 BOVIN

AC 028179; 028179; 11.09 AA.

DT 01.NOV-1997, integrated into UniProtKB/Swiss-Prot.

DT 01-DEC-2000, sequence version 2.

DT 07-MAR-2006, entry version 56.
SWART; SM00210; TSPN; 1.

SWART; SM00214; VWC; 1.

PROSITE; PS00018; EF 2; 1.

PROSITE; PS01166; EGF 2; 1.

PROSITE; PS50026; EGF 2; 2.

PROSITE; PS50027; TSP1; 2.

PROSITE; PS50029; TSP1; 2.

PROSITE; PS50184; VWFC 1; 1.

PROSITE; PS50184; VWFC 2; 1.

CG11 adhesion; EGF-1ike domain.

NON TER

SEQÜENCE 1090 AA; 120978 MW; 5A9320504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB005287; BAA21115.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X87618; CAA60950.1; -; mRNA.
EMBL; X87619; CAA60951.1; -; mRNA.
PIR; S55501; S55501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombospondin-1 precursor.
Name=THBS1; Synonyms=TSP-1, TSP1;
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||||||||||
185 FMGVLQNVRFVF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
```

ö

Gaps

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Endothelial cell;
MEDLINE=R0567617; PubMed=2430973; DOI=10.1083/jcb.103.5.1635;
Lawler J., Hynes R.O.;
"The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different proteins.";
Proteins.";
Cell Biol. 103:1635-1648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 1-397.
MEDLINE=8715/592; PubMed=303036;
Kobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.;
"Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLECTIDE SEQUENCE OF 1-374.
MEDLINE=86287276; PubMed=3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
"Characterization of a cDNA enrocding the heparin and collagen binding domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
MEDIATINE=89139590; PubMed=2918029; DOI=10.1083/jcb.108.2.729;
MEDIATINE=89139590; Prazier B.A., Kim D.D., Deckwerth T.L.,
Baumgartel D.M., Rotwein P., Frazier W.A.;
"Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region.";
J. Cell Biol. 108:729-736(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                      91.7%; Score 55; DB 1; Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                        ODD6ADF3E5FA031A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
TSP1 HUMAN
TSP1 HUMAN
TSP1 HUMAN
AC P07996; Q15667;
DT 01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1988, sequence version 1.
DT 07-MAR-2006, entry version 78.
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.13;
0; Mismatches
                    similarity
                                                                                                                                                                                                                                                                                                                                       ٨
                                                                                                                                                                                                                                                                                                                                     )5 S -:
129534 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3iochemistry 25:8418-8425(1986).
      Name=THBŠ1; Synonyms=TSP, TSP1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombospondin-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FAGVLONVREVE 12
                                                                                                                                                                                                                                                                                                                                                          1170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
    592
6599
650
650
650
705
705
705
813
813
813
814
810
910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins.'
                       DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
DISULFID
    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYP type-1 1.
TYP type-1 2.
TYP type-1 2.
TYP type-1 3.
EGF-like 1.
EGF-like 2.
EGF-like 3.
TYP type-3 1.
TYP type-3 2.
TYP type-3 4.
TYP type-3 4.
TYP type-3 5.
TYP type-3 5.
TYP type-3 5.
TYP type-3 6.
TYP type-3 6.
TYP type-3 6.
TYP type-3 6.
TYP type-3 7.
TYP type-3 6.
TYP type-3 7.
TYP type-3 6.
TYP type-3 7.
TYP type-3 6.
TYP type-3 7.
TYP type-3 6.
TYP type-3 7.
TYP type-3 7.
TYP type-3 6.
TYP type-3 7.
TYP type-3 6.
TYP type
                                                                                                     INTERPRO) IFROUGALD GET 3.

INTERPRO; IPROUGALD GET 3.

INTERPRO; IPROUGALD GET 3.

INTERPRO; IPROUGALD GET 3.

INTERPRO; IPROUGALD GET 11 ke.

INTERPRO; IPROUGALD GET 11 ke.

INTERPRO; IPROUGALD GET 11 ke.

INTERPRO; IPROUGALD TERP 1.

INTERPRO; IPROUGALD TERP 3.

INTERPRO; IPROUGALD TERP 3.

INTERPRO; IPROUGALD TERP 1.

INTERPRO; IPRO; INTERPRO; INTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombospondin-1.
/FTId=PRO_0000035841.
TSP N-terminal.
708
1067
1085
270
274
423
423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
708
1067
1085
270
274
391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGION
MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
```

S

```
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
       CARBOHYDRATE-LINKAGE SITES ASN-248 AND ASN-1067.

PubMed=16335952; DOI=10.1021/pr0502065;
Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
Moore R.J., Smith R.D.; Grotreeme analysis by immunoaffinity subtraction,
T. Muman plasma N-glycoproteome analysis by immunoaffinity subtraction,
T. Protecome Res. 412070-2080(2005).
J. Protecome Res. 412070-2080(2005).
J. Protecome Res. 412070-2080(2005).
J. FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
Cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
T. FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
Cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
Taminin, type v collagen and integrins alpha-V/beta-1, alpha-
V/beta-3 and alpha-III/beta-3.
Cell-to-matrix: Contains 1 TSP C-terminal (TSPC) domain.
Cell-to-matrix: Contains 1 TSP type-1 domains.
Cell-to-matrix: Contains 7 TSP type-3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
[5]
MUCLEOTIDE SEQUENCE OF 1-166.
MEDLINE-89291870; PubMed=2544587;
Laherty C.D., Gierman T.M., Dixit V.M.;
"Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.";
J. Biol. Chem. 264:11222-11227(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22338361; PubMed=12450399; DOI=10.1021/bi026463u;
Huwiler K.G., Vestling M.M., Annis D.S., Mosher D.F.;
"Biophysical characterization, including disulfide bond assignments,
of the anti-angiogenic type 1 domains of human thrombospondin-1.";
Biochemistry 41:14329-14339(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                          NUCLECTIDE SEQUENCE OF 1028-1170.

La Fleur M., Jobin C., Gauthier J., Kreis C.G.;

Expression of thrombospondin in chronic inflammation: neutrophils
from synovial fluids synthesize a novel 3.9 kb TSP mRNA.";

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                    CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441; TISSUB-Platelet; TISSUB-Platelet; TISSUB-Platelet; TISSUB-Platelet; MEDINE-21125860; PubMed=11067851; DOI=10.1074/jbc.Mo08073200; Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J., Mosher D.F., Peter-Katalinic J.; "C.mannosylation and O-fucosylation of the thrombospondin type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M25631; AAA36741.1; -; mRNA.
EMBL; X14787; CAA28370.1; -; mRNA.
EMBL; X14787; CAA28370.1; -; mRNA.
EMBL; M14326; AAA61237.1; ALT SEQ; mRNA.
EMBL; J04835; AAA61237.1; ALT SEQ; mRNA.
EMBL; M99425; AAB59366.1; -; mRNA.
PDB; 1LSL; X-RAY; A=434-546.
PDB; 1LSL; X-RAY; A=434-1170.
PDB; 1Z78; X-RAY; A=19-233.
PDB; 1ZA4; X-RAY; A=19-237.
PDB; 2ERF; X-RAY; A=19-237.
PDB; 2ERF; X-RAY; A=19-257.
PDB; 2ERF; X-RAY; A=19-257.
PDB; 2ERF; X-RAY; A=19-257.
PDB; 2ERF; X-RAY; A=19-257.
                                                                                                                                                                                                                                                                                                                                                                                                                                  THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSG0000137801; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 276:6485-6498(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC; HGNC:11785; THBS1.
MIM; 188060; gene.
Reactome; P07996; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlycoSuiteDB; P07996;
OGP; P07996; -.
                                                                                                                                                                                                                                                                                                                                                                                module.";
```

```
TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
TSP type-1 3.
TSP type-1 3.
TSP type-3 1.
TSP type-3 1.
TSP type-3 4.
TSP type-3 4.
TSP type-3 4.
TSP type-3 7.
TSP type-3 6.
TSP type-3 7.
TSP type-3 6.
TSP type-3 6.
TSP type-3 7.
TSP C-terminal.
TSP C-terminal.
TSP C-terminal.
TSP C-terminal.
TSP C-terminal.
TSP C-terminal.
                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00214; VWC; 1.
PROSITE; PS000224; VWC; 1.
PROSITE; PS00186; EGF_2; 1.
PROSITE; PS00205; EGF_3; 2.
PROSITE; PS002092; TSP1; 3.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_1; 1.
3D-structure; Calcium; Cell adhesion; EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=CAR 000210.
O-linked [Puc. . .).
/FIId=CAR 000211.
N-linked [GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-linked (GlcNAc. ..).
N-linked (GlcNAc. ..) (Potential).
C-linked (Man).
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0004866; F:endopptidase inhibitor activity; TAS.
GO; GO:000471; F:signal transducer activity; TAS.
GO; GO:0007275; P:development; TAS.
InterPro; IPRO13320; CoA_like_subgrp.
InterPro; IPRO6210; EGF_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Frid=cAR 000208.
O-linked (Fuc. ).
/Frid=cAR 000209.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombospondin-1.
/FIId=PRO_0000035842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=CAR 000205.
Olinked (Fuc. ).
/FTId=CAR 000206.
C-linked (Man).
/FTId=CAR 000207.
C-linked (Man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSP N-terminal.
                                                                             InterPro; IPR00142; EGF 3.

InterPro; IPR001881; EGF Ca bd.

InterPro; IPR00209; EGF like.

InterPro; IPR0313032; EGF like reg.

InterPro; IPR00184; Islain_G_TSP_N.

InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heparin-binding; Repeat; Signal.
                                                                                                                                                           InterPro; IRR000884; TSP1.
InterPro; IRR000884; TSP1.
InterPro; IRR000865; TSP 1.
InterPro; IRR001365; TSP 2.
InterPro; IRR001007; VWF C.
Pfam; PF00009; EGF; 2.
Pfam; PF02412; TSP 3; 12.
Pfam; PF02412; TSP 3; 12.
Pfam; PF02412; TSP 3; 12.
Pfam; PF02735; TSP C; 1.
Pfam; PF00033; VWC; 1.
PRINTS; PR01705; TSP185.
SWART; SW00191; EGF; 3.
SWART; SW00101; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 708
1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   429
429
584
587
690
758
781
817
840
840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOTIF
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
```

φ

```
REMEL; M62469; AAA50611.1; JOINED; Genomic_DNA.

REMEL; M62469; AAA50611.1; JOINED; Genomic_DNA.

REMEL; J05660; AAA44431.1; -; Genomic_DNA.

REMEL; REMORGA10; Cond_like_subgrp.

REMEL; REMORGA10; Cond_like_subgrp.

REFERCY; REMORGA10; Cond_like_subgrp.

REFERCY; REMORGA10; REG_like

REFERCY; REMORGA20; EGF_like

REMEL; REPOLOTION; WF_C.

REMEL; REMORGA20; REPLEFERT.

REMORT; SMOOLOT; TSPP.1; TSPP.2;

REMORT; SMOOLOT; TSPP.1; TALEFERT.

REMORT; REMORT; REMORT; REMC_1; TSPP.2;

REMORT; REMORT; REMORT; REMC_2;

REMC_2; REMC_2;

REMC_2; REMC_2;

REMC_2; REMC_2;

REMC_2; REMC_2;

REMC_2; REMC_2;

REMC_2
                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombospondin-1.
/FTId=PRO_0000035843.
TSP N-terminal.
                                                                                                                                        EMBL, M62470; AAA50611.1; -; Genomic_DNA.

EMBL, M65451; AAA50611.1; JOINED; Genomic_DNA.

EMBL, M62451; AAA50611.1; JOINED; Genomic_DNA.

EMBL, M62452; AAA50611.1; JOINED; Genomic_DNA.

EMBL, M62453; AAA50611.1; JOINED; Genomic_DNA.

EMBL, M62454; AAA50611.1; JOINED; Genomic_DNA.

EMBL, M62455; AAA50611.1; JOINED; Genomic_DNA.

EMBL, M62456; AAA50611.1; JOINED; Genomic_DNA.

EMBL, M62459; AAA50611.1; JOINED; Genomic_DNA.

EMBL, M62459; AAA50611.1; JOINED; Genomic_DNA.

EMBL, M62460; AAA50611.1; JOINED; Genomic_DNA.

EMBL, M62461; JAA50611.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic_DNA.
Genomic_DNA.
Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic_DNA.
Genomic_DNA.
Genomic_DNA.
Genomic_DNA.
-!- SIMILARITY: Contains 7 TSP type-3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rsP type-1 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA50611.1; JOINED; C
AAA50611.1; JOINED; C
AAA50611.1; JOINED; C
AAA50611.1; JOINED; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VWFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA50611.1; JOINED;
AAA50611.1; JOINED;
AAA50611.1; JOINED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221
373
429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
316
379
                                                                                                                                                                                           EMBL, M62451, P
EMBL, M62452, P
EMBL, M62454, P
EMBL, M62454, P
EMBL, M62456, P
EMBL, M62456, P
EMBL, M62456, P
EMBL, M62456, P
EMBL, M62461, P
EMBL, M62463, P
EMBL, M62464, P
EMBL, M62466, P
EMBL, M62466, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAIN
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN SEQUENCE OF 19-37.

X PubMed=8654563; DOI=10.1016/0014-5793(96)00460-7;

PubMed=8654563; DOI=10.1016/0014-5793(96)00460-7;

A Chen H., Aschlimann D., Nowlen J., Mosher D.F.;

"Expression and initial characterization of recombinant mouse thrombospondin 1 and thrombospondin 3.";

L FEBS Lett. 387:36-41(1996).

- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type V collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-IIb/beta-3.

- SUBUNIT: Homotrimer; disulfide-linked.

- SIMILARITY: Belongs to the thrombospondin family.

- SIMILARITY: Contains 3 EGF-like domains.

- SIMILARITY: Contains 1 TSP C-terminal (TSPC) domain.

- SIMILARITY: Contains 1 TSP V-terminal (TSPN) domain.

- SIMILARITY: Contains 3 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE OF 1-490.
MEDIJNE=90375546; PubMed=2398070;
Bornstein P., Alfi D., Devarayalu S., Framson P., Li P.;
"Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";
J. Biol. Chem. 265:16691-16698(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development.", J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=92128941; PubMed=1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
Jenkins N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
MEDLINE-22147683; PubMed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
Dixtt V.M.;
                                                                                                                                                                                                                                                                   Score 55; DB 1; Length 1170;
Pred. No. 0.13;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of the murine thrombospondin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994, integrated into UniProtKB/Swiss-Prot. 01-JUN-1994, sequence version 1. 01-JUN-1996, entry version 57. Thrombospondin-1 precursor. Name=Thb81; Synonyms=T8p1;
  Interchain (Probable)
                       Interchain (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1170 AA.
                                                                                                                                                                                                                                                                      91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                 208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 11:587-600(1991)
                                                                                                                                                                                                                                                                                             Local Similarity 91.7
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                       1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
270
274
3391
3391
447
447
504
504
508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSP1 MOUSE
P35441;
                       DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                 DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rspl_mouse
                                                                                                                                                                                                                                                                                                                         Matches
HID DET THE PRINT THE PRIN
                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Graninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Graninci P., Kasukawa T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic W.B., Brenner S.E., Batalov S., Forrest A.R., Sahimokawa K., Bajic W.B., Brenner S.E., Batalov S., Forrest A.R., Bailey T.L., Andesi-Impionbato A., Apweiler R., Aturaliya R.M., Banter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., RA Grow M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Crow M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., At lerrardo D., Down T., Engetrom P., Fagiolini M., Faulkner G., RA Fletcher C.F., Fukushima T., Furuno M., Fucaki S., Gariboldi M., Georgii-Hemming P., Gingers T.R., Colobori T., Green R.E., Georgii-Hemming P., Gingers T.R., Hensch T.K., Hirokawa N., RA Hill D., Huminidecki L., Iacono M., Ikeo G., Kitamura H., Jak M., Karapin A., Katoh M., Kawawa Y., Kelso J., Kitamura H., Jak M., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuawa S., Miki H., Mignone F., Miyake S., Morris K., Matsuda H., Matsuzawa S., Miki H., Mignone R., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Rotte B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Seriguchi K., Sample I.R., Sandelin A., Schneider C., Schonbach C., Setiguchi K., Sample I.R., Sandelin A., Schneider C., Mattick J., Tang S., Taylor M.S., Tegner J., Takakawa T., Tammoda K., Tan S.L., Tang S., Taylor M.S., Tegner J., Takakawa T., Tammoda K., Tan S., L., Yang K., Sandelin A., Schneider C., Mattick J., Mannola M., Suzuki M., Machano H., Nakano K., Ninomish N., Mashio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki J., Havashizaki Y., Itoh M., Kato T., Kawajashiza H., Kawashima T., Suzuki M., Nakani M., Nakani M., Nakani M., Nakani M., Nakani M., Nakashi M.,
                                                               NUCLECTIDE SEQUENCE.
STRAIN-C57BL/6J; TISSUE-Aorta and vein;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
Carninci P., Hayashizaki Y.;
MHigh-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAIN=CSTBL/6J; TISSUE=Aorta and vein;
MEDLINE=22354689; PubMed=1246681; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S
Dalla E., Dragami T.A., Fletcher C.F., Fortreet A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godaik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=16141073; DOI=10.1126/science.1112009;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The transcriptional landscape of the mammalian genome.";
Science 309:1559-1563(2005).
                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Aorta and vein;
PubMed=16141072; DOI=10.1126/science.1112014;
  Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki
        ö
TSP type-1 2.

TSP type-1 3.

EGF-like 2; calcium-binding (Potential).

TSP type-3 1.

TSP type-3 2.

TSP type-3 4.

TSP type-3 5.

TSP type-3 5.

TSP type-3 5.

TSP type-3 6.

TSP type-3 6.

TSP type-3 6.

TSP type-1 6.

TSP type-1 6.

TSP type-1 7.

TSP type-3 6.

TSP type-1 7.

Type-1 1.

TSP type-1 7.

Type-1 1.

TSP type-1 1.

TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mus musculus , mouse).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adult male aorta and vein CDNA, RIXEN full-length enriched library, clone:A530055N06 product:thrombospondin 1, full insert sequence. Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1025 1025 F -> L (1n Ref. 2).
1170 AA; 129647 MW; 0443E493615E7F06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-0CT-2005, integrated into UniProtKB/TrEMBL.
11-0CT-2005, sequence version 1.
07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 1;
Pred. No. 0.13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q3TR40_MOUSE PRELIMINARY; PRT; 1170 AA.
Q3TR40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           930
1167
1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                      DOMAIN
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                          REGION
                                                   DOMAIN
                                                                    DOMAIN
                                                                                         DOMAIN
                                                                                                            DOMAIN
                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q3TR40
ID Q3
ID Q3
AC Q3
DT 11
DT 11
DT 07
DE AG
GN Na
CGN MA
```

σ

```
Q71SA3
           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSTRAIN-C57BL/64; TISSUB-Aorta and vein;
MEDLINE-21085660; PubMed-11217851; DOI=10.1038/3505500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gjobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Brownstein M.J., Bult C., Fletcher C., Fullita M., Wagner L., Washio T.,
Brownstein M.J., Bult C., Fletcher C., Fullita M., Cariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamico N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
A Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Tesadale R.D., Tomita M.,
Nerardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
Wilming L.G., Wynshawa Boris A., Yanagiswa M., Yang I., Yang L.,
Yuan Z., Zavolan M., Zimmer A., Carnicci P., Hayatsu N.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
A Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                      Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare fiull-length cDNA libaries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20530913; PubMed=11076861; DoI=10.1101/gr.152600; Shibbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii K., Katsunai T., Tashiro H., Itoh M., Yamamoto R., Mataminoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Yamamoto R., Mataminoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuniki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuniki M., Rikiki integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Aorta and vein;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Arakawa T. Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
```

```
ö
                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley;
Iwabu A., Hirohata S., Kusachi S., Nakamura K., Murakami T.,
Ninomiya Y., Tsuji T.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55; DB 2; Length 1170;
Pred. No. 0.13;
0; Mismatches 1; Indels
                                                                                                                                                                                                                        EMBL; AK163092; BAE37190.1; -; mRNA.
MG1; MG1:98737; Thbs1.
G0; G0:0005615; C:extracellular space; IDA.
G0; 00:0005615; C:extracellular space; RCA.
G0; G0:0005615; P:negative regulation of angiogenesis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1170 AA; 129619 MW; 55BF04A20D91B194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006210; EGF.
InterPro; IPR006210; EGF.
InterPro; IPR00142; EGF.3.
InterPro; IPR00142; EGF.3.
InterPro; IPR001302; EGF.1ike.
InterPro; IPR001302; EGF.1ike.
InterPro; IPR0013129; Laminin.G.TSP.N.
InterPro; IPR0013129; Laminin.G.TSP.N.
InterPro; IPR001367; tSp.3.
InterPro; IPR001367; tSp.3.
InterPro; IPR0018059; TSP.C.
InterPro; IPR0018059; TSP.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01705; TSPIREPEAT.
SNART; SM00181; EGF; 3.
SNART; SM00209; TSP1, 3.
SNART; SM00210; TSPN; 1.
SNART; SM00214; VWC; 1.
PROSITE; PS01186; EGF 2; UNKNOWN_1.
PROSITE; PS00026; EGF 3; 2.
PROSITE; PS00022; PSP1; 3.
PROSITE; PS001208; VWFC_1; 1.
PROSITE; PS50024; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; 1.
TSP1REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00008; EGF; 2. Pfam; PF00009; TSP 1; 3. Pfam; PF02412; TSP 2; 12. Pfam; PF05735; TSP C; 1. Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FOGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q71SA3_RAT
Q71SA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
```

```
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08CGB2
1D 08
AC 08
DT 01
DT 01
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina R.F., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1170 AA; 129671 MW; 6F38D3DCE733060F CRC64;
                                            GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005199; F:structural molecule activity; IEA.
GO; GO:007155; P:call adhesion; IEA.
InterPro; IPR013320; ConA_like_subgrp.
InterPro; IPR006210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBOYOL MOUSE

1D 000YOL MOUSE

AC 080YOL MOUSE

DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 17.
DT 07-FEB-2006, entry version 17.
DE Thrombospondin 1.
DE Thrombospondin 1.
DE Mame=Thb81;
OC Muse musculus (Mouse).
OC Muroidea; Muriae; Buarchontoglires; Glires; R OC Muroidea; Muriae; Muriae; Mus.
OC Muroidea; Muriae; Muriae; Mus.
OC Muroidea; Muriae; Muriae; Mus.
OC NCBI_TaxID=10090;
RN (1)
RN NUCLECTIDE SEQUENCE.
RX NEDLINE=22388257; PubMed=12477932; DOI=10.1073/
RA Strausberg R.L., Feingold E.A., Grouse L.H., Schemer R. Strausberg R.L., Feingold E.A., Grouse L.H., Schemer R. Altechul S.F., Zeeberg B., Buetow K.H., Schaefe RA Hopkins R.F., Zordan H., Moore T., Max S.I., Wa Hopkins R.F., Jordan H. Moore T., Max S.I., Wa Brownstein M.J., Usdin T.B., Toshiyuki S., Carr R. Raha S.S., Loquellano N.A., Peters G.J., Abrams R. Bosak S.A., McEwan P.J., McKernan K.J., Malek i. R. Richards S., Worley K.C., Hale S., Garcia A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 2;
Pred. No. 0.13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003, integrated into UniProtKB/TrEMBL. 01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                     SWART; SM00181; EGF; 3.
SWART; SM00209; TSP1; 3.
SWART; SM00210; TSP1; 1.
SWART; SM00214; VWC; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS00206; EGF 3; 2.
PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS01208; VWFC 1; UNKNOWN 1.
SEQUENCE 1170 AA; 129671 MW; 6F38D3
                                                                                                                                           InterPro; IPR000742; EGF 3.
InterPro; IPR001881; EGF Ca bd.
InterPro; IPR06209; EGF like.
InterPro; IPR013032; EGF like reg.
InterPro; IPR013129; Laminin G ISP N.
               EMBL; AF309630; AAQ14549.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                      InterPro; IPR003367; tsp_3.
InterPro; IPR008859; TSP_C.
InterPro; IPR001007; VWF_C.
Pfam; PP000009; EGF; 2.
Pfam; PP00090; TSP_1; 3.
Pfam; PP05735; TSP_2; 12.
Pfam; PP05735; TSP_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                          PR01705; TSP1REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.78;
                                                                                                                                                                                            InterPro, IPR013032, EGF_11)
InterPro, IPR003129, Laminio
InterPro, IPR000884, TSP1.
InterPro, IPR008085, TSP_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
È
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.7%; Score 55; DB 2; Length 1171; 91.7%; Pred. No. 0.13; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50092; TSPI, 3.
PROSITE; PS12108; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
SEQUENCE 1171 AA; 129690 WW; 12E077B50C64E2D3 CRC64;
                                                                                                                                                                                                                           Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                         EMBL; BC050917; AAH50917.1; -; mRNA
```

ö

```
MEDLINE=22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;
R. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toobhlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwam P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcha A.M., Gay L.J., Hulyk S.W.,
A Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Salska U., Smailus D.E.,
B. Mennerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Mammary gland;

TISSUE-Mammary gland;

TISSUE-Mammary gland;

TISSUE-Mammary gland;

TISSUE-Mammary gland;

TO TISSUE-Mammary gland;

TO Open R., Ravasi T., Eachard B., Wells C., Kodzius R., Shimokawa K., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Rayama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Rayama R., Ravasi T., Aldinis V., Allen J.E., Dallay Baris M., Wilming L.G., Aldinis V., Allen J.E.,

Davis M.J., Wilming L.G., Aldinis V., Allen J.E.,

A mhoesi-Impiomabto A., Apweiler R., Aturaliya R.N., Banley T.L.,

A mhoesi-Impiomabto A., Apweiler R., Aturaliya R.N., Banley T.L.,

A crowe M.L., Dallas E., Dalrymple B.P., Fagiolini M., Paulkner G.,

A Growe M.L., Dallas E., Dalrymple B.P., Fagiolini M., Paulkner G.,

A illecther C.F., Fukushima T., Furuno M., Futakis, Gariboldi M.,

R Fletcher C.F., Fukushima T., Furuno M., Futakis, Gariboldi M.,

A Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

A Jake M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

R Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,

A Lillson R., Makilam S., Madan Babu M., Madera M., Marchiam I.,

Matsuda H., Matsuawa S., Miki H., Mignone F., Miyake S., Morris K.,

Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,

Nishighon R., Nishighawa S., Nishikawa S., Nori F., Ohara O.,

RA Roat B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euzechontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
enriched library, clone: G930018021 product: thrombospondin 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor
                                                                                                                                                                                                                                             STRAIN-CZECH II; TISSUE-Mammary tumor metastatized to lung. Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
length enriched librar
full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CZECH II; TISS arose spontaneously;
                                                                                                                                                                                                                                                                       arose spontaneously;
                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
```

RC TISSUE-Mammary gland;

RX MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okzazki Y. Furuno M., Kaibukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Madareli R., Hill D.P., Bult C., Hume D.A., Queckenbush J.,

RA Badareli R., Hill D.P., Bult C., Hume D.A., Queckenbush J.,

RA Balka J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R., Lyons P.A.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R., Lyons P.A.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R., Lyons P.A.,

RA Kanai A., Kawaji I., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Sandeu N.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Sandeu N.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Yarani C., Yarani C., Watzun C., Wang Y., Watzune N., Sakai K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Shinagawa T., Rogers J.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Ra Shiraki T., Waki Waterston R., Lander E.S., Rogers J.,

Ra Hara A., Havanhizaki V., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Takenda Y., Sperling S., Stupka E., Sugiura K., Itakenda R., Takenda Y., Takenda Y., Takenda K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Veda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Bult C., Yamanishi H., Zabarovsky E., Zhu S., Zimen A., Hide W., Bult C., A Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., A Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., A lida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., A Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Birney E., Hayashizaki Y., $^{\prime}$ "Analysis of the mouse transcriptome based on functional annotation of Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., TISSUE=Mammary gland;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005). "The transcriptional landscape of the mammalian genome."; TISSUE=Mammary gland; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; Science 309:1559-1563(2005). 60,770 full-length cDNAs."; Nature 420:563-573(2002). NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE

```
NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAIN
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                   TISSUE-Mammary gland;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninol P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matuminoto H., Sakaguchi S., Inegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishika I., Matamatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rishika I., Matsu Saguencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.

TISSUB=Mammary gland;
Arakwa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994, sequence version 1.
07-MAR-2006, entry version 54.
Thrombospondin-1 precursor.
Name=thbs1; Synonyms=tsp1;
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Maphibia; Batraofia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 91.7%; Score 55; DB 2; Length 1171; Local Similarity 91.7%; Pred. No. 0.13; hes 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muramatsu M., Hayashizaki Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994, integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC042422; AAH42422.1; -; mRNA.
EMBL; AK145202; BAE26293.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                   Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P07996; 1LSL.
                                                                                                                     Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSP1 XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P3544B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSP1_XELA

1D TSP1_XE

DT 01-JUN

DT 01-JUN

DT 01-JUN

DT 07-MAR

DE Thromb

GN Xenop

OC Sukar)

OC Amphil

OC Amphil

OX NOBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
    RAPARA RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            용
```

```
R. T. CLOLIALS CONCRIGATION OF THE STATE OF
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                       Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1193 AA; 133256 MW; 6E8781648FCEC7F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R GO; GO:005575; C:extracellular region; IEA.
GO; GO:0005575; C:extracellular region; IEA.
GO; GO:0005575; C:extracellular region; IEA.
GO; GO:000510; F:calcium ion binding; IEA.
GO; GO:000510; F:protein binding; IEA.
GO; GO:0005115; F:protein binding; IEA.
GO; GO:0005125; F:protein binding; IEA.
GO; GO:0005125; F:protein binding; IEA.
R InterPro; IPR001881; EGF_3.
R InterPro; IPR001881; EGF_1A.
R InterPro; IPR001881; EGF_1A.
R InterPro; IPR001881; TSP 1.
R InterPro; IPR001885; TSP 1.
R Ffam; PP000107; WFC.
R Ffam; PP000107; WFC.
R Ffam; PP00103; EGF 12.
R 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; CAAE01014723; CAG03524.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 2;
Pred. No. 0.13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00214; VWC; 1.
PROSITE; PS01186; EGF 2; UNKNOWN_1.
PROSITE; PS50026; EGF=3; 2.
PROSITE; PS50092; TSP1, 3.
PROSITE; PS50184; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-2005, sequence version 1.
21-FBB-2006, entry version 10.
Thrombospondin 1 variant (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q59E99 HUMAN PRELIMINARY;
Q59E99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSPIREPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS, PR01705, TSPIREPEA
SWART; SW00181, EGF; 2.
SWART; SW00210; TSP1, 3.
SWART; SW00210; TSP1, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 FMGVLQNVRFVF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                  preliminary data.
                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
059899 HUM
1D 05989
AC 05989
DT 26-AP
DT 21-FB
DE Throm
OS HOMO
OC Mamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15496914; DOI=10.1038/nature03025;
Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Eruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
19-JUL-2006, entry version 8.
Chromosome 14 SCAF14123, whole genome shotgun sequence. (Fragment)
ORFNames=GSTENGO0022976001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Eukaryota, Meoperygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                        (Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                    (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                 attachment site (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW; A9F036D6516C0F24 CRC64;
     Heparin-binding (Potential)
                                                 (GlCNAC. . . )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 1
Pred. No. 0.13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1193 AA.
                                                                                                                                                                                                                                            similarity.
                                                                                                                                                                                                                                                                        similarity.
similarity.
                                                                                                                                                                                                                                                                                                                            similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                 similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity
similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity
                              Cell attac
N-linked
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 TETNG
Q4S758 TETNG PRELIMINARY;
Q4S758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1173 AA; 130020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 FQGVLQNVRFVF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FAGVLQNVRFVF 12
  235
931
155
158
250
250
363
705
711
711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                       CARBOHYD
                                                                                  CARBOHYD
                                                                                                              CARBOHYD
                                                                                                                                                               CARBOHYD
                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
```

Query

셤

ö

Gaps

ö

```
Search completed: June 5, 2006, 22:42:46 Job time : 109.931 secs
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                       TISSUB=Aorta endothelial cell;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%; Score 55; DB 2; Length 1225; 91.7%; Pred. No. 0.14; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01026; EGF_3; 2.
PROSITE; PS010208; VWFC_1; 1.
PROSITE; PS01084; VWFC_2; 1.
PROSITE; PS0184; VWFC_2; 1.
Cell adhesion; EGF_1ike domain.
NON_TER
SEQUENCE 1225 AA; 134849 MW; 988B16E57157B12 CRC64;
                                                                                                Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                            EMBL; AB209912; BAD93149.1; -; mRNA.
SMR; Q59E99; 886-939, 889-1225.
ENSGONO00137801; Homo sapiens.
GO; GO: 0005576; C:extracellular region; IEA.
GO; GO: 0005509; F:calcium ion binding; IEA.
GO; GO: 0005510; F:heparin binding; IEA.
GO; GO: 0005198; F:structural molecule activity; IEA.
GO; GO: 0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-2004, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 1. 07-FEB-2006, entry version 7. Thrombospondin 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 AA.
                                                                                                                                                                                                                                                                                  InterPro; IPR013320; ConA_like_subgrp.
InterPro; IPR006210; EGF.
                                                                                                                                                                                                                                                                                                         InterPro; IPR000742; EGF 3.
InterPro; IPR01881; EGF Ca bd.
InterPro; IPR06209; EGF like reg.
InterPro; IPR013032; EGF like reg.
InterPro; IPR013129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000884; TSP1.
InterPro; IPR001865; TSP 1.
InterPro; IPR001865; TSP 1.
InterPro; IPR001865; TSP 2.
InterPro; IPR001865; WF C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1705; TSPIREPEAT.
SMART; SM00181; BGF; 3.
SMART; SM00209; TSP1; 3.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PÉan, PP00008, EGF, 2.
PÉan, PF00090, TSP 1; 3.
PÉan, PF02412, TSP 2; 12.
PÉan, PF05735, TSP C; 1.
PÉan, PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.77
These 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 FQGVLQNVRFVF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FAGVLONVRFVF 12
                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSU903_PIG
QSU903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
Q5U903 P1G
AC Q5U903.
DT 07-DEC.
DT 07-PEBC.
DT 07-FEBC.
DT Thrombx
GN Name=TI
GS Sus Sus
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
ö
                                                                                                                                                                                             Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.3%; Score 50; DB 2; Length 249; 100.0%; Pred. No. 0.25; Live 0; Mismatches 0; Indels
                                                                                                                       Zhang K., Mauco G., Hauet T.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AA; 27560 MW; 465D664BE0329C32 CRC64;
                                                                                                                                                                                                                                                                         EMBL; AY773342; AAV38110.1; -; mRNA
                                                                                                                                                                                                                                                                                   EMBL) A1/3212 A27.21.

INTERPTO; IRRO00884; TSP1.

INTERPTO; IRRO01007; VWF_C.

PEam; PF00099; TSP 1; 2.

PEAM; PF00099; YWC; 1.

PRINTS; PR01705; TSPIREPEAT.

SWART; SW00214; VWC; 1.

PROSITE; PS50092; TSP1; 1.

PROSITE; PS50092; TSP1; 1.

PROSITE; PS50092; TSP1; 1.

PROSITE; PS50092; TSP1; 1.

NON TER 1 1.

NON TER 249 A4; 27560 MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVLQNVRFVF 11
                                                                                                NUCLEOTIDE SEQUENCE.
                                            NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
```

THIS PAGE BLANK (USPTO)

```
91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 FOGVLONVRFVF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 482, App
Sequence 97, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 11112, Ap
Sequence 11112, Ap
Sequence 6441, Appl
Sequence 6441, Appl
Sequence 64641, Appl
Sequence 4641, Appl
Sequence 1111, Appl
Sequence 1111, Appl
Sequence 1111, Appl
Sequence 1111, Appl
Sequence 28350, Appl
Sequence 16431, Appl
Sequence 16431, Appl
Sequence 28350, Appl
Sequence 28888, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8164, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                     5, 2006, 22:43:07; Search time 23.8966 Seconds (without alignments) 43.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2
Sequence 4
Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-002-482

US-09-939-853A-97

US-09-939-853A-97

US-09-939-853A-98

US-08-949-012-11112

US-09-949-016-11112

US-09-949-016-11112

US-09-949-016-11112

US-09-949-016-11112

US-09-949-016-11112

US-09-949-016-11112

US-09-949-016-11396

US-09-134-000C-6441

US-09-134-00C-6441

US-09-270-767-46451

US-09-270-767-46451

US-09-270-767-4641

US-09-252-991A-28888

US-09-252-991A-28888

US-09-012-652-4

US-08-0902-655A-4

US-08-0116-622-4

US-09-116-622-4

US-09-116-622-4

US-09-116-622-4

US-09-116-622-4

US-09-116-622-4

US-09-119-621-4

US-09-119-621-4

US-09-119-621-4
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      650591 seqs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                               1 FAGVLQNVRFVF 12
                                                                                                                                                                                                      US-10-030-735-26
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 831
1170
11170
11170
11045
11172
11172
740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9911.7
9911.7
9911.7
9911.7
9911.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
991.7
9
                                                                                                                            June
                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                            ..
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                          Run
```

```
Sequence 482, Application US/09949002
Sequence 482, Application US/09949002
Batent No. 690016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CL000790
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEC ID NOS: 10823
SOFTWARE: FRAESEC for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 97, Application US/09939853A

Sequence 97, Application US/09939853A

Patent No. 6989232

GENERAL INFORMATION:

APPLICANT: Burgess et al.

TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-099

CURRENT APPLICATION NUMBER: 05/29/939,853A

CURRENT FILING DATE: 2001-08-27

PRIOR FILING DATE: 2000-08-25

PRIOR PLICATION NUMBER: 60/267,300

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR PLICATION NUMBER: 60/269,961

PRIOR PLICATION NUMBER: 60/277,337

PRIOR PLILING DATE: 2001-03-20

PRIOR PLILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                        28, Appl
25, Appl
10, Appl
10, Appl
10, Appl
10, Appl
10, Appl
10, Appl
10608, Appl
3, Appl
4, Appl
4, Appl
4, Appl
4, Appl
5, Appl
6, Appl
6, Appl
7, Appl
8, Appl
8,
                                                                                                                                                                                                                                                                                                                                                                                                                                              84, Appl
3732, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                   42044,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
                                                   Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                               Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
     Sequence
Sequence
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 2; Length 825;
Pred. No. 0.023;
0; Mismatches 1; Indels
US-09-328-352-4361
US-08-687-590-28
US-08-484-9938-10
US-08-484-9938-10
US-08-484-1588-10
US-08-484-1588-10
US-08-480-150A-10
US-08-480-150A-10
US-09-270-767-42057
US-09-270-767-42057
US-09-270-767-3
US-09-270-767-43187
US-09-270-767-43187
US-09-270-767-44184
US-09-270-767-44144
US-09-270-767-44144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-134-001C-3732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
  444444444444444A
```

ò

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Lander, Eric S.
APPLICANT: Leader, James S.
APPLICANT: Ireland, James S.
APPLICANT: Ireland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, Stacey
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
FURRENT FILING DATE: 1090-07-07
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR SPLING DATE: 2000-07-26
PRIOR SPLING DATE: 2000-07-26
SPRIOR FILING DATE: 2000-07-26
SEQ ID NOS: 2551
SOCITUM NO 2
SESCIID NO 2
SESCIID NO 2
SESCIID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 2; Length 1170;
Pred. No. 0.034;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%; Score 55; DB 1; Length 1170; 91.7%; Pred. No. 0.034; tive 0; Mismatches 1; Indels
                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. 9.678
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELEPHONE: (212) 278-0400
TELEPAK: (212) 391-0526
TELEX:
                                 US/08/313,288B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-002-350
; Sequence 350, Application US/09949002
; Patent No. 6900016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-657-472-2
; Sequence 2, Application US/09657472
; Patent No. 6727063
                                                               January 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                           20:
                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FQGVLQNVRFVF 219
   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gequence 98, Application US/09939853A

patent No. 6989222

GENERAL INFORMATION:

APPLICATIVE:

TITLE OF INVENTION: No. 6989232e1 Proteins and Mucleic Acids Encoding Same
FILE REFERENCE: 21402-099

CURRENT PILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR APPLICATION NUMBER: 60/226,300

PRIOR FILING DATE: 2001-02-08

PRIOR PILING DATE: 2001-02-08

PRIOR PILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOFTWARE: Patentin Ver. 2.1

FENCENT: 60/3
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Sequence 2.0, Application US/08313288B |
| Sequence 2.0, Application US/08313288B |
| Patent No. 5756502 |
| GENERAL INFORMATION: |
| APPLICANTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN NUMBER OF SEQUENCES: 20 |
| NUMBER OF SEQUENCES: 20 |
| NUMBER OF SEQUENCES: 20 |
| STREET: 1185 Avenue of the Americas |
| STREET: 1185 Avenue of the Americas |
| STREET: 1185 Avenue of the Americas |
| STREET: 10036 |
| COUNTY: New York |
| COUNTY: New York |
| COUNTY: READABLE FORM: |
| MEDIUM TYPE: Floppy disk |
| COMPUTER: Floppy disk |
| COMPUTER: PREADABLE FORM: |
| SOFTWARE: Patentin Release #1.0, Version #1.30 |
| SOFTWARE: Patentin Release #1.0, Version #1.30 |
| Paten
                                                                                                                                                                                                                                                           91.7%; Score 55; DB 2; Length 831; 91.7%; Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%; Score 55; DB 2; Length 831; 91.7%; Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                              SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 97
LENGTH: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 FOGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 91.7
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FAGVLQNVRFVF 12
NUMBER OF SEQ ID NOS: 159
                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
```

g 8

ö

ö

```
SQUENCE 6333, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| PAPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| FILE REFERENCE: CLOO1307
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR PILING DATE: 2000-10-03
| PRIOR PILING DATE: 2000-10-03
| PRIOR PILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| WINBER OF SEQ ID NOS: 2000-10-03
| SEQ ID NOS: 2000-10-04
| CREATION NUMBER: FAMING NOS: 2000-10-04
| CREATION NOMBER: FAMING NOS: 2000-10-05
| CREATION NOS: 2000-10-06
| CREATION NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 1; Length 1172;
Pred. No. 20;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.3%; Score 41; DB 2; Length 1172;
66.7%; Pred. No. 20;
ive 1; Mismatches 3; Indels
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                   CURENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEBHONE: (212) 278-0400
TELEBHONE: (212) 391-0526
TELERA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 1172 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 |:|||| ||
202 FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 8; Conserv
          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-949-016-6333
                                                                         10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-313-288B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRNERAL INFORMATION:
GRAELAL INFORMATION:
GRAELAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WINH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PAPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 11112
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT PRILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 350
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.3%; Score 41; DB 2; Length 1045; 66.7%; Pred. No. 17; 3; Indels iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55; DB 2;
Pred. No. 0.034;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11112, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7.
Seat Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 FRGLLONVHLVF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Human
US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Human
US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-313-288B-19
```

ò 셤 ö

Gaps

ö

Gaps

g

```
RESULT 13
US-09-270-767-45864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          쉽
       Sequence 6441, Application US/09134000C

Patent No. 6617156

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

SPRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 6441

LENGTH: 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Genellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Brandt, Petran
APPLICANT: Brandt, Petran
APPLICANT: Brandt, Petran
APPLICANT: Cino, Paul M
APPLICANT: Cino, Paul M
APPLICANT: Octoberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Weichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA sequences
TITLE OF INVENTION: US 99/23535
CURRENT APPLICATION NUMBER: DE 198 46 493.2
EARLIER PLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-07
MUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (11)..(11)
; OTHER INFORMATION: Amino acid 11 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-6441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.7%; Score 37; DB 2; Length 2475; 58.3%; Pred. No. 2.8e+02; ive 2; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-413-814-48
; Sequence 48, Application US/09413814
; Patent No. 6225064
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Sorangium cellulosum US-09-413-814-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.3%;
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |:| |: |::
728 FCGILGNINFIY 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||| |: |:|
123 FAGVSSNLSFLF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE
US-09-134-000C-6441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEO ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Sequence 61365, Application US/09270767

Sequence 61366, Application US/09270767

GENERAL INFORMATION:
APPLICANT: Homburgar et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SSOFTWARE: PatentIn Ver. 2.0

LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46451, Application US/09270767

Sequence 46451, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SSOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45864 Application US/09270767

Pagenence 45864 Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 45864

LENGTH: 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 304;
                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2; Length 61;
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 2;
Pred. No. 44;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-45864
                                                                                                                                                                                                                                                                                       TYPE: PRT ; ORGANISM: Drosophila melanogaster US-09-270-767-61396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                              60.0%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.3.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 FFGVVINVRLLF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ||: ||| :|
44 FFGVVTNVRLLF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
```

```
RESULT 15
US-09-489-03A-8120
Sequence 8120, Application US/09489039A
Sequence 8120, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
CURRENT PELICATION NUMBER: US 60/117,747
PRIOR FILLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8120
LENGTH: 476
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                   Query Match 60.0%; Score 36; DB 2; Length 335; Best Local Similarity 58.3%; Pred. No. 48; Matches 7; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.0%; Score 36; DB 2; Length 476; Best Local Similarity 54.5%; Pred. No. 71; Matches 6; Conservative 3; Mismatches 2; Indels
; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-46451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT;
CRGANISM: Klebsiella pneumoniae
US-09-489-039A-8120
                                                                                                                                                                                                                                | | | | | | :|
159 FPGXLQNRRLIF 170
                                                                                                                                                                                                   1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AGVLQNVRFVF 12
                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
```

Search completed: June 5, 2006, 22:48:57 Job time: 24.8966 secs

33 AGTLKNMRYAF 43

g

THIS PAGE BLANK (USPTO)

```
TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserv
              991.77
991.77
991.77
991.77
991.77
991.77
991.77
$\text{Q} \text{Q} \t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
Sequence 28, Appl
Sequence 40, Appl
Sequence 1020, Appl
Sequence 1022, Appl
Sequence 1042, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 453, Appl
Sequence 453, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 461, Appl
Sequence 11, Appl
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                              5, 2006, 23:46:43 ; Search time 78.6207 Seconds (without alignments) 70.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                  GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-741-600-1020
US-10-741-600-1022
US-10-741-600-1022
US-11-043-806-454
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-451
US-11-043-806-451
US-11-043-806-451
US-11-043-806-451
US-11-043-806-458
US-11-043-806-458
US-11-043-806-458
US-11-043-806-458
US-11-043-806-458
US-10-206-733-1
US-10-206-733-1
US-10-206-141-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-295-027-1170
US-10-211-462-38
US-10-231-956A-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-021-660-114
US-10-008-093-2
                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                             2097797 segs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                           length: 0
length: 2000000000
                                                                                                                                                                                                                                              1 FAGVLQNVRFVF 12
                                                                                                                                                                                                      US-10-030-735-26
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    831
855
11000
11100
11150
11170
11170
11170
11170
11170
                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
No.
```

```
DESCRIPTION NO. 19200-19.28

Sequence 28, Application US/10474213

Bequence 28, Application No. 1920040214248A1

GENERAL INPORMATION:

APPLICANT: Roberts, David D

APPLICANT: ROBERTS, Henry C

TITLE OF INVENTION: USE OF SEMENOGELIN IN THE DIAGNOSIS, PROGNOSIS AND TREATMENT OF TITLE OF INVENTION: UNMER: 124329

FILE REFERENCE: 224329

FULE REFERENCE: 224329

FULE REFERENCE: 2003-10-06

PRIOR FILING DATE: 2003-04-03

PRIOR PLING DATE: 2002-04-06

PRIOR PLING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.2

SEQ ID NO 28

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-419-462-40
US-10-419-462-40
Sequence 40, Application US/10419462
Publication No. US20040053392A1
GENERAL INFORMATION:
APPLICANT: Kevin J.
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
TITLE REFERENCE: W110-720005
CURRENT APPLICATION NUMBER: US/10/419,462
CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOUTWARE: Patentin version 3.2
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                   38, Appl
548, Appl
548, App
1376, Ap
2, Appl
594, App
595, App
516, Appl
516, Appl
516, Appl
517, Appl
518, Appl
518, Appl
518, Appl
                                                                                                                                                                                                                                                             6, Appli
6, Appli
                                                                                                                                                                                                                                                                           Sequence 6, Appli
Sequence 1251, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                     Sequence
Sequence
Sequence
                                     Sequence
Sequence
Sequence
                                                                                                                                                      Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                         Sequence
                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12;
US-10-419-462-38

US-10-741-600-1019

US-10-741-600-1021

US-10-782-968-38

US-10-849-989-44

US-10-831-997-2

US-10-831-997-2

US-10-995-561-594

US-10-995-561-595

US-11-037-713-51

US-11-046-644-28

US-11-046-644-28

US-11-046-646-28

US-11-046-649-6

US-11-046-649-6

US-10-997-699-6

US-10-997-699-6

US-10-997-699-6

US-10-997-699-1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 4; I
Pred. No. 0.00077;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic peptide
US-10-474-213-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FAGVLONVRFVF 12
                   11170
11170
11170
11170
11170
11170
11170
11170
11170
11170
```

N

```
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO.01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1022
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                       Gaps
                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 6; Length 459;
Pred. No. 0.045;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 432;
                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 5;
Pred. No. 0.042;
0; Mismatches
Pred. No. 0.042;
                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i LOCATION: (1)...(432)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-741-600-1022
                                                                                                                                                                                                    ; Sequence 1022, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1047, Application US/09925301; Patent No. US20020052308A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%;
91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                   208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FOGVLONVRFVF 219
Best Local Similarity 91.7
Matches 11; Conservative
                                                             1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
                                                                                                                                                                                     US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-043-806-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                               8
                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-782-968-40
| Sequence 40, Application US/10782968
| Sequence 40, Application US/10782968
| Publication No. US20050065324A1
| GENERAL INFORMATION:
| APPLICANT: Kevin J. Williams
| APPLICANT: Williams, Kevin J.
| TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
| TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
| TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
| TITLE OF INVENTION NUMBER: US/10/782,968
| CURRENT FILING DATE: 2004-02-20
| PRIOR PILING DATE: 2003-04-21
| NUMBER OF SEQ ID NOS: 53
| SOFTWARE: PatentIn version 3.2
| LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1020, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001499

FURENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997

SOUTHARE: FSELSEQ for Windows Version 4.0

LENGTH: 432
                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                ; OTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-419-462-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Thrombospondin Region plus N-terminal domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 240;
                                                                                                                                             Length 240,
                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.7%; Score 55; DB 5; Best Local Similarity 91.7%; Pred. No. 0.022; Matches 11; Conservative 0; Mismatches 1
                                                                                                                                           Score 55; DB 4;
Pred. No. 0.022;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.7%; Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)...(432)
OTHER INFORMATION: Xaa = Any Amino Acid
                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                           Query Match 91.7%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                    190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 FOGVLONVRFVF 201
                                                                                                                                                                                                                           1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-782-968-40
  LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

ò

```
Sequence 452, Application US/11043806
Fublication No. US2060051774A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOW-B Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT APPLICATION NUMBER: US/11/043,806
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-043-806-455

US-11-043-806-455

Sequence 455, Application US/11043806

Sequence 455, Application US/11043806

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CORRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 6; Length 685;
Pred. No. 0.071;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.7%; Score 55; DB 6; Length 804;
91.7%; Pred. No. 0.084;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 453, Application US/11043806; Publication No. US20060051774A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 91.7%;
il Similarity 91.7%;
11; Conservative
                                                                 208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 804
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                         RESULT 10
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                   8 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 454, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
APPLICANT: COMPUTED ILIGATION IN TITLE OF INVENTION:
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REPRENCE: 1847.1003
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
LENGTH: 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 456, Application US/11043806
Sequence 456, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
SEQ ID NO 8: 575
LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PeatentIn Ver. 2.0
SEQ ID NO 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.7%; Score 55; DB 6; Length 578; Best Local Similarity 91.7%; Pred. No. 0.058; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                       Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 6;
Pred. No. 0.056;
                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 3;
Pred. No. 0.046;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FOCVLONVREVE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 FOGVLONVRFVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Homo sapiens
US-11-043-806-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-043-806-456
                                                                                                                                                                                                                                                                            TYPE: PRT
```

셤

```
208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FOGVLONVRFVF 219
                                                                                                     Query Match 91.7
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                 1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
     US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-11-043-806-461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-043-806-461
                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 98, Application US/09939853A

publication No. US2004003163A1

publication No. US2004003163A1

publication No. US2004003163A1

publication No. US2004003163A1

APPLICANT: Burgess et al.

TITLE OF INVENTION: No. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFRENCE: 21402-099

CURRENT PILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOFTWARE: PATENT PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION. No. US20040039163Alel Proteins and Nucleic Acids Encoding Same
FITE REPRENENCE: 2.1402-099
FITE REPRENENCE: 2.1402-099
CURRENT APPLICATION NUMBER: US/09/939,853A
CURRENT RILING DATE: 2001-08-27
FRIOR APPLICATION NUMBER: 60/228,191
FRIOR APPLICATION NUMBER: 60/267,300
FRIOR FILING DATE: 2000-08-25
FRIOR APPLICATION NUMBER: 60/267,300
FRIOR FILING DATE: 2001-02-20
FRIOR FILING DATE: 2001-02-20
FRIOR FILING DATE: 2001-02-20
FRIOR FILING DATE: 2001-03-20
FRIOR FILING DATE: 2001-03-20
FRIOR FILING DATE: 2001-03-20
FRIOR FILING DATE: 2001-03-20
FRIOR FILING DATE: 2010-03-20
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö,
                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                      Score 55; DB 6; Length 828;
Pred. No. 0.087;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 3; Length 831;
Pred. No. 0.088;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 97, Application US/09939853A; Publication No. US20040039163A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.7%;
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FOGVLONVREVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FAGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FAGVLQNVRFVF 12
                                                     TYPE: PRT
GRGANISM: Homo sapiens
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-939-853A-97
LENGTH: 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

```
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer.
TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer.
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 461
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                          Gaps
                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Score 55; DB 3; Length 831;
Pred. No. 0.088;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vuery Match
91.7%; Score 55; DB 6; Length 855;
Best Local Similarity 91.7%; Pred. No. 0.09;
Matches 11; Conservative 0; Mismatches 1. Traff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June 6, 2006, 00:00:11
Job time: 78.6207 secs
                                                                                                                                                                                                                                                                                ; Sequence 461, Application US/11043806; Publication No. US20060051774A1; GENERAL INFORMATION:
```

Perfect score:

Title:

Run on:

Sequence:

Scoring table:

Searched:

Database

```
Sequence 1348, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: ERCURNCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVERTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579P9025
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN Version 3.3
SEQ ID NO 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ TRANSE: Patentin version 3.3
SEQ ID NO 15318
LENGTH: 182
12464, A
12464, A
12462, A
12462, A
16526, A
16526, A
16526, A
16526, A
16526, A
16526, A
1159, A
12003, A
12003, A
1159, A
1159, A
1159, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                      Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
US-10-953-349-12464
US-10-953-349-12463
US-10-953-349-12463
US-10-953-349-12463
US-10-953-349-16526
US-10-953-349-16526
US-10-953-349-16526
US-10-953-349-16526
US-10-953-349-16526
US-10-953-349-16526
US-10-953-349-1759
US-10-953-349-17509
US-10-953-349-12003
US-10-953-349-12003
US-10-953-349-12003
US-10-953-349-12003
US-10-953-349-12003
US-10-953-349-12003
US-10-953-349-12003
US-10-953-349-12003
US-10-953-349-12003
US-10-953-349-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 6;
Pred. No. 9.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15318, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 63.6 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||:|| :|
181 AGVLENVSAIF 191
    2 AGVLONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max
    RESULT 2
US-10-953-349-15318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-953-349-15318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-1348
    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25318, 7

5462, Ap

51318, Ap

5132, Ap

32501, Ap

32499, Ap

3996, Ap

3996, Ap

3997, Ap

39138, Ap

39138, Ap

39138, Ap

2010, Ap

2010, Ap

2010, Ap

2010, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1348, Ap
Sequence 15318, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA New:*

1. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

4. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                                                                  // Search time 3.72414 Seconds
(without alignments)
37.266 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                        GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-1348

US-10-953-349-15318

US-10-953-349-5462

US-10-953-349-5461

US-11-203-697-4132

US-11-203-697-4132

US-10-953-349-32501

US-10-953-349-32501

US-10-953-349-3995

US-10-953-349-3995

US-10-953-349-15282

US-10-953-349-15282

US-10-953-349-15282

US-10-953-349-39136

US-10-953-349-2644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                      58871 segs, 11565156 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                    6, 2006, 00:00:38
                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                              1 FAGVLQNVRFVF 12
                                                                                                                                                                                                                                                            US-10-030-735-26
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq
Maximum DB seq
```

Result No.

ઠે 셤

```
Sequence 32501, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION

APPLICANT: ALEXANDROV, Nickolai et al.

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT APPLICATION NUMBER: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE PATENTIN VEISION 3.3
                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                     Score 33; DB 7; Length 608;
Pred. No. 50;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%; Score 32; DB 7; Length 297; 70.0%; Pred. No. 36; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 53.3%; Score 32; DB 6; Length 570; Best Local Similarity 60.0%; Pred. No. 73; Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 413. Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REPERENCE: H1-A0106
CURRENT PELING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
                    CURRENT APPLICATION NUMBER: US/11/203,828
CURRENT FILING DATE: 2005-08-15
PRIOR PILING DATE: 2005-08-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 5
LENGTH: 608
                                                                                                                                                                                                                                                                                     55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                       Query Match 55.0
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 53.3
Best Local Similarity 70.0
Matches 7; Conservative
      FILE REFERENCE: MYOG:58US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 GVVFNVRVVF 243
                                                                                                                                                                                                                                                                                                                                                                                                 ::||||| :
463 IVQNVRFTY 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GVLQNVRFVF 12
                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-203-828-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4132
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             4 VLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-953-349-32501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-293-697-4132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-293-697-4132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 32501
LENGTH: 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5.15.3.4.
Sequence 5.20060107345A1
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION WUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 5461
LENGTH: 329
TYPE: PRT
                                                                                                                                                                                                                                                                                APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE REFERENCE: 2750-1579FUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 5462
LENGTH: 290
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: INHIBITION OF KU AS A TREATMENT FOR CARDIOVASCULAR IITLE OF INVENTION: DISEASES
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 6; Length 290;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.0%; Score 33; DB 6; Length 329; 63.6%; Pred. No. 26; 2; Indels tive 2; Mismatches 2; Indels
                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
  60.0%; Pred. No. 8.6;
                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                   ; Sequence 5462, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-203-828-5

Sequence 5, Application US/11203828

Publication No. US20060110390A1

GENERAL INFORMATION:
APPLICANT: LEIWAND, LESLIE

APPLICANT: SUCHAROV, CARMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Arabidopsis thaliana
US-10-953-349-5461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:|: || ||
141 AGLLEEVREVF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 AGLLEEVREVF 190
                                                                                                1:| |: |||
104 GLLMNMNFVF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AGVLONVREVE 12
                                                                   3 GVLQNVRFVF 12
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                 US-10-953-349-5462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-953-349-5461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
```

ઠે 셤 ò

g ઠે

```
Sequence 3997, Application US/10953349
Publication No. US20060107345A1
Publication No. US20060107345A1
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-10-953-349-3996
Sequence 3996, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 4025-2
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 6; Length 1234;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 6; Length 1237;
Pred. No. 2.6e+02;
                                                                                                                                                     Score 31; DB 6; Length 298;
Pred. No. 56;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                         LENGTH: 298
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3996
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9347
LENGTH: 298
                                                                                                                                                           51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.7%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.7%;
55.6%;
                                                                                                                                      Query Match
Best Local Similarity 55.67
Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.0.
Lag 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1122 ILENVRLVY 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1125 ILENVRLVY 1133
                                                                                                                                                                                                                                                               |::| |:|:
88 GIIQGVKFI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VLQNVRFVF 12
                                                                                                                                                                                                                                      3 GVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 VLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-10-953-349-3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3996
LENGTH: 1237
                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12499, Application US/10953349

Sequence 12499, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, NICKOLAI et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: UNMBER: US/10/953,349

CURRENT APPLICATION UNMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 32499

LENGTH: 581
                                                                                                                                                     Sequence 32500, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799U3.
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 32500
LENGTH: 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799USE
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 6;
Pred. No. 74;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 6;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 9347, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Triticum aestivum
US-10-953-349-32500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Triticum aestivum US-10-953-349-32499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.00
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.3
Best Local Similarity 60.0
Matches 6; Conservative
                                            1||| ||:::
414 AGVLYNVQYM 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 AGVLYNVQYM 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 AGVLYNVQYM 434
                      2 AGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGVLQNVRFV 11
                                                                                                                    RESULT 8
US-10-953-349-32500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-953-349-32499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-953-349-9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
```

ઠ 硆 .. 0

0; Gaps

Score 30; DB 6; Length 77; Pred. No. 20; 2; Mismatches 2; Indels

```
Search completed: June 6, 2006, 00:12:57
Job time : 3.82414 secs
                                                    50.0%;
                                                 Query Match 50.0
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                           ::| ||| |
24 IVQGVRFAF 32
                                                                                                                                             4 VLONVRFVF 12
    US-10-953-349-15282
                                                                                                                                                                                            셤
US-10-953-349-3995
Squence 3995, Application US/10953349
Squence 3995, Application US/10953349
Squence 3995, Application US/10953349
Squence 3995, Application US/20060107345A1
GRNERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 3995
LENGTH: 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15282, Application US/10953349

Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION WUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 15282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15283, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
THE APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE PATENTIN VERSION 3.3
SEQ ID NO 15283
LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 30; DB 6; Length 74; 55.6%; Pred. No. 19; 2; Indels tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Arabidopsis thaliana US-10-953-349-3995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|||||
1225 ILENVRLVY 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::| ||| |
21 IVQGVRFAF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-15283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-10-953-349-15283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-10-953-349-15282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

Tue

```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

- protein search, using sw model OM protein

June Run on:

5, 2006, 22:08:53 ; Search time 91.1379 Seconds (without alignments) 60.201 Million cell updates/sec

US-10-030-735-27 Title: Perfect score:

1 FOGVAQNVRFVF 12 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

2589679 segs, 457216429 residues Searched: 2589679 Total number of hits satisfying chosen parameters:

88

seq length: 0 seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

.. Database

A_Geneseq_8:* 1: geneseqp1980s:*

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:*geneseqp2003bs:*geneseqp2004s:* geneseqp2005s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:

SUMMARIES

Description	Aab35368 Alpha3bet	Aab35352 Alpha3bet	•	Abg72834 Thrombosp	Adl70641 Human thr	Adq39359 Human myo	Adq39357 Human myo	Aau02916 Angiotens	Aab43602 Human can	Aau02915 Angiotens	Adn02474 TSF polyp	Aau02914 Angiotens	Aau02913 Angiotens	Aab00042 Human thr	Aau74771 Human thr	Abb82285 Human thr	Aab74450 Human var	Aab90800 Human she	Aae25030 Human thr	Aau75315 Human thr	Abp96780 Human COP	Abu03474 Angiogene	Abg74673 Human THB
di .	AAB35368	AAB35352	AAB35378	ABG72834	ADL70641	ADQ39359	ADQ39357	AAU02916	AAB43602	AAU02915	ADN02474	AAU02914	AAU02913	AAB00042	AAU74771	ABB82285	AAB74450	AAB90800	AAE25030	AAU75315	ABP96780	ABU03474	ABG74673
% Query Match Length DB	12	12 4	12 4	12 6	240 8	432 8	432 8	459 4	466 3	546 4	548 7	555 4	731 4	1152 3	1152 5	1152 5	1170 4	1170 4	1170 5	1170 5	1170 6	1170 6	1170 6
Query Match	100.0	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8
Score	61	26		26	26	26	26	26	56	56	26	26	26	26	26	26	26	26	26	26	26	26	26
Result No.	1	~	m	4	'n	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Aae36226 Human THB Abr62059 Human thr Adn39852 Cancer/an Adj76124 Marker ge Adj75296 Marker ge Adj7639 Human thr Add26070 Thrombosp Adg26070 Thrombosp Adg39358 Human myo Adg39358 Human thr Aab37781 Human thr Aab37781 Alpha3bet Aab35374 Alpha3bet Aab35374 Alpha3bet	Aab35371 Alpha3bet Aab35376 Alpha3bet Aab35380 Alpha3bet
AAE36228 ADN39852 ADN39852 ADV76124 ADV761296 ADV36874 ADV33858 ADC33358 ADC33358 ADC33356 ADC33356 ADC33356 ADC33356 ADC33355 ADC33356 ADC33356 ADC33356 ADC33356 ADC33356 ADC33356 ADC33356 ADC333364 AAB35374 AAB35374	AAB35371 AAB35376 AAB35380
111170 111170 1170 117	
	••••
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	51 51 51
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	4 4 4 8 4 4 5

ALIGNMENTS

RESULT 1 AAB35368

AAB35368 standard; peptide; 12 AA.

AAB35368;

(first entry) 08-MAY-2001 Alpha3betal integrin binding peptide #33.

Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.

Synthetic.

WO200105812-A2.

25-JAN-2001.

12-JUL-2000; 2000WO-US018986.

99US-0144549P. 15-JUL-1999; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Krutzsch HC; Roberts DD,

WPI; 2001-182656/18.

New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and cancer

Claim 4; Page 34; 84pp; English.

The present invention provides a number of peptides which bind to alphalbetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention

Sequence 12 AA;

```
ABG72834 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001; 2001US-0281994P.
                                                                                                                                                                                                                                                                                                                                                              91.8%;
91.7%;
                                                                                                          12-JUL-2000; 2000WO-US018986
                                                                                                                             99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                        FOGVLONVRFVF 12
                                                                                                                                                                                     WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                            the invention
                                                                                                                                                                                                                                                                                                                                               Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200281630-A2
                                                                    WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-APR-2002;
                                                                                                                             15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2002.
                                                                                      25-JAN-2001
                                                                                                                                                                    Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG72834;
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                       cancer.
                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG72834
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of peptides which bind to alphalbetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoioid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention
                                                                                                                                                                                    Alphaßbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                    New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
100.0%; Score 61; DB 4; Length 12; 100.0%; Pred. No. 3.4e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 4; I
Pred. No. 0.00034;
0; Mismatches 1;
                                                                                                                                                                    Alpha3betal integrin binding peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha3betal integrin binding peptide #43.
                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                           AAB35352 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB35378 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.8%;
91.7%;
                                                                                                                                                                                                                                                                                       12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                               Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 91.
                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVAQNVRFVF 12
                                       1 FOGVAQNVRFVF 12
                                                          FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOGVLONVRFVF
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-182656/18.
Query Match
Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12 AA;
                                                                                                                                                                                                                                                WO200105812-A2.
                                                                                                                                                                                                                                                                                                          15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-2001
                                                                                                                                                08-MAY-2001
                                                                                                                                                                                                                                                                    25-JAN-2001
                                                                                                                                                                                                                              Synthetic
                                                                                                                              AAB35352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB35378;
                                                                                                                                                                                                                                                                                                                                                                                                                   cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                 AAB35352
ID AAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB35378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
```

```
Applaables al integril, anglogenesis; cell proliferation; cancer;

Mibhabheral integril, anglogenesis; cell adhesion; cell motility.

Michaelte: Cettinopathy; restenonesis; cell adhesion; cell motility.

Michaelte: Michaelte: Cettinopathy; restenonesis; cell adhesion; cell motility.

Michaelte: Michaelte: Cettinopathy: Cell adhesion; cell adhesion;
```

```
The invention relates to diagnosing cancer other than prostate cancer in a male mammal, comprising assaying a test sample for increased level of semenogelin, or cancer in a female by assaying for the presence of semenogelin. Administering a semenogelin protein or polypeptide fragment or a semenogelin-specific antibody or active fragment, or a recombinant vector expressing the protein or antibody, is useful for inducing an immune response to a cancer in a mammal, where the cancer is not prostate cancer, particularly of epithelial origin such as lung cancer, papillary renal cell carcinoma, colon cancer, especially small-cell lung cancer (SCLC), or a melanoma. The present sequence represents the amino acid
                                          A new diagnosis for cancer other than prostate cancer in a mammal useful to detect cancer including lung cancer, particularly small cell lung cancer and melanoma comprises detecting semenogelin in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma
                                                                                                                                                                                                                                                                                                       sequence of the thrombospondin-1 sequence containing synthetic peptide
which binds to alpha-3-beta-1 integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151. .164
/note= "Fibrinogen binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23. .32
/note= "Heparin binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human thrombospondin-1 N-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL70641 standard; protein; 240 AA.
                                                                                                        Example 1; Page 14; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                               91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2003; 2003WO-US026023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2002; 2002US-0405494P.
21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVAONVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FQGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WILL/) WILLIAMS K J.
              WPI; 2003-103329/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-226901/21.
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004018995-A2
                                                                                                                                                                                                                                                                                                                                                     Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL70641;
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
ò
```

the present sequence is that or the N-returnata omeaan to mutant thrombospondia. (1929) ADJ0639. The invention relates to TSP fragments (80-100, 40-55 or 20-35 kDa mol.w.) found in plasma, and their use in clinical assays for cancer and for generation of antibodies and other concernations of the plasma, and their use in clinical assays for cancer and for generation of the Fragment or Dortion involves: (1) using an epitope shared by TSP and the TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion to obtain a epitope present in TSP but not in the fragment or portion; (2) using an epitope present in TSP but not in the fragment or portion; (2) using an epitope present in TSP but not in the fragment or portion. Suitable ceptiopes are provided ADJ7063-ADJ70631 betection or quantification of the TSP fragment or portion. Suitable complication of the TSP fragment or portion. Suitable ceptiopes are provided ADJ7063-ADJ70631 betection or quantification of the TSP fragment or portion. Suitable complication and the TSP fragment or portion is performed in order to detect the presence. The TSP fragment or portion is performed in order to detect the presence. The TSP fragment or portion is performed in order to detect the presence. The TSP fragment or portion is performed in order to detect the presence. The TSP fragment or portion is performed in order to detect the presence. The TSP fragment or portion is performed in order to detect the presence. The TSP fragment or portion is performed in the TSP fragment or performed in the TSP fragment or portion associated with clotting, a condition associated with clotting a sociated with consumption of platelets, hepartam the tendence of the TSP fragment or production associated with an entire certivation, a condition associated with an entire certivation, an appartame reaction, at a programmal order to the TSP fragment order where the TSP fragment order is the TSP fragment order with vascular intervales and condition associated with a c Human myocardial infarction-associated gene derived protein, SEQ ID 1022. Gaps or leukemia or as calibrators, indicators, immunogens and analytes. .. 0 sequence is that of the N-terminal domain of human Score 56; DB 8; Length 240; Pred. No. 0.01; 1; Indels 0; Mismatches Disclosure; SEQ ID NO 40; 76pp; English ADQ39359 standard; protein; 432 AA. 91.8**%**; 91.7**%**; Query Match
Best Local Similarity >...
11; Conservative 18-NOV-2004 (first entry) 190 FOGVLONVREVE 201 1 FOGVAQNVRFVF 12 Sequence 240 AA; ADQ39359; RESULT 6 ADQ39359 ò 셤 ö

Gaps

ö

1; Indels

Score 56; DB 6; Length 12; Pred. No. 0.00034;

ö

Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.

4

```
has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleotide sequences given in the specification in the individual's nucleic acidg, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention turther comprising at least a contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino caid sequences given in the specification; an isolated polypoptide comprising an amino acid sequence given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid molecule, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypoptide; a method for identifying an agent useful in treating or preventing method in according in in a nucleic acid molecule; a method of detecting a variant activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents the protein of a human myocardial infarction-
sasociated gene containing one or more SNPs of the invention. Note: This
sequence was not shown in the specification. The sequence has come from
an electronic sequence listing downloaded from the WIPO website.
                  Human myocardial infarction-associated gene derived protein, SEQ ID 1020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for identifying an individual who
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                            Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composition for treating or preventing myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.8%; Score 56; DB 8; Length 432; 91.7%; Pred. No. 0.019; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; SEQ ID NO 1020; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iakoubova 0;
                                                                                      cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                              20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                   22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cargill M, Devlin JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                              (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2004-533949/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADQ38529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 432 AA;
                                                                                                                                                                             402004058052-A2.
                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                       15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
AAU02916
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's conclet acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises an isolated nucleic acid molecule comprising at least sontiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprishing an amino acid sequence given in the specification; an antipody fragment; an amplified polymorleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in fragment; an amplified polymorleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in polymorleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and an enthod for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acide of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction. This contains and composition for treating or preventing myocardial infarction. This invention and composition for the invention of an infarction of a human myocardial infarction. This invention and is infarction. This invention and is infarction and i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.8%; Score 56; DB 8; Length 432; 91.7%; Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; SEQ ID NO 1022; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Iakoubova O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ39357 standard; protein; 432 AA.
                                                                                                                                                                                               20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                        22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||| ||||||
208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                               Devlin JJ,
                                                                                                                                                                                                                                                                                                                  (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-533949/51
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADQ38531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 432 AA;
                                                                 WO2004058052-A2
                       Homo sapiens.
                                                                                                           15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                            Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ39357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ39357
SXXXE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

ö

Gaps

. 0

S

AAB43602 standard; protein; 466 AA.

```
granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                        Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                               Angiotensin converting enzyme (ACEV) splice variant protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Khosravi R,
AAU02916 standard; protein; 459 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 16; 519pp; English.
                                                                                                                                                                                                                                                                                                                                         17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Levine Z, David A, Azar I,
                                                                                                                                                                                                                                                                                                                                                                    99IL-00132978
99IL-00133455
                                                    12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS06016.
                                                                                                                                                                                                                                                                                     WO200136632-A2
                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1999;
                                                                                                                                                                                                                                                                                                              25-MAY-2001.
                         AAU02916;
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1c, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated mucleic candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetrophy, muscular diseases such as hypertrophy, immune disorders such as immune complex negatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer, sarcoidosis, nonarcoidotic pulmonary granulomatus diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 459 AA;
```

```
Gaps
                           ö
  Score 56; DB 4; Length 459;
Pred. No. 0.021;
0; Mismatches 1; Indels
91.8%;
                         11; Conservative
              Local Similarity
   Query Match
                           Matches
```

ö

```
1||| ||||||
208 FQGVLQNVRFVF 219
1 FQGVAQNVRFVF 12
```

RESULT 9 AAB43602

```
AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiabetheric; antichematic; antibacterial; antichritic; antichematory; antichyroid; antiallergic; antibacterial; antiviral; corruptic; antipportective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipportatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, appropriates and antagonists from the present invention may be used to treat immune disorders by activating the proliferation, differentiation or mobilisation of continuous corruption to treat disorders of haematopoicit cells, autoimmune disorders, allergic reactions, differentiation or mobilisation of cisorders, allergic reactions, graft versus host disease and organ rejection, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78477 and AAB4240 represent sequences used in the exemplification of
                                                                                                                                                                                       diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiarthritic; antiviral; antidiabetic; antiarthritic; antiviral; antidiameatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; antiangiogenic; caction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                       Human; cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.8%; Score 56; DB 3; Length 466; 91.7%; Pred. No. 0.021; ive 0; Mismatches 1; Indels
                                                                                                                          Human cancer associated protein sequence SEQ ID NO:1047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 1636-1638; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2000; 2000WO-US005882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0124270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 FOGVLONVŘEVĚ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAC77811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1999;
                                                                                  08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

φ

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interlettins, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, unscular diseases such as hypertrophy, immune disorders such as immune complex nephritis.
                                                                                                                                                             Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidoic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                           Angiotensin converting enzyme (ACEV) splice variant protein #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.8%; Score 56; DB 4; Length 546; 91.7%; Pred. No. 0.025; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abnormality such as deep vein thrombosis
AAU02915 standard; protein; 546 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 15; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                     vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Levine Z, David A, Azar I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99IL-00132978.
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS06015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200136632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                   12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001
                                        AAU02915;
```

```
The present invention relates to a novel recombinant adenovirus vector mediated anti-neoplastic composition is prepared through cloning the cDNA sequence from the human peripheral blood cell by specific primer and reverse transcription-polymerase chain reaction (RT-PCR) method for coding TSF polypeptide, construction in human embryonic kidney cell 293 by Addasy system, and packaging and expressing the recombinant adenovirus vector of TSF. It can suppress the growth and transfer of cancer. The present sequence represents the TSF polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction, coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor suppressing polypeptide TSF and gene therapy vector composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin converting enzyme (ACEV) splice variant protein #14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                    adenovirus vector; anti-neoplastic; TSF polypeptide; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56; DB 7; Length 548;
Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                             (TAID-) TAIDA LIFE SCI TECH RES CENT HEMATOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 1; 13pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02914 standard; protein; 555 AA.
                                ADN02474 standard; protein; 548 AA.
                                                                                                                                                                                                                                                                                                           21-AUG-2002; 2002CN-00129408.
                                                                                                                                                                                                                                                                                                                                           21-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-469302/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADN02475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 548 AA;
                                                                                                                                    TSF polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                               Liu P;
                                                                                                  17-JUN-2004
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2001
                                                                                                                                                                                                                                        CN1401387-A.
                                                                                                                                                                                                                                                                          12-MAR-2003
                                                                ADN02474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU02914;
                                                                                                                                                                                                                                                                                                                                                                                                               lan 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
RESULT 11
                 ADN02474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU0291
                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
```

ö

ö

Gaps

ö

208 FQGVLQNVRFVF 219

요 ò

11; Conservative 1 FQGVAQNVRFVF 12

Matches

```
vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                   (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-336004/35.
N-PSDB; AAS06013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 731 AA;
                                                                                         WO200136632-A2
                                                Homo sapiens.
                                                                                                                                                                                                                               17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                      25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                 Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB00042
  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase cinhibitor ic, cellular tumour antigen P53, and vasoactive intestinal caids are useful for identification of variant sequences and detection of cardidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as as sebestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiotensin converting enzyme (ACEV) splice variant protein #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                 Levine Z, David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 4;
Pred. No. 0.026;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU02913 standard; protein; 731 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Fig 14; 519pp; English.
vascular disorder; asbestosis
                                                                                                                                                                                    17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                             99IL-00132978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 FOGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                   (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                            2001-336004/35
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-336004/:
N-PSDB; AAS06014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 555 AA;
                                                                                      WO200136632-A2
                                                                                                                                                                                                                             17-NOV-1999;
10-DEC-1999;
                                                Homo sapiens.
                                                                                                                                      25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU02913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02913
XX AAU0
AC AAU0
XXX AAU0
XXX AAU0
XXX ANG1
XXX A
8XXGXGCCCCCCCCCXXXX4P4P4XXBXXBXXBXXBXXBXX8XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen P53, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases cuch as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection; glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 56; DB 4; Length 731; Pred. No. 0.035; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                   Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361. .416
/label= Type 1 repeat region
                                                                                                                                                                                                                                                                                                   David A, Azar I, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB00042 standard; protein; 1152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Fig 13; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human thrombospondon-1 (TSP-1).
                                                                                99IL-00132978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.8%;
91.7%;
17-NOV-2000; 2000WO-IL000766.
```

Tue Jun

```
Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer.
417. .473
/label= Type 1 repeat region
474. .530
/label= Type 1 repeat region
                                                                                                            (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                              Disclosure; Fig 1; 40pp; English
                                                                                                                                                                                                                                                                                                                                         does not induce drug resistance
                                                                          01-FEB-2000; 2000WO-US002482.
                                                                                           99US-0118053P
                                                                                                                                            WPI; 2000-514823/46.
                                          WO200044908-A2
                                                                                           01-FEB-1999;
                                                          03-AUG-2000
                                                                                                                            Lawler JW;
 Region
                  Region
```

```
New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TYP (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymeric protein) creation). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. Anti-angiogenic therspy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.8%; Score 56; DB 3; Length 1152; 91.7%; Pred. No. 0.058; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

```
190 FQGVLQNVRFVF 201
        11; Conservative
                          1 FQGVAQNVRFVF 12
Best Loca
Matches
                           ò
                                           셤
```

```
AAU74771 standard; protein; 1152 AA
                                Human thrombospondin-1 (TSP-1).
                        (first entry)
                        09-APR-2002
                AAU74771;
```

Thrombospondin-1; TSP-1; cytostatic; angiogenesis; vasotropic; vulnerary; neovascularisation; cell proliferation inhibitor; cancer; solid tumour; haemangioma; acoustic neuromas; netricibroma; trachoma; acoustic neuromas are propertic granulomas; rhemacioid arthritis; ocular angiogenic disease; retinopathy; psoriasis; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rebeosis; angiofibroma; Osler-Webber syndrome; myocardial angiogenesis; haemophiliac joints; plaque neovascularisation; telangiectasia; wound granulation; apoptosis.

Homo sapiens

```
The invention describes a composition comprising cDNA encoding fragments of human thrombospondin-1 (TSP -1), a type 1 repeat polypeptide and potent inhibitor of tumour growth and anglogenesis. The composition is useful for killing cancerous cells (preferably tumour); for reducing volume or inhibiting growth of a tumour (inhibiting neovascularisation in the tumour); for decreasing proliferation of tumour cells; in the treatment of diseases and conditions associated with anglogenic activity or misregulated growth and anglogenesis-mediated diseases such as cancer, solid tumour, tumour metaatasis, benign tumour, (e.g. haemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Type_3 repeat domain
/note= "This region contains 7 type 3 repeats, from
/note= "This region contains 7 type 3 residues 757-792,
residues 793-815, residues 816-853, residues 854-889 and
residues 890-925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition useful for treatment of cancer comprises cDNA encoding amino acids of human thrombospondin-1 or its conservative variant and a
                                                                                    361. 530
/label= Type_1_repeat_domain
/note= "This region contains 3 type 1 repeats, from
residues 361-416, residues 417-473 and residues 474-530"
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                     118. .423
/label= TGF-beta_and_fibronectin_binding_domain
/note= "Transforming growth factor"
                                                             'label= Procollagen homology_domain
'note= "Required in_inhibition of angiogenesis"
                          63. .360
label= Procollagen_homology_region
                                                                                                                                                                                                                                                                                                                                          81. .499 -
label= Anti-angiogenesis_domain
                                                                                                                                                                                                                                                             20. .426
label= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                 77. .483 __ label= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                  70. .601
| label = Calcium_binding_domain
                                                                                                                                                      label= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                    86. .491
label= Cell_binding_domain
                                                                                                                                                                                                                                                                                                   Cell_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 7; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001; 2001WO-US017250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000; 2000US-0207994P.
                                                                                                                                                                                                                                                                                  .434
/label= cr
                                               309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-106273/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200191781-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawler JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carrier.
             Key
Region
                                                    Domain
                                                                                          Domain
                                                                                                                                              Jomain
                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                       Region
```

```
rheumatoid arthritis, psoriasis, ocular angiogenic diseases (e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasias, rebeosis), Osler-Webber syndrome, mycardial angiogenesis is telangiectasia, plaque neovascularisation, haemophiliac joints, angiofibroma or wound granulation. The composition induces apoptosis and inhibits neovascularisation in the tumour cells. This amino acid sequence represents human thrombospondin-1 (TSP-1), on which the recombinant proteins of the invention are based
                                                                                                                                                                                                                                                                                                                                                                               Query Match

91.8%; Score 56; DB 5; Length 1152;
Best Local Similarity 91.7%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                      Sequence 1152 AA;
               88888888888888
```

ó;

Gaps ö

Search completed: June 5, 2006, 22:24:59 Job time: 92.1379 secs

ò g

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June Run on:

5, 2006, 22:25:22 ; Search time 13.9655 Seconds (without alignments) 82.675 Million cell updates/sec

US-10-030-735-27 61 1 FQGVAQNVRFVF 12 Perfect score:

Sequence:

, Gapext 0.5 BLOSUM62 Gapop 10.0 , Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

thrombospondin 2 p thrombospondin 2 p cytochrome P450 2B probable lippic ac carbohydrate kinas thrombospondin 1 -thrombospondin 1 p thrombospondin 1 p hypothetical proce protein F15D4.3 [i hypothetical prote hypothetical prote imidazoleglycerol-leukocidin chain l thrombospondin pre C02C2.2 protein leukocidin chain S leucocidin chain S leucocidin R S com preprotein translo probable penicilli gamma-hemolysin co probable imidazole beta-galactosidase leukocidin chain F leukotoxin LukE (i conserved hypothet hypothetical prote synergohymenotropi SUMMARIES B88349 D81929 TSHUP2 A42587 167791 E72462 C69415 JC5618 A39804 D95336 G64070 B82057 T36795 S35697 S75258 C49238 S68225 JC5468 C70013 В Query Match Length Result

leukocidin chain S	hypothetical prote	hypothetical prote	probable DNA topoi	hypothetical prote
gamma-hemolysin co	regulatory protein	probable malate de	potassium channel	hypothetical prote
hlqC-like protein	probable methylgal	probable malate qu	probable negative	hypothetical prote
JN0626	\$28706	E85860	T03504	T18808
E90043	A26499	H64990	S55349	F69955
PC4078	JC5172	C91016	T39103	S72382
0 0 0	244	0000	000	0 0 0
315	326	24 44 44 44 48 48 48 48 48 48 48 48 48 48	652	154
315	377		688	252
315	531		1142	271
55.7 55.7 55.7	55.7	55.7 55.7 7.7 7.7	55.7 55.7 55.7	54.1 54.1 54.1
0 0 0	444	u u u u	7 7 7 7	
4 4 4		4 4 4 4	7 7 7 7	
9 9 9	. W W W (4 4 4 0 1 5	4 4 4 5 4 3

ALIGNMENTS

Chrombospondin 1 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S57957
R;Lafeuillade, B.; Pellerin, S.; Keramidas, M.; Chambaz, E.M.; Feige, J.J.
R;Lafeuillade, B.; Pellerin, S.; Keramidas, M.; Chambaz, E.M.; Feige, J.J.
R;Lafeuillade, B.; Pellerin, S.; Keramidas, M.; Chambaz, E.M.; Feige, J.J.
R;Dacciption: Opposite regulation of thrombospondin-1 and CISP/thrombospondin-2 expressions S57957
A;Reference number: S57955
A;Reference number: S57955
A;Accession: S57957
A;Accession: S57957
A;Accession: L-229 cLAF>
A;Residues: 1-229 cLAF>
A;Rose-references: UNIPROT:Q28194; UNIPARC:UPI000008740A; EMBL:X89511; NID:g899228; PIDP C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor Gaps ö Score 56; DB 2; Length 229, Pred. No. 0.0013; 0; Mismatches 1; Indels ch 91.8%; .1 Similarity 91.7%; 11; Conservative (Query Match Best Local Similarity Best Loc Matches

ö

190 FOGVLONVRFVF 201 1 FOGVAONVRFVF 12 ò 셤

Cispecies: Homo sapiens (man)
Richae: 23-40g-1987 #sequence revision 03-4ug-1995 #text_change 09-Jul-2004
Cispecies: A. 103-1648, 1986
A. 103-163, 1635-1648, 1986
A. 103-163, 1635-1648, 1986
A. 103-163, 1635-1648, 103-1648, 10

A; Accession: A34274

A;Molecule type: DNA A;Residues: 1-166 <LAH> A;Cross-references: UNIPARC:UPI00001742BF; GB:J04835 R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, I A; Cell Biol. 108, 729-736, 1989 A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the

N

```
A;Title: Characterization of the murine thrombospondin gene.
A;Fitle: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUD:92128941; PMID:1774063
A;Retensin A40558
A;Retensin A40558
A;Retensin A40558
A;Residues: 1-1170 cLAM
A;Residues: 1-1170 cLAM
A;Cross-references: UNIPROT:P35441; UNIPARC:UPI0000028012; GB:M62449; GB:M62450; GB:M62465
B;Bornstein, P.; Affi, D.; Devarayalu, S.; Framson, P.; Li, P.
B;Bornstein, P.; Affi, D.; Devarayalu, S.; Framson, P.; Li, P.
A;Reference number: A37905; MUD:90375546; PMID:2398070
A;Reference number: A37905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Status: preliminary; not compared with conceptual translation
A, Status: preliminary; not compared with conceptual translation
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-1152, P'. 1154-1170 <LAH>
A, Cross-references: UNIPARC: UP10000177496; GB: M87276
A, Note: sequence extracted from NCBI backbone (NCBIP: 81501)
R; Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FRBS Lett. 387, 36-41, 1996
A, Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar
A, Reference number: S68787; MUID: 96234006; PMID: 8654563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 19-26, Xr. 28-37 < CHE>
A; Cross-references: UNIPARC: UD10000177A97
A; Cross-references: UNIPARC: UD10000177A97
C; Complex: homotrimer, disultide linked
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor C; Keywords: calcium binding; glycoprotein; homotrimer
C; Keywords: calcium binding; glycoprotein; homotrimer
F; 1-18/Domain: signal sequence #status predicted < SIGS
F; 1-18/Domain: von Willebrand factor type C repeat homology < VWC>
F; 378-429/Domain: thrombospondin type 1 repeat homology < THR1>
F; 434-490/Domain: thrombospondin type 1 repeat homology < THR2>
F; 431-547/Domain: EGF homology < EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UPI000016D076; GB:J05605; GB:J05606; NID:g201991; PIDN:AAA404 R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M. J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell characterican number: A42587; MUID:92147683; PMID:1371115
A;Reference number: A42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F15D4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20985
S;Smye, R.
S;Smye, R.
Shibmitted to the EMBL Data Library, September 1996
A;Reference number: Z19354
A;Accession: T20985
A;Accession: T20985
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Actus: preliminary;
A;Molecule type: DNA
A;Residues: 1-145 < WIL>
A;Cross-references: UNIPROT:Q93511; UNIPARC:UPI000007BE33; EMBL:Z80344; PIDN:CAB02486.2;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 56; DB 2; Length 1170;
pred. No. 0.0078;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 FQGVLQNVŘEVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVAONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-490 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T20985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A) Description: participates in cell migration and adhesion, and in platelet aggregation c) Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vG (Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer F;1-18/Domain: signal sequence #status predicted <BIG. F;19-1170/Product: thrombospondin 1 #status predicted <MAT. F;378-429/Domain: von Wilebrand factor type C repeat homology <THR1> F;378-429/Domain: thrombospondin type 1 repeat homology <THR2> F;434-490/Domain: thrombospondin type 1 repeat homology <THR2> F;551-586/Domain: EGF homology <EGF2> F;551-586/Domain: EGF homology <EGF2> F;551-586/Domain: EGF homology <EGF2> F;556-528/Region: cell attachment (R-G-D) motif
                                                                             A; Molecule type: mRNA
A; Residues: 1-83, 4, 85-522, 4, 524-1170 < HEN>
A; Cross-references: UNIPARC.UPI0000038AB1; EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
R; Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemiarty 25, 8418-8425, 1986
A; Title: Partial amino acid sequence of human thrombospondin as determined by analysis of A; Reference number: A25812; MUID:87157592; PMID:303036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Modecule type: mRNA
A, Residues: 1-83, 'A', 85-374, 'RC' <DIX>
A, Residues: 1-83, 'A', 85-374, 'RC' <DIX>
A, Cross-references: UNIPARC:UP10000168140; GB:M14326; NID:g340005; PIDN:AAA61237.1; PIDD:
A, Note: parts of this sequence, including the amino end of the mature protein, were dete
R, Sun, X.; Skorstengaard, K.; Mosher, D.F.
Cell Biol. 118, 693-701, 193-
A, Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A, Reference number: A42927; MUID:92348511; PMID:1379247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-83,'A',85-397 <KOB>
A;Cross-references: UNIPARC:UPI000016B0CA; GB:M25631; NID:9538353; PIDN:AAA36741.1; PID:
R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5455, 1986
A;Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787
(A;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;248,360,708,1067/Binding site: carbohydrate (Asn.) (covalent) #status predicted $270,274/Disulfide bonds: interchain #status predicted F;610/Modified site: erythro-beta-hydroxyasparagine (Asn.) #status predicted F;610/Modified site: carbohydrate (Asn.) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
A; Reference number: A30140; MUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 1;
Pred. No. 0.0078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 987-1003 <SUND
A;Cross-feferences: UNIPARC:UPI00001742C0
A;Note: Cys-992 is shown to have a free sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Note: the list of introns may be incomplete C, Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: GDB:THBS1; TSP1; TSP
A,Cross-references: GDB:120438; OMIM:188060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 15q15-15q15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: A42927
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A25812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 23/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
```

ö

Gaps

8

```
Rilabell, T.L.; Byers, P.H. Genomics 17, 225-229, 1993
Affile: Sequence and characterization of the complete human thrombospondin 2 cDNA: poter A; Reference number: A47379; MUID:94010892; PMID:8406456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1.1172 - LABA
A; Residues: 1.1172 - LABA
A; Cross-references: UNIPROT: P35442; UNIPARC: UPI0000046680; GB: L12350; NID: G307505; PIDN: J
A; Cross-references: UNIPROT: D.J.; Disteche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992
A; Title: Thrombospondin II: partial CDNA sequence, chromosome location, and expression of A; Reference number: A42173; MUID: 92217961; PMID: 1559694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GBB:128789; OMIM:188061
A;Cross-references: GBB:128789; OMIM:188061
A;Cross-references: GBB:128789; OMIM:188061
A;Cross-references: GBB:128789; OMIM:188061
A;Map position: 6427-6427
C;Cromplex: homotrimer, disulfide linked
C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; BGF homology; thrombospondin type I repeat homology cMAT>
F;19-1172/Pomain: signal sequence #status predicted cSIG>
F;19-1172/Pomain: thrombospondin type I repeat homology cTHR1>
F;380-431/Domain: thrombospondin type I repeat homology cTHR1>
F;530-589/Domain: thrombospondin type I repeat homology cTHR3>
F;552-591/Domain: BGF homology cBGF>
F;552-591/Domain: BGF homology cBGF>
F;552-691/Domain: BGF homology cBGF>
F;52-691/Domain: BGF homology cBGF>
F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A47379; A42173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: fibroblast
A, Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A42173
A;Nolecule rype: mRNA
A;Residues: 560-1172 < LA2>
A;Cross-references: UNIPARC:UPI00001742C1; GB:M81339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 FRGLLÓNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 58.3
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB: THBS2; TSP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A47379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cispecies: Neisseria meningitidis
Cispecies: Neisseria
Cispecies:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein F15D4.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B88349
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1958
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ and procession published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: B88349
A;Status: preliminary
A;Alecule type: DNA
A;Residues: 1.162 <5TO>
A;Cross_references: UNIPROT:Q93511; UNIPARC:UPI0000179EEB; GB:Chr_II; PIDN:CAB02486.1;
C;Genetics:
A;Gene: F1554.3
A;Map position: 2
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 2; Length 212; Pred. No. 1.3; 2; Mismatches 3; Indels
                                                                                                                                                                    Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 2; Length 162;
Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: serogroup A, strain Z2491
C, Genetics:
A, Gene: hisH; NWA0840
C, Superfamily: amidotransferase hisH; trpG homology
C, Keywords: glycosyltransferase; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                               70.5%; Score 43;
58.3%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.5%;
58.3%;
                                                                                                                                                       Query Match 70.5
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | |||| :|::|
FMGVAOGLRYIF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 FÓGIPÓDTRFYF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 70.5
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                               1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         73 FMGVAQGLRYIF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                           A;Map position: 2
A;Introns: 21/3; 82/1
A;Gene: CESP:F15D4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ઠે

```
carbohydrate kinase, FGGY family homolog - Archaeoglobus fulgidus
C;Species: Obec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69415
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.F.; Felschamann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Gloek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Accession: C69415
A;Coss-references: UMIPROT:O28945; UNIPARC:UPI0000056D86; GB:AE001012; GB:AE000782; NID: C;Superfamily: xylulokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-pulations of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.0%; Score 36; DB 2; Length 586; 54.5%; Pred. No. 41; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                Length 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 505
                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.0%; Score 36; DB 54.5%; Pred. No. 34; tive 4; Mismatches
                                                                                                                                                                                                                                                Score 36; DB Pred. No. 19; 2; Mismatches
                                                                                                                                                                                                                                                59.0%;
63.6%;
                                                                                                                                                                                                             Ouery Match
Best Local Similarity 63.0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||| |:::||
382 EGVALNIKWVF 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 FQGVEEHVRLV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVAQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVAQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 OGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
C69415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable lipoic acid synthetase APE2344 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 31-Dec-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 31-Dec-2004
C;Accession: E72462
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kaference number: A72450; MUID:99310339; PMID:10382966
A;Accession: E72462
A;Accession: E72462
A;Accession: E72462
A;Accession: E72462
A;Residues: 1-295 <KAW>
                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mSNA
A;Cross-references: UNIPARC:UPI000016D077; GB:M64866; NID:g201994; PIDN:AAA40432.1; PID:
C;Superfamily: thrombospondin 1; BGF homology; thrombospondin type I repeat homology <VWC>
F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>
F;380-431/Domain: thrombospondin type I repeat homology <THRI>
F;481-492-549/Domain: thrombospondin type I repeat homology <THR2>
F;485-495/Domain: EGF homology <EGF>
F;652-691/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT: Q64583; UNIPARC: UPI0000174D3C; GB: D17349; NID: g468484; PIDN:
           R;Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.J. Biol. Chem. 266, 12821-12824, 1991
A;Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome. A;Reference number: A39851; MUID:91302287; PMID:1712771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  With the conting and sequencing of a novel rat cytochrome P450 2B-encoding gene. A; Title: Cloning and sequencing of a novel rat cytochrome P450 2B-encoding gene. A; Reference number: I53690; MUD:94124025; PMID:8294026
A; Rocession: I67791
A; Accession: I67791
A; Molecule type: DNA
A; Residues: 1-332 <RES>
A; Residues: 1-332 <RES>
A; Residues: 1-332 <RES>
A; Crosa-references: UNIPROT:064583; UNIPARC:UPI0000174D3C; GB:D17349; NID:g468484
C; Genetics:
A; Introns: S3/3; 112/3; 160/1; 222/3; 270/1
C; Superfamily: human cytochrome P450 CyrsD6; cytochrome P450 homology
C; Superfamily: human cytochrome P450 woology cytochrome P450 homology
C; Reywords: chromoprotein; heme; iron; metalloprotein; transmembrane protein
F; 133-226/Domain: cytochrome P450 homology P45>
F; 274/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytochrome P450 2B15 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: I67791
R;Nakayama, K.; Suwa, Y.; Mizukami, Y.; Sogawa, K.; Fujii-Kuriyama, Y.
Gene 136, 333-336, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 2; Length 1172;
Pred. No. 34;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 2; Length 332;
Pred. No. 14;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 FRGLLÓNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGIAONELFIF 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                 A; Accession: A39851
```

RESULT 9

셤

277

ઠે 셤 RESULT 10

Query Match

ö

Gaps ö

Score 35; DB 2; Length 155; Pred. No. 15; 2; Mismatches 2; Indels

A; Reference number: A82950; MUID: 20437337; PMID: 10984043

67 FEGIADIVRFI 77

셤

```
A;Accession: B83124
A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-155 <STO>
A;Cross-references: UNIPROT:Q9HWJ8; UNIPARC:UPI00000C5C5C; GB:AE004834; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: June 5, 2006, 22:45:01
Job time: 14.9655 secs
                                                                                                                                                                                                                                                                  57.4%;
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 2 QGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                     | | | | | ::| | |
58 QGVAHDMRFDF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CO2C2.2 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Accession: S44740
R;Wilson, R.
submitted to the EMBL Data Library, September 1993
A;Description: Sequence of the C. elegans cosmid C02C2.
A;Reference number: S44737
A;Reference number: S44737
A;Reference type: DNA
A;Status: preliminary
A;Residues: 1-152 <WIL>
A;Coss-references: UNIPARC:UPI00001386F5; EMBL:L23649; NID:g388566; PIC
C;Genetics:
A;Introns: 33/1
C;Superfamily: Caenorhabditis elegans C02C2.2 protein
                                                                                                                                                                                                                                                                                                                                                                                                A MOLECULE TYPE: MRNA
A; Residues: 1-178 «LAW»
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology «VWC»
F; 386 «437/Domain: thrombospondin type 1 repeat homology «THR1»
F; 442-498/Domain: thrombospondin type 1 repeat homology «THR2»
F; 499-555/Domain: thrombospondin type 1 repeat homology «THR2»
F; 499-555/Domain: thrombospondin type 1 repeat homology «THR3»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein PA4183 [imported] - Peeudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Dsep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83124
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                    thrombospondin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Dete: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A33804 # Perro, P.
J. Biol. Chem. 266, 8039-8043, 1991
A;Title: Cloning and sequencing of chicken thrombospondin.
A;Reference number: A39804; MUID:91217026; PMID:2022631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.0%; Score 36; DB 1; Length 1178; 41.7%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 2; Length 152;
Pred. No. 15;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|:||:||208 FRGLLQNIHLIF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : || || |:|
92 YMGVCLNVTFIF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```



```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model Run on: June 5, 2006, 22:09:41 ; Se
--

US-10-030-735-27 61 1 FQGVAQNVRFVF 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2849598 segs, 925015592 residues Searched:

2849598 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:* Датараве :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

65.6 619 2 Q3QA31 GGAMM Q3qa31 shewanellan 65.6 621 2 Q7RGF7 PLAYO Q7rgf7 plasmodium 65.6 629 2 Q2ZSB6_SHEPU Q2zsb6 shewanella 63.9 289 2 Q48AF4_COLP3 Q48AF4_colwellia	
65.6 621 2 Q7RGF7_PLAYO Q7rgf7 plasmodium 65.6 629 2 Q2ZSB6_SHEPU Q2zsb6 shewanella 63.9 289 2 Q48AF4_COLP3 Q48af4 colwellia	2 Q3QA31
65.6 629 2 Q2ZSB6_SHEPU Q2zsb6 shewanella 63.9 289 2 Q48AF4_COLP3 Q48af4 colwellia	2 Q7RGF7
63.9 289 2 Q48AF4_COLP3 Q48af4 colwellia	2 Q2ZSB6
	9 2 048AF4
THE PLANT CHANGE OF THE COLUMN	- Transfer of

Q3xc93 methylobaci Q31fl0 methanospir Q6by75 debaryomyce Q2ltc9 syntrophus Q2ht5 ciona intes Q314%5 desulfovibr Q4xg12 plasmodium Q4iul7 azotobacter Q6d44 erwinia car Q6dy9 magnetite-C P3542 homo sapien Q5xi52 homo sapien Q5xi52 homo sapien Q7rmt3 mus musculu	·	brata; Euteleostomi; actyla; Ruminantia;	:AID-JCP19>3.3.CO;2-0; unik M., Chambaz E.M., corticotropin-induced by adrenocorticotropic	see http://www.uniprot.org/terms Attribution-NoDerivs License (ctivity; IEA.	Length 229; 1; Indels 0; Gaps 0;	
411 2 Q3XC93_METFL 500 2 Q33FL0_METHU 859 2 Q68FY5_DBBHA 1113 2 Q2LTC9_DBLT 1168 2 QYMF2_C1OIN 1720 2 Q3M4W5_DESDG 29 2 Q4XCF3_PLACH 253 2 Q41UT, AZOVI 261 2 Q6DP49_SPROT 1172 1 TSP2_HUWAN 1172 1 TSP2_HUWAN 1172 1 GSFEZ_HUWAN 1172 2 QSRISS_HUWAN 1172 2 QSRISS_HUWAN	ALIGNMENTS PRELIMINARY; PRT; 229 AA.	rated into UniProtKB/Tr nce version 1. version 24. Fragment). ; Chordata; Craniata; V. ; Laurasiatheria; Cetar.	NUCLECTIDE SEQUENCE. MEDLINE=56331130; PubMed=8698834; MEDLINE=56331130; PubMed=8698834; MEDLINE=56331130; PubMed=8698834; Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chamba: Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chamba: Retge J.J.; "Opposite regulation of thrombospondin-1 and corticotropin-: Rescreted protein/thrombospondin-2 expression by adrenocortical hormone in adrenocortical cells."; J. Cell. Physiol. 167:164-172(1996).	pyrighted by the UniProt Consortium, see http perributed under the Creative Commons Attribut. Ins. X8951; CAA61682.1; -; mRNA. RB.; SS7957; SS7957. CG0:0005198; F:structural molecule activity; CG:0007155; P:cell adhesion; IEA. CHEPPO; IPR013129; ConA like subgrp. HEFPO; IPR013129; Laminin_G_TSP_N. ART; SM00210; TSPN; 1. INTER 229 229 SQÜENCE 229 AA; 25015 MW; 90D9EBCE4E6B669C	91.8%; Score 56; DB 2; 91.7%; Pred. No. 0.011; rative 0; Mismatches VVF 12 VVF 201	PRELIMINARY; PRT; 496 AA. integrated into UniProtKB/TrEMBL. sequence version 1.
38 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1 BOVIN E8194 BOVIN	18194; -NOV-1996, in -NOV-1996, en -FEB-2006, en rrembospondin- se taurus (Bov karyota, Meta mmalia; Euthe cora; Bovidae	TUCLECTIDE SEQUENCY MEDLINE=96331330; MEDLINE=96331330; MEDLINE=96331330; MEDLINE=96331330; MEDLINE=96331330; MEDLINE=96331330; MEDLINE=96331330; MEDLINE=96331330; MEDLINE=96331330; MEDLINESSEQUENCESSEQUENCESSEQUENCESSE	Copyrighted by the Universe Consort Distributed under the Creative Commerce	Query Match Best Local Similarity 91. Matches 11; Conservative 1 FQGVAQNVRFVF 12	XENLA FSY84_XENLA FSY84; L-OCT-2003, OCT-2003,
u u u u u u u u u u u a a a a a a a a u u u u	RESULT Q28194 ID	74 F F F F F F F F F F F F F F F F F F F	RA R	;	Query Best Match Qy Db	RESULT Q7SY84 ID Q7 AC Q0 DT 01

214 FOGVLONVRFVF 225

d

MGC64438 protein.

```
RESULT 3
                                                                                                                                                                                Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Sones M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rachages A.C., Grimwood J., Schmutz J., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalsa U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                TISSUE=Whole;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, BC054970; AAH54970.1; -; mRNA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0007155; P:cell adhesion, IEA.

InterPro; IPR013320; ConA like subgrp.

InterPro; IPR003129; Laminin.G_TSP_N.

InterPro; IPR00884; TSP1.

InterPro; IPR00884; TSP1.

InterPro; IPR008085; TSP1.

InterPro; IPR00909; TSP1.

Pfam; PP00090; TSP1; 2.

Pfam; PP00090; TSP1; 2.

PRINTS; PR01705; TSP1REPEAT.

SMART; SM00210; TSP1; 1.

SMART; SM00210; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50092; TSP1; 2.
PROSITE; PS01209; VWFC_1; UNKNOWN_1.
PROSITE; PS01209; VWFC_1; UNKNOWN_1.
SEQUENCE 496 AA, 54843 MW; E4FD2F07CB7EF51B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 18%; Score 56; DB 2; Local Similarity 91.7%; Pred. No. 0.025; les 11; Conservative 0; Mismatchem
                Kenopus laevis (African clawed frog)
                                                                        Xenopus; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Whole;
                                                                            Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                             TISSUE=Aortic endothelium;
Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin stimulatory effect of
                                                                                                                                                                             STRAIN=Holstein; TISSUE=Tooth;
MEDLINE=98173773; PubMed=9507054; DOI=10.1016/S0167-4838(97)00188-X;
Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                              "cDNA cloning of bovine thrombospondin 1 and its expression in odontoblasts and predentin.";
TSPI BOVIN STANDARD; PRT; 1170 AA. (28178; 028179; 028179; 01-NOV-1997, integrated into UniProtKB/Swiss-Prot. 01-NOV-2000, sequence version 2. (7-MAR-2006, entry version 56. Name-THSB1; Synonyms-TSP-1, TSP1; Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA] OF 1-18 AND 710-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; ABO05287; BAA21115.1; -; mRNA.
EMBL; K87619; CAA60950.1; -; mRNA.
EMBL; K87619; CAA60951.1; -; mRNA.
PIR; S55501; S55501.
HSSP; P07996; ILSL.
SMR; Q28178; 549-1169.
GWCSQuitcDB; Q28178; -.
InterPro; IPR001320; ConA_like_subgrp.
InterPro; IPR00610; EGF.
InterPro; IPR00142; EGF.
InterPro; IPR00181; EGF_like.
InterPro; IPR00181; EGF_like.
InterPro; IPR00181; EGF_like.
InterPro; IPR00181; EGF_like.
InterPro; IPR001881; EGF_like.
InterPro; IPR001881; TSP1.
InterPro; IPR001881; TSP1.
InterPro; IPR001881; TSP1.
InterPro; IPR001881; TSP1.
InterPro; IPR001007; VWF_C.
Pfam; PP00009; TSP1.
Pfam; PP00009; TSP1.
                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 1382:17-22(1998).
                                                                                                                                                                  NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                    Inoue H
```

. 0

Gaps

ö

1; Indels

1 FOGVAQNVRFVF 12

ð

Best Loca Matches

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 25:8418-8425(1986)
                                                                                                                             208 FOGVLONVRFVF 219
  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                        1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins.";
                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                           WWFC.

TSP type-1 3.

TSP type-1 3.

EGF-like 2; calcium-binding (Potential).

EGF-like 3.

TSP type-3 1.

TSP type-3 2.

TSP type-3 2.

TSP type-3 3.

TSP type-3 3.

TSP type-3 5.

TSP type-3 5.

TSP type-3 7.

TSP type-1 3.

TSP type-1 4.

N-linked (GlcNAc. .) (Potential).

N-linked (GlcN
                   Pfam, PF00093; VWC; I.

RRINTS; PR01705; TSPIREPEAT.
SMART; SM00209; TSPI; 3.

SMART; SM00210; TSPI; 1.

SMART; SM00214; VWC; 1.

SMART; SM00214; VWC; 1.

RROSITE; PS0022; EGF 1; FALSE_NEG.
RROSITE; PS0026; EGF 2; 1.

RROSITE; PS0029; TSPI; 3.

RROSITE; PS01208; VWFC_1; 1.

R
PF05735; TSP_C; 1.
PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      708
1067
1085
270
274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
708
1067
1085
270
274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451
462
504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGION
MOTIF
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
TISSUB=Endothelial cell;
MEDLINE=87057617; PubMed=2430973; DOI=10.1083/jcb.103.5.1635;
Lawler J., Hynes R.O.;
"The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 1-374.
MEDLINE=86287276; PubMed=3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
"Characterization of a cDNA encoding the heparin and collagen binding domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLECTIDE SEQUENCE OF 1-397.
NUCLECTIDE SEQUENCE OF 1-397.
NUCLECTIDE SEQUENCE OF 1-397.
NEDLINE S., Eden-Mccutchan F., Framson P., Bornstein P.,;
Nobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.,;
"Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE OF 1-166.
MEDLINE-89291870; PubMed=2544587;
Laherty C.D., Gierman T.M., Dixit V.M.;
"Characterization of the promoter region of the human thrombospondingene. DNA sequences within the first intron increase transcription.";
J. Biol. Chem. 264:11222-11227(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89139590; PubMed=2918029; DOI=10.1083/jcb.108.2.729; Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L., Baundartel D.M., Rotwein P., Frazier W.A.; "Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region."; Coll Biol. 108:729-736(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE OF 1028-1170.

La Fleur M., Jobin C., Gauthier J., Kreis C.G.;

Expression of thrombospondin in chronic inflammation: neutrophils from synovial fluids synthesize a novel 3.9 kD TSP mRNA.";

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441;
THR-450; TRP-498 AND THR-507.
TISSUE-Platelet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21125860; PubMed=11067851; DOI=10.1074/jbc.M008073200;
                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   TSP1 HUMAN STANDARD; PRT; 1170 AA. 007956; 015667; 01-806-1988, integrated into UniProtKB/Swiss-Prot. 01-AUG-1988, sequence version 1. 01-AUG-1988, synonyms=TSP, TSP1; Homo sapiens (Human)
                              0.061;
                                                                        Mismatches
Score 56;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins.";
J. Cell Biol. 103:1635-1648(1986)
                                                                                                                                                                                                                                                                                                                                                                                                               A LO DITION OF THE SEASON OF T
```

```
4447
451
462
504
508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
DORR RODOR STATE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYDRATE-LINKAGE SITES ASN-248 AND ASN-1067.

Pubmed=16335952; DOI=10.1021/pro502065;
A Liu T., Qian W.-J., Gartesenko M.A., Camp D.G. II, Monroe M.E.,
A Liu T., Qian W.-J., Gartesenko M.A., Camp D.G. II, Monroe M.E.,
A Moore R.J., Smith R.D.;
"Human plasma N-glycoproteome analysis by immunoaffinity subtraction,
Apdrazide chemistry, and mass spectrometry.";
J. Proteome Res. 4.2070-2080(205).
J. FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
lamini, type V collagen and integrins alpha-V/beta-1, alpha-
V/beta-3 and alpha-IIb/beta-3.

CHEMILARITY: Contains 1 TSP C-terminal (TSPC) domain.
CHEMILARITY: Contains 1 TSP C-terminal (TSPN) domain.
CHEMILARITY: Contains 7 TSP type-1 domains.
CHEMILARITY: Contains 7 TSP type-1
CHEMILARITY: Contains 7 TSP type-3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                  MEDLINE=22338361; PubMed=12450399; DOT=10.1021/bi026463u;
Huwiler K.G., Vestling M.M., Annis D.S., Mosher D.F.;
"Biophysical characterization, including disulfide bond assignments,
of the anti-angiogenic type 1 domains of human thrombospondin-1.";
Biochemistry 41:14329-14339(2002).
Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J., Mosher D.F., Peter-Katalinic J.; "C-mannosylation and O-fucosylation of the thrombospondin type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A FINGULATION STATEMENT ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; ILSL; X-ray; A=434-546.
PDB; IUX6; X-ray; A=834-1170.
PDB; 1ZA8; X-ray; A=19-233.
PDB; ZERF; X-ray; A=19-257.
PDB; ZERF; X-ray; A=19-257.
SMR; P07996; 549-1169.
Glycosuitedb; P07996; -.
GGP; P07996; -.
Ensembl; ENSG0000137801; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M25631; AAA36741.1; -; mRNA.

EMBL; X04665; CAA28370.1; -; mRNA.

EMBL; X14787; CAA32889.1; -; mRNA.

EMBL; M1326; AAA61237.1; ALT SEQ; mRNA.

EMBL; J04835; AAA61178.1; -; Genomic_DNA.

EMBL; M99425; AAB59366.1; -; mRNA.
                                                                                                                                                                                                                        THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES.
                                                                                                                                                   Biol. Chem. 276:6485-6498(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000884; TSP1.
InterPro; IPR003605; TSP_1.
InterPro; IPR003657; tsp_3.
InterPro; IPR008859; TSP_C.
InterPro; IPR001007; VWF_C.
Pfam; PF00008; EGF; 2.
Pfam; PF00090; TSP_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A26155; TSHUP1.
PDB; 1LSL; X-ray; A:
                                                                                                                         nodule.
           A STATE STAT
```

```
TSP type-1 1.
TSP type-1 1.
TSP type-1 2.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2; calcium-binding (Potential).
EGF-like 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 4.
TSP type-3 5.
TSP type-3 6.
TSP type-3 7.
TSP type-3 7.
TSP type-3 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                PROSITE; PS00022; EGF 1; FALSE_NEG.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50024; TSP1; 3.
PROSITE; PS01208; VWFC 2; 1.
3D-structure; Calcium; Cell adhesion; EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-11nked (Man).
O-linked (Fuc. .).
FTId=CAR 000210.
N-FTId=CAR 000211.
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-linked (GlcNAc. ..).
N-linked (GlcNAc. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heparin-binding (Potential).
Cell attachment site (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 1; Length 1170;
Pred. No. 0.061;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interchain (Probable)
Interchain (Probable)
                                                                                                                                                                                                                                                 Thrombospondin-1.
/FTId=PRO_0000035842.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=CAR 000208.
O-linked (Fuc. .)
/FTId=CAR 000209.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-linked (Man).
/FTId=CAR 000205.
O-linked (Fuc. . .)
/FTId=CAR_000206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                000207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-linach
/Frid=CAR 000zu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-linked
                                                                                                                                                                                                                       Heparin-binding; Repeat; Signal.
Pfam; PF02412; TSP_3; 12.
Pfam; PF05735; TSP_C; 1.
Pfam; PF00093; VWC; 1.
PRINTS; PR01705; TSP1REPEAT.
SMART; SM00181; EGF; 3.
SMART; SM00210; TSP1; 3.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91...
Best Local 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGVAONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1001
2070
2070
4423
4488
5413
5411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      914
950
1170
232
928
248
360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441
```

```
MOTIF
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
REGION
                                                 EMBL;
EMBL;
                                                                                     EMBL;
EMBL;
EMBL;
                                                                                                                                      EMBL;
EMBL;
                                                                                                                                                                        EMBL;
EMBL;
                EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLECTIDE SEQUENCE OF 1-490.
MEDLINE=90375546; PubMed=2398070;
Bornstein P., Alfi D., Devarayalu S., Framson P., Li P.;
"Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";
J. Biol. Chem. 265:16691-16698(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development."; J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                             MEDLINE=92128941; PubMed=1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
Jenkins N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
MEDLINE=22147683; PubMed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                 "Characterization of the murine thrombospondin gene.";
                                                                                              01-JUN-1994, integrated into UniProtKB/Swiss-Prot. 01-JUN-1994, sequence version 1. 07-MAR-2006, entry version 57. Name-Thbb1; Synonyms=TBp1; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M62470; AAA50611.1; -; Genomic DNA.
EMBL; M62451; AAA50611.1; JOINED; Genomic DNA.
EMBL; M62421; AAA50611.1; JOINED; Genomic DNA.
EMBL; M62423; AAA50611.1; JOINED; Genomic DNA.
EMBL; M62453; AAA50611.1; JOINED; Genomic DNA.
EMBL; M62454; AAA50611.1; JOINED; Genomic DNA.
EMBL; M62455; AAA50611.1; JOINED; Genomic DNA.
EMBL; M62455; AAA50611.1; JOINED; Genomic DNA.
EMBL; M62459; AAA50611.1; JOINED; Genomic DNA.
EMBL; M62451; AAA50611.1; JOINED; Genomic DNA.
EMBL; M62451; AAA50611.1; JOINED; Genomic DNA.
                                                                   PRT; 1170 AA
                                                                                                                                                                                                                                                                                                                                                                                    Genomics 11:587-600(1991).
                                                                   STANDARD;
                                                                                                                                                                                                                                                                              [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                           RESULT 5

TOPI MOUSE

TO 1-JUN-1994,

DT 01-JUN-1994,

DT 01-JUN-1994,

DT 01-JUN-1994,

DT 01-JUN-1994,

DT 01-JUN-1994,

OS BUKARYOLA;

RA DO BUKARYOLA;

RA LAMIE JAILE

RA CONTIGNE

RA LAMIE JAILE

CC CONTIGNE

CC LONTIGNE

CC LONTIGNE

CC LONTIGNE

CC LONTIGNE

CC CONTIGNE

CC CONTIGNE

CC LONTIGNE

CC CONTIGNE

CC CO
```

φ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Aorta and vein;
PubMed=16141072; DOI=10.1126/science.1112014;
PubMed=16141072; DOI=10.1126/science.112014;
Carninci P., Kaeukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V. Brenner S. B., Batalov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/67; TISSUE=Aorta and vein;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
Adult male aorta and vein cDMs, RIKEN full-length enriched library, clone:A530055N06 product:thrombospondin 1, full insert sequence.
   .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0443E493615E7F06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
N-linked (GlcNAc.
Interchain (Probable)
Interchain (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 1;
Pred. No. 0.061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
I[2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                             similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1170 AA
                                                                         similarity.
similarity.
                                                                                                                                                                                                                                               similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                    similarity
similarity
                                                                                                                                                                                                                                                                                           similarity
similarity
                                                                                                                                                                                                                                                                                                                        similarity
similarity
                                                                                                                                                                                                                                                                                                                                                      similarity
                                                                                                                                                                                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                                                                                                               similarity
                                                                                                        similarity
                                                                                                                                                                                                                                                                                                                                                                                 similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1170 AA; 129647 MW;
                                              MESULI 0

OTTR40_MOUSE

DAC 03TR40_MOUSE

DAC 03TR40_MOUSE

DT 11-0CT-2005, integrated into Un

11-0CT-2005, sequence version 1

DT 07-FEB-2006, entry version 5.

DE Adult male aorta and vein cDNA,

Clone:A530055N06 product:thromb

GN Name-Thbs1;

OC Eukaryota; Metazoa; Chordata; C

Musmambia; Butheria; Buarchontog

OC Muroidea; Muridae; Murinae; Mus

OX NCBI TaxID=10090;

RN [1]

RN NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Aorta a

RN MEDIJNE=99279253; Pubbled=103496

RA MEDIJNE=99279253; Pubbled=103496

RN MEDIJNE=99279253; Pubbled=103496

RA CARNING: P., Hayashizaki V.;

RN NUCLEOTIDE SEQUENCE.

RN MEDIJNE=99279253; Pubbled=103496

RN MEDIJNE=99279253; Pubbled=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similario,
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVAQNVRFVF 12
                                                                                                                  DISULFID
                                                                                                                                                                                                                                     DISULFID
                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                              DISULFID
                                                             DISULFID
                                                                           DISULFID
                                                                                       DISULPID
                                                                                                        DISULFID
                                                                                                                     DISULFID
                                                                                                                                                               DISULFID
                                                                                                                                                                             DISULFID
                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  datches
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

```
Bansal W., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.W., Chiu, K.P., Choudhary V., Christoffeel A., Gollolland G., Childrich C., Charles C., Childrich C., Charles C., Childrich C., Charles C., Childrich C., Charles C., Chieffeel C., Childrich C., Charles C., Chieffeel C., Childrich C., Charles C., Chieffeel C., Chiefeel C., Chiefeel C., Chiefeel C., Chiefeel C., Chieffeel C., Chie
```

```
InterPro; IPR008859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPLINE-2108560; PubMed=11217851; DOI=10.1038/3505500;
REDLINE-2108560; PubMed=11217851; DOI=10.1038/3505500;
REDLINE-2108560; PubMed=11217851; DOI=10.1038/3505500;
RAMAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishin Y.,
A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Radto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Gissi C., King B., Kochiwa H.,
Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Nymbha-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Nymbha-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Aorta and vein; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazati Y., Muramatsu M., Hayashizati Y.; Shibata K., Itoh M., Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Tashiro H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE-Aorta and vein;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori P. Iida J., Imamura K., Imocani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AK163092; BAE37190.1; -; mRNA.

MGI; MGI:99737; Thbs1.

MGI; MGI:99737; Thbs1.

MGI; MGI:095615; C:extracellular space; IDA.

GO; GO:0005615; C:extracellular space; RCA.

GO; GO:016525; P:negative regulation of angiogenesis; IDA.

InterPro; IPR0067210; BGF.

InterPro; IPR001881; EGF.

InterPro; IPR006209; EGF.

InterPro; IPR013032; EGF_like_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Sprague-Dawley;
Iwabu A., Hirohata S., Kusachi S., Nakamura K., Murakami T.,
Ninomiya Y., Tsuji T.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 56; DB 2; Length 1170;
Pred. No. 0.061;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1170 AA; 129619 MW; 55BF04A20D91B194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMR; Q71SA3; 834-1169.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0007155; P:cell adhesion; IEA.

InterPro; IPRO13120; Cona like subgrp.

InterPro; IPRO00742; EGF_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q71SA3;
Q71SA3;
05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000742; BGF 3.
InterPro; IPR001881; BGF Ca bd.
InterPro; IPR004209; BGF like.
InterPro; IPR013032; BGF like reg.
InterPro; IPR03129; Laminin G TSP N.
                                   InterPro; IFROUGES; TSP 1.
InterPro; IFROUGES; TSP 1.
InterPro; IFROUGES; TSP 2.
InterPro; IFROUGES; TSP 2.
InterPro; IFROUGES; TSP 2.
InterPro; IFROUGOS; TSP 2.
Pfam; PPO0000; TSP 1; 3.
Pfam; PPO0000; TSP 1; 3.
Pfam; PPO5735; TSP 2; 1.
Pfam; PPO5735; TSP 2; 1.
PRINTS; PRO1705; TSP 1; 1.
PRINTS; PRO1705; TSP 1; 3.
SMART; SM00210; TSPN; 1.
SWART; SM00210; TSPN; 1.
PROSITE; PS50024; VWC; 1.
PROSITE; PS50024; VWC; 1.
PROSITE; PS50025; TSP 3; 2.
PROSITE; PS50026; TSP 3; 2.
PROSITE; PS50026; TSP 3; 2.
PROSITE; PS50026; TSP 3; 3.
PROSITE; PS50184; VWFC 2; 1.
Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF309630; AAQ14549.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSP 1.
tsp 3.
TSP C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.7%,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Tsp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q71SA3 RAT
```

α

```
01-MAR-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBCGB2_MOUSE PRELIMINARY; PRT; 1171 AA.
QBCGB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1705; TSPEREPEAT.
SMART; SM00181; EGF; 3.
SMART; SM00210; TSP1; 3.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50029; TSPI; 3.
PROSITE; PS50184; VWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_2; 1.
SEQUENCE 1171 AA; 129690 MW; 12E077
                   EMBL; BC050917; AAH50917.1; -; mRNA
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POSCORDS CONTROL OF CO
SO DE RESERVAÇÃO DE RESERVAÇÃO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glíres; Rodentía; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 2; Length 1170;
Pred. No. 0.061;
0; Mismatches 1; Indels
                                                                                                                                                                                 SMART; SM00181; EGF; 3.
SMART; SM00209; TS11; 3.
SMART; SM00210; TSPN; 1.
SMART; SM00210; TSPN; 1.
PROSITE; PS0026; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50026; TSP1; 3.
PROSITE; PS50184; VWFC 1; UNKNOWN 1.
PROSITE; PS0184; VWFC 2; 1.
SEQUENCE 1170 AA; 129671 MW; 6F38D3DCE733060F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6; TISSUB=Brain;
Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003, integrated into UniProtKB/TrEMBL.
01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBOYQ1 MOUSE PRELIMINARY; PRT; 1171 AA. QBOYQ1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.8%;
91.7%;
                                                                                                                                                           PRINTS; PR01705; TSP1REPEAT
                      Pfam; PF00008; EGF; 2. Pfam; PF00009; TSP 1; 3. Pfam; PF02412; TSP 2; 12. Pfam; PF05735; TSP C; 1. Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombospondin 1 (Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library, clone:G930018021 product:thrombospondin 1, full insert sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauener R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CZECH II; TISSUE-Mammary tumor metastatized to lung. Tumor
Ensembl; ENGUNGSCOROUGO040152; Mus musculus.

R GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0016525; P:negative regulation of angiogenesis; IDA.
GO; GO:0016525; FSP.
GO; GO; GO; GO; GO; GO; GO;
GO; GO; GO; GO; GO;
GO; GO; GO; GO;
GO; GO; GO;
GO; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56; DB 2; Length 1171;
Pred. No. 0.061;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50184; VWFC_2; 1.
1171 AA; 129690 MW; 12E077B50C64E2D3 CRC64;
```

σ

RC TISSUE-Mammary Jahad;

RA PARAMELEGIATO72; DONE-10.1126/science.1112014;

RA PARAMELEGIATO72; DONE-10.1126/science.1112014;

RA Mandeel-Ediato72; DONE-10.1126/science.1112014;

RA Mandeel-Inginombarco A. Agweller R., Atturaliya R. N., Bailary T.L.,

Banisal M., Baxter L., Beigal K. W., Bersano T., Bono H., Chalk A.M.,

RA Banisal M., Baxter L., Beigal K. W., Bersano T., Bono H., Chalk A.M.,

RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

G. Growe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA Growe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA Growe M.L., Larbor T., Engstrom P., Fagiolini M., Faulkner G.,

RA Growe M.L., Larbor T., Engstrom P., Fagiolini M., Faulkner G.,

RA Georgii-Hemming P., Gingeras T.R., Golobori T., Green R.E.,

Gustincich S., Harbers M., Hayashi Y., Hensch T. K., Hirokawa N.,

RA Hill D., Huminiecki L., Lacono M., Ikeo K., Iwama A., Ishikawa T.,

Anteno H., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,

Anteno H., Matuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

Mutson R., Malliam S., Madan Babu M., Makauchi H., Ng P.,

Aliuni S., Mowilliam S., Madan Babu M., Nakauchi H., Ng P.,

Anteno H., Salnado V., Pang K.C., Pavan W.J., Pavesi G., Peacol G.,

RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,

Schiguchi Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Sheng Y.,

Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,

Schonbach C., Sakiguchi K., Semple C.A., Seno S., Sessa L., Shang Y.,

Shamond S., Tang S., Taylor M.S., Tegner J., Tekin M.,

Namanishi H., Zabarovsky, E., Zhu S., Liu B.T., Brusk Y.,

Ramonja K., Tan S.L., Tang S., Hume D.A., Kai C., Saski D., Tackman J.,

Ramonja K., Tan S.L., Tang S., Hume D.A., Kai C., Saski D., Sanchi J.,

Ramonda Y., Tang M., Rato T., Kawaji H., Kawashima T., Kolima M., Rato T., Kawashima T., Kolima M., Rato T., Kawashima T., Kolima M., Rato T., Kawashima T., Kolima M., Ra Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schort R.M., Schmitz J., Myers R.M., Schein J.E., Ones S.J.M., Marra M.A., Schein J.E., Schonerch A., Schein J.E., Jones S.J.M., Marra M.A., TISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999). NUCLEOTIDE SEQUENCE. STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) mouse cDNA sequences." arose spontaneously; NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE Strausberg R.

"The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005). [5] NUCLEOTIDE SEQUENCE.

RECOURSE SEQUENCE.

RA NUCLESCIBE, SEQUENCE.

RA ORACARÍ Y., FUTUNO M., KASUKAWA T., Adachi J., Bono H., Kondo S.,

NA NACACARÍ Y., FUTUNO M., KASUKAWA T., Adachi J., Bono H., Kondo S.,

RA VARARÍ Y., FUTUNO M., SASICO R., SUZUKÍ H., YAMANARA I., KYOSAWA H.,

NA NAKAJGO I., OSAICO R., SUZUKÍ H., YAMANARA I., KYOSAWA H.,

RA BAIGARELII R., HILL D. P., BULT C., HUME D.A., QUACKENDUBH J.,

RA BAIGA J., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA GABSTERIANG T., GAIRDOLI M., GISBI C., GOAZIK A., GOUGH J.,

RA GARAI T., GARIBOLI M., GISBI C., GOAZIK A., GOUGH J.,

RA GARAI T., KAWAJI H., KAWASAWA N., JACKON I.J., JATVÍS B.D.,

RA KANAJ A., KUROCHKIN I.V., Lee Y., Lenhard B., Lyons P.A.,

RA KORAJA A., KUROCHKIN I.V., Lee Y., Lenhard B., Lyons P.A.,

RA MAGAGHIM T., NUMATA K., OKHOO T., PRAVIN W.J., PERTER G., PESOLE G.,

RA RAVARI T., Reed J.C., Reed D.J., Raid J., RIMB B.C.,

RA RAVARI T., Reed J.C., Reed D.J., Raid J., RIMB B.C.,

RA RAVARI T., Reed J.C., Reed D.J., Raid J., SHIMA B. K.,

RA SANGALIN A., Schneider C., Semple C.A., Setcu M., Shimada K.,

RA VERARO R., WAGHER T., WAHLESTECH C., WANG Y., WARCHARE Y., WAGHER N.,

RA VERARO R., WAGHER T., KONDO H., NAKAMURO M., SARARUME N.,

RA VILLAN E., RANIALUME W., IMOCRANI R., INDA M., YANG I., YANG I.,

RA KINIMIN I.G., WANDA W., ZINARAWA T., FUKUGA S.,

RA SHIRAK T., WAKI K., KAWAI J., AIZAWA K., SINARAWA T., FUKUGA S.,

RA HARA A., HASHIZUME W., IMOCRANI R., ISHNIH Y., ITOH M., KAGWA T.,

RA HARA A., YASHINO M., WALERSTON R., LANGAR A.,

RA YASHURISHI M., SARAI Y.,

RA YASHURISHI M., RAYASHIRA Y.,

RA YASHURISHI M., SARAI Y.,

RA YASHURISHI M., RAYASHIRA K., ISHNIH Y., ITOH M., KAGWA T.,

RA HARANA W., YOSHIMO M., SARAKU S., ITOH M., NACORER S.,

RA HARANA M., YOSHIMO M., WALENBERTON R., ILANGAR A.,

RA HARANA M., YOSHIMO M., SARAI Y.,

RA HARANA M., YOSHIMO M., WALENBERTON R., ILANGAR A.,

RA HARANA M., YOSHIMO M., WALENBERTON R., ILANGAR A.,

RA HARANA M. Rewai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Itoh M., Itoh M., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh A. Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Yamanaka I., R. Ajzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Fuell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., R. Kuell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., R. Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Rabi E., Suzuki R., Toni Burdo I., Pesole G., Quackenbush J., R. Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., R. Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., R. Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., L. Wottone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., T. "Puntzional annotation of a full-length mouse cDNA collection."; Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of $60,770~{\rm full-length~cDNAs."};$ TISSUE-Mammary gland;

MEDLINE-2049374; PubMed-11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630(2000). RIKEN Genome Syploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; TISSUE=Mammary gland; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; TISSUE=Mammary gland; PubMed=16141073; DOI=10.1126/science.1112009; Science 309:1564-1566(2005). Nature 420:563-573(2002). Nature 409:685-690(2001). NUCLEOTIDE SEOUENCE NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE

```
4492

5590

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

6690

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66900

66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa M., Sitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoro R., Matsunioto H., Sakaguchi S., Ikegami T., Kashikaja K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771 (2000).
                                                                                                                                                                                                                                                                                                                                             Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Sulmatsu M., Hayashizaki Y., Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=thbāl; Synonyms=tspl;
Skoropus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.8%; Score 56; DB 2; Length 1171; 91.7%; Pred. No. 0.061; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC042422; AAH42422.1; -; mRNA.
EMBL; AK145202; BAE26293.1; -; mRNA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994, sequence version 1. 07-MAR-2006, entry version 54. Thrombospondin-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 91.7
nes 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSP1 XENLA
AC P3544;
DT 701-JUN-1994,
DT 01-JUN-1994,
DS TANABORDING;
CC ENARTYCLA, R
RT "Cloning, ch
RT "Clon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              datches
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
C copyrighted With the Charlet Commons Attribution. Wobering License C Distributed under the Creative Commons Attribution. Wobering License C Distributed under the Creative Commons Attribution. Wobering License C BME. 10278; 1. NOTAMONTATED COS; MRNA.

RESP, POT968.1116.1.

RESP, POT968.1.

RESP, POT968.1116.1.

RESP, POT968.1.

RESP, POT968.116.1.
```

g

ઠે

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collagen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-DEC-2004, integrated into UniProtKB/TrEMBL.
21-DEC-2004, sequence version 1.
21-FEB-2006, entry version 12.
31-FEB-2006, entry version 12.
0RFNames=DKEY-11E23.1-001;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            91.8%; Score 56; DB 2; Length 1225; 91.7%; Pred. No. 0.064; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     1225 AA; 134849 MW; 9888B16E57157B12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL928866; CAI20599.1; -; Genomic_DNA.
SMR; QSSPG5; 751-804, 754-1089.
Ensembl; ENSDAG0000010785; Danio rerio.
GO; GO:0005509; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:000515; F:heparin binding; IEA.
GO; GO:000515; F:protein binding; IEA.
GO; GO:000518; F:protein binding; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR013320; ConA like subgrp.
InterPro; IPR01340; EF hand_Ca_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSSPGS BRARE PRELIMINARY; PRT; 1090 AA.
QSSPGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF 3.
EGF Ca bd.
EGF like.
EGF like reg.
InterPro; IPR001007; VWF_C.

Pfam; PP00008; EGF; 2.

DR Pfam; PP002412; TSP_1; 3.

Pfam; PP02412; TSP_2; 12.

DR Pfam; PP05735; TSP_C; 1.

Pfam; PP05735; TSP_C; 1.

DR PRINTS; PR01705; TSP18EPEAT.

DR SMART; SM00210; TSP1; 3.

DR SMART; SM00210; TSP1; 3.

DR SMART; SM00210; TSP1; 3.

DR SMART; SM00214; VWC; 1.

DR PROSITE; PS01186; BGF_2; 1.

DR PROSITE; PS01086; EGF_3; 2.

DR PROSITE; PS01086; TSP1; 3.

PROSITE; PS01086; VWFC_1; 1.

R PROSITE; PS010814; VWFC_2; 1.

R PROSITE; PS01084; VWFC_2; 1.

R SEQÜENCE 1225 AA. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 FOGVLONVRFVF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 91.7
Les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVAONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR013032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR008085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barker D.;
Submitted (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo applens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
TISSUE-Aorta endothelial cell;
TISSUE-Aorta endothelial cell;
TISSUE-Aorta endothelial cell;
Chocki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Chara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 1; Length 1173; Pred. No. 0.061;
                       By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB209912; BAD93149.1; -; mRNA.

SNR; Q59E99; 886-939, 889-1225.

Ensembl; ENSGORO0137801; Homo sapiens.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005101; F:heparin binding; IEA.

GO; GO:0005115; P:protein binding; IEA.

GO; GO:0007155; P:cell adhesion; IEA.

InterPro; IPR001320; ConA_like_subgrp.

InterPro; IPR000742; EGF 3.

InterPro; IPR000742; EGF 3.

InterPro; IPR001881; EGF Ca bd.

InterPro; IPR001801; EGF 2.

InterPro; IPR001801; EGF 1.

InterPro; IPR001801; EGF 1.

InterPro; IPR001801; EGF 1.

InterPro; IPR001801; Laminin_G TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q59E99 HUMAN PRELIMINARY; PRT; 1225 AA.
Q59E99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-APR-2005, sequence version 1.
21-FBB-2006, entry version 10.
Thrombospondin 1 variant (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                          91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPRO0884; TSP1.
IPRO08085; TSP 1.
IPRO03367; tsp_3.
IPRO08859; TSP_C.
                                                                                                                                                                                                                                                                                                                                                                                                   AA; 130020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 FQGVLQNVRFVF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 91.7 les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
                       DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                            DISULFID
                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                      DISULPID
                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
```

DER NOOR BURN DER NOOR DE NOOR DE

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                       EMBL; CAAE01014723; CAG03524.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
050903 PIG
D 050903 PIG
AC 050903.
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DT 17-FEB-2006, entry version 7.
DE Thrombospondin 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY773342; AAV38110.1; -; mRNA.
Interpro; IPR000884; TSP1.
Interpro; IPR008085; TSP_1.
Interpro; IPR01007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01186; EGF 2; UNKNOWN 1. PROSITE; PS50026; EGF 3; 2. PROSITE; PS50092; TSP1; 3. PROSITE; PS501208; WWFC 1; 1. PROSITE; PS50184; WWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03/03; MS; 1.
PRINTS; PR01705; TSPIREPEAT.
SMART; SM00181; EGF; 2.
SMART; SM00210; TSP1; 3.
SMART; SM00210; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 FMGVLQNVRFVF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 83.3
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whede-15496914; DOI=10.1038/nature03025;

A Daillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Andraud S., Jaffe D., Fisher C., Lutfalla G., Dossat C., Segurens B.,

Anthouard V., Jubin C., Castelli V., Ratinha M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Ratinha M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Ratinha M., Vacherie B.,

Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

Rellis M., Volff J.-N., Guigo R., Zody M.C., Meelrov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Rahn D., Robinson-Rechavi M.,

Landet V., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2005, sequence version 1.
SI-FEB-2006, entry version 8.
Chromosome 14 SCAF14/23, whole genome shotgun sequence. (Fragment)
ORFNames-GSTENG00022976001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon nigroviridis (Green puffer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
Genoscope, Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.6%; Score 51; DB 2; Length 1090;
83.3%; Pred. No. 0.6;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1090 AA; 120978 MW; 5A9320504A22D836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q4S758 TETNG PRELIMINARY; PRT; 1193 AA. 04S758;
                                                                                                                                                                                                                                                                                SMART; SM00181; EGF; 2.
SMART; SM00210; TSP1; 2.
SMART; SM00210; TSP1; 2.
SMART; SM00210; TSP1; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01018; EF HAND 1; UNKNOWN_1.
PROSITE; PS01018; EGF_2; 7.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS50029; TSP1; 2.
PROSITE; PS50184; VWFC_2; 1.
Cell adhesion; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                         PRINTS; PR01705; TSP1REPEAT.
                                                                                             Pfam; PF00008; EGF; 1. Pfam; PF00009; TSP 1; 2. Pfam; PF02412; TSP 3; 12. Pfam; PF05735; TSP C; 1. Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 83.3
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=99883;
                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                          InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
104 8758
107 8755
10 96 8755
10 96 8755
11 9 - JI
11 9 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
         DOR NO DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metăzoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 2; Length 1193;
Pred. No. 0.66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER 1 1 SEQUENCE 1193 AA; 133256 MW; 6E8781648FCEC7F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
Zhang K., Mauco G., Hauet T.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
SME (49758; 811-1148)

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005519; F:calcium ion binding; IEA.

GO; GO:0005119; F:pertium ion binding; IEA.

GO; GO:0005119; F:pertium ion binding; IEA.

GO; GO:0005159; F:protein binding; IEA.

GO; GO:0007155; P:cell adhesion; IEA.

InterPro; IPR006210; EGF.

InterPro; IPR00142; EGF.

InterPro; IPR013032; EGF.

InterPro; IPR013032; EGF.

InterPro; IPR013032; EGF.

InterPro; IPR001007; VWF.C.

R Ffam; PF00008; TSP.1.

R Ffam; PF00019; TSP.1; 3.

R Ffam; PF00019; TSP.1; 3.

R Ffam; PF00512; TSP.2; 1.
```

```
completed: June 5, 2006, 22:42:41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: June
Job time: 109.931 secs
        DR VALUE OR CONTRACTOR CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whedel5496914; DOI=10.1038/nature03025;
Whomed=15496914; DOI=10.1038/nature03025;
Maillon O. Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
Maillon O., Aury J.-M., Brunet C., Ozouf-Costaz C., Bernot A.,
Macaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
M. Blemont C., Skalli Z., Cattolico L., Poulain J., De Barardinis V.,
A parra G., Lardier S., Brottier P., Coutanceau J.-P., Gouzy J.,
Rellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
M. "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2005, sequence version 1.
21-FBB-2006, entry version 8.
Chromosome 10 SCAF15019, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENG00032374001;
Tetraodon nigroviridis (Green puffer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Tetradontoidea; Tetraodontidae; Tetraodon.
NCBI_TAXID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
Genoscope, Whitehead Institute Centre for Genome Research,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.0%; Score 50; DB 2; Length 249; 90.9%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                              249 AA; 27560 MW; 465D664BE0329C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QARLES; 834-887, 837-1171.
GO:0005576; C:extracellular region; IEA.
GO:0008201; F:heparin binding; IEA.
GO:000515; F:protein binding; IEA.
GO:000519; F:protein binding; IEA.
GO:000519; F:structural molecule activity; IEA.
GO:0007155; F:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; CAAE01015019; CAG10667.1; -; Genomic_DNA.
SMR; Q4RLRS; 834-887, 837-1171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O4RLR5_TETNG PRELIMINARY; PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
Pfam; PF00090; TSP_1; 2.
Pfam; PF00093; VWC; 1.
SMART; SM0209; TSP1REPEAT.
SMART; SM02214; VWC; 1.
SMART; SM02214; VWC; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50184; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 90.5
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 QGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
04 RLRS TET
19-JT
119-JT
119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
        STTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

```
Gaps
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                       Score 50; DB 2; Length 1171;
Pred. No. 1;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                           1171 1171
1171 AA; 129304 MW; 865F3749693F7FCE CRC64;
InterPro; IPR000742; EGF 3.
InterPro; IRR001801; EGF Ca bd.
InterPro; IPR0013032; EGF Tike reg.
InterPro; IPR003129; Laminin G TSP N.
InterPro; IPR000884; TSP 1.
InterPro; IPR008085; TSP 1.
                                                                   82.0%;
                                                                                                                                                                                                                                                                                   83.3%;
                                                                                                                                                                                                                                                                                                                               Local Similarity 83.3
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                 1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                 Cell adhesion.
                                                                                                                                                                                                                                           NON TER
SEQUENCE
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                      Best Loca
Matches
```

THIS PAGE BLANK (USPTO)

```
Sequence 97, Application US/09939853A
; Patent No. 6989232
; Fatent No. 6989232
; GENERAL INFORMATION:
; APPLICANT: Burgess et al.
; TITLE OF INTERTION: No. 6989232el Proteins and Nucleic Acids Encoding Same TITLE OF INTERTION: No. 6989232el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099
; CURRENT PAPLICATION NUMBER: US/09/939,853A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/228,191
; PRIOR APPLICATION NUMBER: 60/226,300
; PRIOR FILING DATE: 2001-02-08
; PRIOR FILING DATE: 2001-02-08
; PRIOR FILING DATE: 2001-02-08
; PRIOR FILING DATE: 2001-02-20
; PRIOR FILING DATE: 2001-02-20
; PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 91.8
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 FOGVLONVŘEVĚ 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVAQNVRFVF 12
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 97, Appl
Sequence 98, Appl
Sequence 20, Appl
Sequence 11112, A
Sequence 11112, A
Sequence 6133, Appl
Sequence 6133, Appl
Sequence 6136, Appl
Sequence 6136, Appl
Sequence 6136, Appl
Sequence 19467, Appl
Sequence 15, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42057, A
3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                          (without alignments)
43.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                     /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Sequence Sequence Sequence
                                                                                             5, 2006, 22:43:07; Search time 23.8966 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
          GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-949-002-482
US-09-939-853A-97
US-09-939-853A-97
US-08-313-288B-20
US-09-949-012-1112
US-09-949-016-11112
US-09-949-016-11112
US-09-949-016-6333
US-09-252-991A-20515
US-09-213-288B-19
US-09-252-991A-20515
US-09-270-767-61396
US-09-270-767-61396
US-09-270-767-61396
US-09-270-767-45864
US-09-270-767-45864
US-09-270-767-45864
US-09-289-15
US-09-289-15
US-09-299-15
US-09-303-518D-466
US-09-303-518D-464
US-09-303-518D-464
US-10-124-807-19
US-09-303-518D-464
US-10-124-807-19
US-09-303-518D-464
US-10-124-807-29
US-09-303-518D-464
US-10-124-807-29
US-09-303-518D-464
                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    650591 segs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                              Patents AA:*
                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 10
                                                                                                                                                                              1 FOGVAQNVRFVF 12
                                                                                                                                                   US-10-030-735-27
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
                                                                                                                                                                                                           Scoring table:
                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein
                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
```

```
Sequence 402, Application US/09949002

Sequence 402, Application US/09949002

Patent No. 690016

GENERAL INPORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: WITH SEPTIMENCE: CLOOO790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 482
LENGTH: 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                  8227, Ap
14310, A
6682, Ap
4256, Ap
6576, Ap
14, Appl
                                                                           Appl
Appl
Appl
Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                      23,
221,
221,
221,
221,
                  Sequence Sequence Sequence
                                               Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                  Sequence
 Sequence
          Sequence
                                                                                                                                               Sequence
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56; DB 2; Length 825;
Pred. No. 0.011;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
               US-09-121-207
US-09-121-207
US-09-489-039A-14310
US-09-134-000C-6882
US-09-134-000C-6576
US-09-134-000C-6576
US-09-134-000C-6576
US-09-124-807-23
US-09-124-807-23
US-07-868-353A-13
US-07-868-353A-15
US-08-407-804-22
US-08-407-804-22
US-08-407-804-24
US-09-124-807-22
                                                                                                                                                                           US-09-124-807-24
                                                                                                                                                                                                       ALIGNMENTS
```

```
Sequence 350, Application US/09949002; Patent No. 6900016; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVAQNVRFVF 12
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98, Application US/09939853A

| Sequence 98, Application US/09939853A
| Patent No. 6989212
| GENERAL INFORMATION:
| APPLICANT: Burgess et al.
| TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099
| CURRENT APPLICATION NOWBER: US/09/939,853A
| CURRENT APPLICATION NUMBER: US/09/939,853A
| CURRENT APPLICATION NUMBER: 60/226,191
| PRIOR FILING DATE: 2001-08-25
| PRIOR FILING DATE: 2001-02-08
| PRIOR FILING DATE: 2001-02-08
| PRIOR PLING DATE: 2001-03-20
| PRIOR APPLICATION NUMBER: 60/269,961
| PRIOR PILING DATE: 2001-03-20
| PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-313-288B-20
; Sequence 20, Application US/08313288B
; Sequence 20, Application US/08313288B
; Patent No. 575502
; GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: OVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
; STATE: New York
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 831;
                                                                                                                                                                                                Length 831;
                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                Score 56; DB 2;
Pred. No. 0.011;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56; DB 2
Pred. No. 0.011
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.8%;
91.7%;
                                                                                                                                                                                                     91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                  208 FOGVLONVREVE 219
  NUMBER OF SEQ ID NOS: 159
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.8
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                   1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Mus musculus
US-09-939-853A-98
                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                    US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                   SEQ ID NO 97
LENGTH: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                    셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Tander, Staces
APPLICANT: Tander, James S.
APPLICANT: Daley, George O.
APPLICANT: Michele
APPLICANT: Michele
APPLICANT: Michele
CURRENT APPLICANTON: SINGLE WICLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICANTON NUMBER: US 60/153,357
FRIOR APPLICANTON NUMBER: US 60/120,947
FRIOR FILING DATE: 1999-09-10
FRIOR FILING DATE: 2000-07-26
FRIOR APPLICATION NUMBER: US 60/225,724
FRIOR FILING DATE: 2000-07-26
FRIOR APPLICATION NUMBER: US 60/225,724
FRIOR APPLICANTON TOWNER: US 60/225,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 2; Length 1170;
Pred. No. 0.016;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 1; Length 1170;
Pred. No. 0.016;
0; Mismatches 1; Indels
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09657472 Patent No. 6727063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1170 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FOGVLONVRFVF 219
```

```
Sequence 6333 Application US/09949016
; Sequence 6333 Application US/09949016
; Retent No. 681239
GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION UNMERR: US/09/949,016
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6333
LIBRIGHT: 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 2; Length 1172;
Pred. No. 65;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 1172;
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
CONFOTER: IBM PC compatible
CONFOTER: IBM PC compatible
CONFOTER: IBM PC compatible
CONFOTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White John P. 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1907-0400
TELEFRAX: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 1172 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|: || ||
202 FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 FRGLLÓNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
    STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 7; Conserv
                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-313-288B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-11112

US-09-949-016-11112

Sequence 11112, Application US/09949016

Patent No. 6012339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11112
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CLO00790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-00-09
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FRASEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 2; Length 1170;
Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.3%; Score 38; DB 2; Length 1045; 58.3%; Pred. No. 57; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08313288B Patent No. 5750502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 FRGLLONVHLVF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Human
US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-313-288B-19
                                                                                                                                                                                                                                                   SEO ID NO 350
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
```

g

ö

ö

g ઠે

```
55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 FFGVVTŇVRLLF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||||:|
151 KGVAQNIR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QGVAQNVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-270-767-45864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-270-767-61396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-303-518D-460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
; Sequence 20515, Application US/0925291A; Sequence 20515, Application US/0925291A; Sequence 20515, Application US/0925291A; Patent No. 6551795; GENERAL INFORMATION:
; APPLICATION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; TITLE OF INVENTION NUMBER: US/09/252,991A; CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; PRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 20515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCOMPATION:

APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Brandt, Petra
APPLICANT: Broeker, Helmut
APPLICANT: Cino, Paul M
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Hofle, Gerhard
APPLICANT: Hofle, Gerhard
APPLICANT: Mueller, Joachim
APPLICANT: Meller, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35, DB 2; Length 206;
Pred. No. 36;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2; Length 247
Pred. No. 6.1e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-270-767-61396
. Sequence 61396, Application US/09270767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 57.4%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.4%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 FAGVSSNLSFLF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||| ::|| |
109 QGVAHDMRFDF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-413-814-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45864, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1995-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SSEQ ID NO 45864
LENGTH: 304
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6196
LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 227;
                                                                                                                                                                                                                                                                                                                                          Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.7%; Score 34; DB 2; 75.0%; Pred. No. 64; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                       Score 34; DB 2;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Scarlato, Vincenzo
APPLICANT: Manaignani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisserial Antigens
FILE REFERENCE: CHIROl60
CURRENT APPLICATION NUMBER: US/09/303,518D
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 1098
SOFTWARE: Patentin version 3.1
SEQ ID NO 460
LENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:

NAME/KEY: misc feature

LOCATION: (12)...(12)

CTHER INFORMATION: Xaa= any amino acid
US-09-303-518D-460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 460, Application US/09303518D Patent No. 6914131
                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Neisseria meningitidis
```

```
RESULT 15
US-09-248-796A-19467
; Sequence 19467, Application US/09248796A
; Sequence 19467, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
; FILE REFRENCE: 107196.132
; CURRENT APPLICATION NUMBER: US 60/074,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR APPLICATION NUMBER: US 60/096,409
; RIOR APPLICATION NUMBER: US 60/096,409
; RIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19467
                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                 Score 34; DB 2; Length 304;
Pred. No. 89;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.7%; Score 34; DB 2; Length 347; Best Local Similarity 77.8%; Pred. No. 1e+02; Matches 7; Conservative 1; Mismatches 1; Indels
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; CHER INFORMATION: Xaa means any amino acid
US-09-270-767-45864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: June 5, 2006, 22:48:54 Job time: 23.8966 secs
                                                                                                                               Query Match 55.7%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                  287 FFGVVTNVRLLF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19467
                                                                                                                                                                                                                         1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 GVAKNVRIV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GVAQNVRFV 11
                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```



```
Sequence 28, Appl
Sequence 40, Appl
Sequence 1020, Appl
Sequence 1022, Appl
Sequence 462, Appl
Sequence 454, Appl
Sequence 456, Appl
Sequence 461, Appl
Sequence 461, Appl
Sequence 461, Appl
Sequence 461, Appl
Sequence 11, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , App
Appli
                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                     (without alignments)
70.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, A Sequence 2, Ap Sequence 114,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                             5, 2006, 23:46:43 ; Search time 78.6207 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seguence
version 5.1.9
- 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-474-213-28
US-10-419-462-40
US-10-741-600-1020
US-10-741-600-1022
US-11-043-806-462
US-11-043-806-454
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-451
                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                             2097797 segs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         protein search, using sw model
                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
GenCore (c) 1993 .
                                                                                                   US-10-030-735-27
61
1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   555
578
685
828
831
831
1000
11105
11150
11169
11170
11170
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9911.8
                                                              June
                                                                                                    Title:
Perfect score:
                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein -
                                                                                                                          Sequence:
                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                               Database
                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
```

```
US-10-474-213-28

US-10-474-213-28

Sequence 28, Application US/10474213

Sequence 28, Application No. US20040214248A1

Sequence 28, Application No. US20040214248A1

SEQUENCE CONTROL OF C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-419-462-40

US-10-419-462-40

Publication No. US20040053392A1

Sequence 40, Application US/10419462

Publication No. US20040053392A1

GENERAL INFORMATION:

APPLICANT: Kevin J.

APPLICANT: Williams, Kevin J.

TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents

TITLE OF INVENTION: UNABER: US/10/419,462

CURRENT APPLICATION NUMBER: US/10/419,462

CURRENT FILING DATE: 2003-04-17

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
   38, Appl
1018, Ap
1019, Ap
1021, Ap
38, Appl
548, Appl
1376, Ap
1376, Ap
596, App
596, App
596, App
596, Appl
596, Appl
61, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
Sequence
                                                          Sequence
Sequence
Sequence
                                                                                                                                                   Sequence
                                                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                        US-10-741-600-1018

US-10-741-600-1019

US-10-741-600-1021

US-10-782-968-38

US-10-849-999-44

US-10-631-467-548

US-10-995-561-595

US-10-995-561-595

US-10-995-561-595

US-11-046-648-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 4; 1
Pred. No. 0.00033;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-467-657-2428
US-10-285-394-153
US-09-822-682-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic peptide US-10-474-213-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOGULONVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVAQNVREVF 12
11170
11170
11170
11170
11170
11170
11170
11170
11170
11170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
11;
   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
```

ò

```
APPLICANT: Compugen Ltd
APPLICANT: Compugen Ltd
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 462
LENGTH: 459
                                                                                                                                                                                                 Sequence 1022, Application US/10741600

Sequence 1022, Application US/20741600

Sublication No. US20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL,
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.8%; Score 56; DB 6; Length 459; 91.7%; Pred. No. 0.021; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 5;
Pred. No. 0.019;
0; Mismatches
    Pred. No. 0.019;
                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COTHER INFORMATION: Xaa = Any Amino Acid US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1047, Application US/09925301; Patent No. US2020052308A1; GENEAL INFORMATION: APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-043-806-462
; Sequence 462, Application US/11043806
; Publication No. US20060051774A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.8%;
91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91...
Local Similarity 91...
Local Similarity 91...
                                                                                        208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
  Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVAONVREVE 12
                                                                1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
                                                                                                                                                                        RESULT 5
US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-043-806-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                    ð
                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                 US-10-782-968-40
Sequence 40, Application US/10782968
Sequence 40, Application US/10782968
Sequence 40, Application No. US20050065324A1
Sequence 40, Application No. US20050065324A1
GENERAL INFORMATION:
APPLICANT: Williams, Kevin J.
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
FILE REFERENCE: WIL07-20005
FILE REFERENCE: WIL07-20005
CURRENT APPLICATION NUMBER: US/10/419,462
PRIOR APPLICATION NUMBER: US/10/419,462
PRIOR FILING DATE: 2003-04-21
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-741-600-1020
US-10-741-600-1020
US-10-741-600-1020
US-10-741-600-1020
US-10-741-600-1020
US-10-741-600-1020
US-20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
CIDERAL APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 1020
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-782-968-40
                                                                                        ; OTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-419-462-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 432;
                                                                                                                                                       Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                 1; Indels
                                                                                                                                                       Score 56; DB 4;
Pred. No. 0.0099;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 5;
Pred. No. 0.0099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.8%; Score 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCATION: (1)...(432)
CTHER INFORMATION: Xaa = Any Amino Acid
US-10-741-600-1020
                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                    Query Match 91.8%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                     190 FOGVLONVRFVF 201
                                                                                                                                                                                                                                           1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVAONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
        LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                         FEATURE:
```

a

```
RESULT 10
US-11-043-066-452
Sequence 452, Application US/11043806
Sequence 452, Application No. US20060051774A1
GENERAL INFORMATION:
TITLE OF INVENTION: Under 1043
TITLE OF INVENTION: Uhereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: Uhereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: US-11/003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
SEQ ID NOS: 575
LENGTH: 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-043-806-455
US-11-043-806-455
Sequence 455, Application US/11043806
Sequence 455, Application US/11043806
Sequence 456, Application No. US20060051774A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: WUMBER: US/11/043,806
CURRENT APPLICATION NUMBER: US/11/043,806
SURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 453, Application US/11043806
Publication No. US20060051774A1
Publication No. US20060051774A1
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
LENGTH: 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 6; Length 685;
Pred. No. 0.033;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.8%; Score 56; DB 6; Length 804; 91.7%; Pred. No. 0.039; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.8%;
91.7%;
                                                        208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVAONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-11-043-806-456

US-11-043-806-456

Sequence 456, Application US/11043806

PUDLICATION: US20060051774A1

GENERAL INFORMATION: Compugen Ltd

TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: UMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 456

LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 454, Application US/11043806

Publication No. US20060051774A1

GENERAL INFORMATION:

APPLICATOR COMPUSED Ltd

TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

CURRENT APPLICATION UNDER: US/11/043,806

CURRENT APPLICATION UNDER: 2005-01-27

NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
SOFTWARE: PeacentIn Ver. 2.0
SEQ 1D NO 1047
                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 3; Length 466;
Pred. No. 0.021;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.8%; Score 56; DB 6; Length 578; 91.7%; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 6; Length 555;
Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.8%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 FOGVLONVRFVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 454
LENGTH: 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: June
Job time: 78.6207 secs
US-09-939-853A-98
                                                                                                                                                                                                                                                                             US-11-043-806-461
                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-938-853A-97

Sequence 97, Application US/09939853A

Sequence 97, Application US/09939853A

Sequence 97, Application US_0040039163A1

GENERAL INFORMATION:

APPLICANT: Burgess et al.

ITLE OF INVENTION: No. US20040039163A1el Proteins and Nucleic Acids Encoding Same

ITLE OF INVENTION: No. US20040039163A1el Proteins and Nucleic Acids Encoding Same

ITLE OF INVENTION: No. US20040039163A1el Proteins and Nucleic Acids Encoding Same

ITLE OF INVENTION: NOWBER: 2001-08-25

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR PILING DATE: 2001-02-08

PRIOR PILING DATE: 2001-02-08

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR APPLICATION NUMBER: 60/267,337

PRIOR PILING DATE: 2001-03-20

NUMBER OF SEC ID NOS: 159

SEC ID NO 97

LENGTH: 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VB-09-939-853A-98

Sequence 98, Application US/09939853A

Sequence 98, Application US/09939853A

Sequence 98, Application NG US20040039163A1

SERVERAL INFORMATION:

APPLICANT: Burgese et al.

TITLE OF INVENTION: NO. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR PILING DATE: 2001-08-25

PRIOR PILING DATE: 2001-08-06

PRIOR PILING DATE: 2001-02-08

PRIOR PILING DATE: 2001-02-08

PRIOR PILING DATE: 2001-02-08

PRIOR PILING DATE: 2001-03-20

PRIOR PILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SEQ ID NO 98

LENGTH 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                ó
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 3; Length 831;
Pred. No. 0.041;
0; Mismatches 1; Indels
                                                                                                                 DB 6; Length 828;
                                                                                                                                                             1; Indels
                                                                                                               Score 56; DB 6;
Pred. No. 0.041;
0; Mismatches
                                                                                                             Query Match 91.8%;
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                         208 FÓGVLÓNVRFVF 219
                                                                                                                                                                                                              1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVAQNVRFVF 12
; LENGTH: 828
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Homo sapiens
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                    g
```

```
APPLICANT: Compugen Ltd
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 461
LENGTH: 855
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Query Match

91.8%; Score 56; DB 3; Length 831;
Best Local Similarity 91.7%; Pred. No. 0.041;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.8%; Score 56; DB 6; Length 855; 91.7%; Pred. No. 0.042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6, 2006, 00:00:10
                                                                                                                                                                                                                                          Sequence 461, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
                                                                                                                   208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 FOGVLÓNVŘFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                         1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Homo sapiens
US-11-043-806-461
```

```
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PU22 CURRENT APPLICATION NUMBER: US.10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SEQ ID NOS: 4025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6894, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: ||||| :
461 KAIVQNVRFTY 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-10-953-349-6894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-203-828-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-203-828-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6891, Ap Sequence 6893, Ap Sequence 1159, Ap Sequence 1159, Ap Sequence 1151, Ap Sequence 1157, Ap Sequence 29201, Ap Sequence 29202, Ap Sequence 9203, Ap Sequence 9203, Ap Sequence 1689, App Sequence 1689, App Sequence 1899, App Sequence 24927, Ap Sequence 24926, Ap Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                         (without alignments)
37.266 Million cell updates/sec
                                                                                                                                                               6, 2006, 00:00:38 ; Search time 3.72414 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-203-828-5
US-10-953-349-6894
US-10-953-349-6893
US-10-953-349-1159
US-10-953-349-1159
US-10-953-349-1159
US-10-953-349-1159
US-10-953-349-1159
US-10-953-349-91203
US-10-953-349-91203
US-10-953-349-9203
US-10-953-349-9203
US-10-953-349-9203
US-10-953-349-9203
US-11-121-154-49
US-11-121-986-599
US-11-121-986-599
US-11-122-986-599
US-11-122-986-599
US-11-122-986-599
US-11-122-986-599
US-11-123-986-599
US-10-953-349-24926
US-10-953-349-24926
US-10-953-349-24926
US-10-953-349-24926
US-10-953-349-24926
US-10-953-349-24926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA_New:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58871 seqs, 11565156 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                     US-10-030-735-27
61
1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99979999777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           June
                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2222221111111111
22222211111111111
24321099435111111111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
```

```
ö
                                         167, App
169, App
18, App
33, Appl
24, Appl
24, Appl
15283, A
14976, A
23541, A
23541, A
23541, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/11203828

Publication No. US2006011039041

GENERAL INFORMATION:

APPLICANT: LEINWAND, LESLIE

APPLICANT: LEINWAND, LESLIE

APPLICANT: SUCHAROV, CARMEN

TITLE OF INVENTION: INHIBITION OF KU AS A TREATMENT FOR CARDIOVASCULAR

TITLE OF INVENTION: DISEASES

FILE REFERENCE: MYOG:58US

CURRENT APPLICATION NUMBER: US/11/203,828

CURRENT FILING DATE: 2004-08-15

PRIOR APPLICATION NUMBER: 60/604,435

PRIOR FILING DATE: 2004-08-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATENTIN VOE: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                     Sequence Seq
                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 7; Length 608;
Pred. No. 35;
3; Mismatches 3; Indels
                                       US-11-122-986-167
US-10-122-986-169
US-10-11-286-18
US-10-511-937-2413
US-11-124-94
US-11-124-94
US-11-247-437-2
US-10-953-349-15282
US-10-953-349-15282
US-10-953-349-14978
US-10-953-349-14977
US-10-953-349-14977
US-10-953-349-14976
US-10-953-349-14976
US-10-953-349-14976
US-10-953-349-14976
US-10-953-349-14976
US-10-953-349-14976
US-10-953-349-23341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.1%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Mus musculus
  44444444444
```

```
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 14717, 9941, 19310, c;
TITLE OF INVENTION: Hematological Disorders Using 252, 304, 1980, 14717, 9941, 19310, c;
FILE OF INVENTION: MABER: US/11/242,505A
CURRENT APPLICATION NUMBER: US/11/242,505A
CURRENT APPLICATION NUMBER: US 10/290,078
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR PRILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 10/320,351
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-953-349-1158

Sequence 1158, Application US/10953349

Sequence 1158, Application US/20060107345A1

Sequence 1158, Application No. US20060107345A1

SEQUENCE 1158, APPLICANT: ALEXANDROV, Nickolai et al.

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION INVENTION: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT PILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PUS2 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SEQ ID NOS: 40252 SEQ ID NO 1159 LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 6; Length 164;
Pred. No. 21;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 7; Length 980;
Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1159, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Arabidopsis thaliana
US-10-953-349-1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVAONVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 FEAVVDRVRLVF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 FOGLSGNERF 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FQGVAQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-242-505A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-953-349-1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                      Sequence 6893, Application US/10953349
Fublication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONNED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION VUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 6893
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-553-149-6892
Sequence 6892, Application US/10953349
Sequence 6892, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 6892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                          ή;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                          <u>.</u>
                                          Score 32.5; DB 6; Length 157; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32.5; DB 6; Length 208; Pred. No. 14; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                          1; Indels
                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%; Score 32.5; 72.7%; Pred. No. 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-11-242-505A-36
Sequence 36, Application US/11242505A
Publication No. US20060099656A1
GENERAL INFORMATION:
APPLICANT: Carroll, Joseph M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana US-10-953-349-6892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana US-10-953-349-6893
                                          53.3%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.3
Best Local Similarity 72.7
Matches 8; Conservative
                                             Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQGTVADNVRY 125
                                                                                                                                     1 FQG-VAQNVRF 10
                                                                                                                                                                 1 FQG-VAQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 FOGTVADNVRY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOG-VAQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
US-10-953-349-6894
                                                                                                                                                                                                                                                                          US-10-953-349-6893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
Query Match 50.8
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                1 FQGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  82 FEAVVDRVRLVF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||| :|||:
246 RGVATSVRFL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 QGVAQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-953-349-3915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-196-749-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILLE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILLING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN version 3.3
                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                        Score 31; DB 6; Length 249;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 7; Length 297;
Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 6; Length 250;
Pred. No. 34;
                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4132, Application US/11293697

Publication No. US20060105376A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TILE OF INVENTION: Novel full length cDNA

FILE REFERENCE: H1-A0106

CURRENT APPLICATION UNMBER: US/11/293,697

CURRENT FILING DATE: 2005-12-05

PRIOR APPLICATION NUMBER: US/10/108,260

PRIOR APPLICATION DATE: 2002-03-28
                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
; SEQ ID NO 1158
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Arabidopsis thaliana
US-10-953-349-1157
                                                                                                        50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.8%;
                                                                                        Query Match
Best Local Similarity 50.0
Best Local Similarity 50.0
                                                                                                                                                                                                          167 FEAVVDRVRLVF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 FEAVVDRVRLVF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4132
LENGTH: 297
                                                                                                                                                                           1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 GVVFNVRVVF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-11-293-697-4132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                              US-10-953-349-1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-293-697-4132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1157
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                            ઠ
                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

RESULT 10

```
Subjunction 195, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

TITLE REPERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT PILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

FERRIT OF 1915
Sequence 9204. Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITTLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 6; Length 315;
Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 6
Pred. No. 51;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 160, Application US/10196749
; Publication No. US20060094864A1
                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT , ORGANISM: Arabidopsis thaliana US-10-953-349-3915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                    50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang, Zemin
```

```
6, 2006, 00:12:56
    APPLICANT: ALEXANDROV, Nickolai et al
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                     h 50.8%;
Similarity 50.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 FEAVVDRVRLVF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|| |||
513 GLAQGVRF 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GVAQNVRF 10
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June Job time: 3.82414 secs
                                                                                                                                                                                                                                                                              US-10-953-349-9202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-11-316-521-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-316-521-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILIG DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40222
SOFTWARE: Patentin version 3.3
SEQ ID NO 9203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 6; Length 400;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 6; Length 392;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior Application data removed - See File Wrapper or PALM. WINDER OF SEQ ID NOS: 612
SEQ ID NO 160
LENGTH: 392
FILE REFERENCE: P3430R1C340

CURRENT APPLICATION NUMBER: US/10/196,749

CURRENT FILING DATE: 2002-07-16

PRIOR PLING DATE: 2002-01-15

PRIOR PLING DATE: 2002-01-15

PRIOR PLING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR PLING DATE: 1997-0-10-17

PRIOR PRIOR DATE: 1997-10-24

PRIOR PLING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063540

PRIOR PLING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063541

PRIOR PLING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063541

PRIOR PLING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 9202, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-953-349-9203

Sequence 9203, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Arabidopsis thaliana US-10-953-349-9203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 FEAVVDRVRLVF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.8
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVAQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 FRGVAASFRF 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FQGVAQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Homo Sapien
US-10-196-749-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-953-349-9202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
Sequence 39, Application US/11316521

Sequence 39, Application WS/11316521

Publication No. US20060111848A1

GENERAL INPORMATION:

APPLICANT: Carlow, Clotilde K.S.

TITLE OF INVENTION: Identification and Use of Cofactor Independent Phosphoglycerate

TITLE OF INVENTION: He Same

FILE REFERENCE: NEB-230-PCIP-US

CURRENT PILING DATE: 2005-12-22

PRIOR APPLICATION NUMBER: US 60/483,566

PRIOR APPLICATION NUMBER: PG-27

PRIOR APPLICATION NUMBER: PG-27

PRIOR APPLICATION NUMBER: PG-27

PRIOR APPLICATION NUMBER: PG-27

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin version 3.2

SEQ ID NO 39

LENGTH: 557
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY TITLE OF INVENTION: ENCONDED THERBY TITLE OF INVENTION: ENCONDED THERBY CURRENT APPLICATION NUMBER: 105/10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: Patentin version 3.3 SEQ ID NO 9202 LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.8%; Score 31; DB 7; Length 557; 75.0%; Pred. No. 80; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 6; Length 401;
Pred. No. 56;
1; Mismatches 5; Indels
```

```
GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                        Copyright
```

Į,	
mode.	
M8	
using	
search,	
protein	
protein	
Ö	

22:08:53; Search time 91.1379 Seconds (without alignments) 60.201 Million cell updates/sec 5, 2006, June Run on:

US-10-030-735-28 59 1 FQGVLQNVRFVA 12 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 seqs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* A_Geneseq_8 Database

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2001s:* geneseqp2002s:* geneseqp1990s:* geneseqp2000s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

SUMMARIES

ID Description	AAB35366 Alpha3bet		AAB35352 Alpha3bet	AAB35378 Alpha3bet	ABG72834 Thrombosp	ADL70641 Human thr	ADQ39359 Human myo	_	AAU02916 Angiotens	AAB43602 Human can	AAU02915 Angiotens	ADN02474 TSF polyp	AAU02914 Angiotens	AAU02913 Angiotens	AAB00042 Human thr	AAU74771 Human thr	ABB82285 Human thr	AAB74450 Aab74450 Human var	AAB90800 Aab90800 Human she	AAE25030 Aae25030 Human thr	AAU75315 Human thr	ABD96780 AMD96780 HILL
82	4	4	4	4	9	8	8	œ	4	m	4	7	4	4	m	Ŋ	Ŋ	4	4	Ŋ	Ŋ	¥
Length	12	11	12	12	12	240	432	432	459	466	546	548	555	731	1152	1152	1152	1170	1170	1170	1170	1170
ដូ	100.0	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	•	93.2	93.2	93.2
Score	. 65	55	55	22	22	55	55	55	55	55	55	55	55	55	25	25	22	22	55	55	22	55
ΙZ	1	7	e	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22

1170 6 ABG74673 1170 6 AAE36228 1170 7 ABR62059 1170 8 ADJ76124 1170 8 ADJ76124 1170 8 ADJ76236 1170 8 ADJ7639 1170 8 ADG29358 1170 8 ADG29358 1170 8 ADG29358 1170 8 ADG39356 1170 8 ADG39356 1170 9 AEB87781 1170 9 AEB87781 1170 9 AEB87781 1170 9 AEB87781 1170 9 AEB87781 1170 9 AAE95373 12 4 AAB35364 12 4 AAB35364 12 4 AAB35317	Abg74673 Human THB Aae36228 Human THB Abr62059 Human thr Adm39852 Cancer/an	Marker Marker Human	Ad135874 Human Chr Adq26070 Thrombosp Adp54179 Human PRO Adq39358 Human myo	Adg39356 Human myo Adg39355 Human myo Ad221688 Thrombosp Aeb87781 Human thr Aeb46751 Human thr	Alpha3 Alpha3 Alpha3	Aab35364 Alpha3bet Aab35374 Alpha3bet Aab35347 Alpha3bet
	ABG74673 AAE36228 ABR62059 ADN39852	ADJ76124 ADJ75296 ADL70639	ADL35874 ADQ26070 ADP54179 ADQ39358	ADQ39356 ADQ39355 ADZ21688 AEB87781 AEB46751	AAB35373 AAB35381 AAB35355	AAB35364 AAB35374 AAB35347
					000	
			93.2.2	93.2	88.1 88.1 86.4	86.4 4.6 4.4 4.4
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ក ស ល ល ល ល	ល ល ល ល ល ល ល ល				51 51
555 557 558 558 558 558 558 558		3038	3 3 3 1 1 4 3 3 4 1 1 1 1 1 1 1 1 1 1 1	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		4 4 4 ይ 4 3

ALIGNMENTS

Alpha3betal integrin binding peptide #31. Ą. AAB35366 standard; peptide; 12 (first entry) 08-MAY-2001 AAB35366; AAB35366

Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.

Synthetic.

WO200105812-A2.

25-JAN-2001.

12-JUL-2000; 2000WO-US018986.

99US-0144549P. 15-JUL-1999; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Krutzsch HC; Roberts DD,

WPI; 2001-182656/18.

New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and cancer

Claim 4; Page 34; 84pp; English.

The present invention provides a number of peptides which bind to alphaibetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention

Sequence 12 AA;

```
Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                  Sequence 12 AA;
                                                            WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200105812-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999;
                                                                                                                 15-JUL-1999;
                                                                                                                                                    Roberts DD,
                                                                              25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001
                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB35378;
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                  cancer.
                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                           AAB35378
δ
                                                                                                                                                                                                                                                                                                                                                                                     원
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of peptides which bind to alphaibetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention
                                                                                                                                                                    Alpha3beta1 integrin, angiogenesis, cell proliferation, cancer, diabetic retinopathy, restenosis, atherosclerosis, rheumatoid arthritis, macular degeneration, psoriasis, cell adhesion, cell motility.
                                                                                                                                                                                                                                                                                                                                                   New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
100.0%; Score 59; DB 4; Length 12; 100.0%; Pred. No. 0.00015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 11;
                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.00085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 4;
Pred. No. 0.0008
0; Mismatches
                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha3betal integrin binding peptide #17.
                                                                                                                                                    Alpha3betal integrin binding peptide #25.
                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Æ
                                                                                                AAB35360 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2.
100.08; FL
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 34; 84pp; English.
                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB35352 standard; peptide; 12
                                                                                                                                                                                                                                                             12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                               99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-2001 (first entry)
                                                                                                                                   08-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                  Roberts DD, Krutzsch HC;
                                                 FOGVLQNVRFVA 12
                 12; Conservative
                                   FOGVLONVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGULQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11 AA;
                                                                                                                                                                                                                            WO200105812-A2
                                                                                                                                                                                                                                                                               15-JUL-1999;
                                                                                                                                                                                                                                             25-JAN-2001
                                                                                                                                                                                                          Synthetic
Query Match
Best Local S
Matches 12
                                                                                                                   AAB35360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB35352
                                                                                                                                                                                                                                                                                                                                                                                cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
                                                                               RESULT 2
                                                                                         AAB35360
                                                   g
                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SXSXSXS 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                   ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
Alpha3beta1 integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides that bind to or are recognized by alpha3-betal integrins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 4; Lostred. No. 0.00093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha3betal integrin binding peptide #43.
                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%; bcc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB35378 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0144549P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                                                                                   12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                                                                             99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLQNVRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
tes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention
```

renal cell carcinoma, colon cancer, especially small-cell lung cancer (SCLC), or a melanoma. The present sequence represents the amino acid sequence of the thrombospondin-1 sequence containing synthetic peptide which binds to alpha-3-beta-1 integrin

ö

Gaps

ö

Length 12; 0; Indels

93.2%; Score 55; DB 6; L 100.0%; Pred. No. 0.00093; ive 0; Mismatches 0;

93.2%;

11; Conservative

Query Match Best Local Similarity Matches 11; Conserv

Sequence 12 AA;

8888888

ઠે 셤

```
New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                            WPI; 2001-182656/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG72834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                       cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
ABG72834
ID ABG72834

셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

```
ö
                                                                   The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to diagnosing cancer other than prostate cancer in a male mammal, comprising assaying a test sample for increased level of semenogelin, or cancer in a female by assaying for the presence of semenogelin. Administering a semenogelin protein or polypeptide fragment or a semenogelin-specific antibody or active fragment, or a recombinant vector expressing the protein or antibody, is useful for inducing an immune response to a cancer in a mammal, where the cancer is not prostate cancer and semenogelin is a marker. The invention is used to diagnose cancer, particularly of epithelial origin such as lung cancer, papillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A new diagnosis for cancer other than prostate cancer in a mammal useful to detect cancer including lung cancer, particularly small cell lung cancer and melanoma comprises detecting semenogelin in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; thrombospondin-1; cytostatic; immunostimulant; cancer; epithelial cancer; lung cancer; papillary renal cell carcinoma; colon cancer; small-cell lung cancer; SCLC; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                93.2%; Score 55; DB 4; Length 12; 100.0%; Pred. No. 0.00093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombospondin-1 sequence containing synthetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES
Example 2; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG72834 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 14; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-2002; 2002WO-US010535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2001; 2001US-0281994P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-103329/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                         invention
                                                                                                                                                                                                                                                                                                                                                Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200281630-A2
```

```
The present sequence is that of the N-terminal domain of human thrombospondin-1 (TSP) ADI/70639. The invention relates to TSP fragments (80-100, 40-55 or 20-35 kDa mol.vd.) found in plasma, and their use in clinical assays for cancer and for generation of antibodies and other binding agents. A method that distinguishes TSP from a TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion as a target for a binding molecule, e.g. an antibody, to obtain a quantitation of TSP plus TSP fragment or portion; (2) using an epitope present in TSP but not in the fragment or portion; 05 using an equantitation of TSP only; and (3) using the difference between (1) and (2) as a quantitation of the amount of TSP fragment or portion. Suitable epitopes are provided ADI/7062-ADI/70639. Detection or quantification of the TSP fragment or portion is performed in order to detect the presence, or monitor the course, of a disease or condition selected from cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes.
                                                                                                                                                                         Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                151. .164 // /note= "Fibrinogen binding region"
                                                                                                                                                                                                                                                                                                                "Heparin binding region"
                                                                                                                                                                                                                                                                           "Heparin binding region"
                                                                                                                                      Human thrombospondin-1 N-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 40; 76pp; English.
                                                                                                                                                                                                                                              Location/Qualifiers
                              ADL70641 standard; protein; 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-AUG-2002; 2002US-0405494P.
21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2003; 2003WO-US026023.
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                            .82
                                                                                                                                                                                                                                                                  23. .32
/note= '
                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WILL/) WILLIAMS K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-226901/21.
                                                                                                                                                                                                                                                                                                                                                                                     WO2004018995-A2.
                                                                                                                                                                                                             Homo sapiens
                                                                                                      20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-2004
                                                                   ADL70641;
                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                    Region
                  ADL70641
RESULT
```

```
cremal failure, remal disease, atopic dermatitis, vasculitis, acute vasculitis, remal allograff, asthma, diabetes mellitus, myocardial inforcation, liver disease, splenectomy, dermatchyoshis, polyareritis nodosa, systemic lupus erythematosus, lupus erythematosus, Kawasaki syndrome, non-specific vasculitis, juvenile rheumatoid arthritis, chemical purpura, an inflammatory condition, a condition associated with platelet activation, a condition associated with nintravascular platelet activation, a condition associated with intravascular coagulation, a condition associated with clotting, a condition associated with nintravascular coagulation, a condition associated with consumption of platelets, heparin cativation, a condition associated with nintravascular coagulation, a condition associated with nintravascular coagulation, a condition associated with section, an appartame reaction, and acondition associated with actopic dermatitis, eczema, hypersonsitivity, scleroderma, conditions associated with plugging of reaction, an aspartame reaction, and a condition associated with a cryofibringen, carcinoma, lamban, lauren, cancer, inthe vascular invasion, internal cancer, is the respiratory system, of cancer, is encer, is encer, is encer, interpreted with a cryofibringen, and according the respiratory system, intervale cancer, is encer, intervale cancer, intervale canc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human myocardial infarction-associated gene derived protein, SEQ ID 1022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%; Score 55; DB 8; Length 240
100.0%; Pred. No. 0.027;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iakoubova O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ39359 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-ASEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 FQGVLQNVRFV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Devlin JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004058052-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ39359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
               ð
```

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's converse firsk for myocardial infarction in the individual. The invention further comprises an isolated nucleic acid molecule comprising at least cortiguous nucleotides where one of the nucleotides is an SNP given in further comprising an amino acid sequence given in the specification one of the mucleotides is an SNP given in the specification and sequence given in the specification, an isolated polypeptide or its antigen-binding comprising an amino acid sequence given in the specification; an amplified polymucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in containing a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and contained for identifying an agent useful in treating or preventing an composition for treating or preventing myocardial infarction. The novel detection may be used in gene therapy. The composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction. This sequence was not shown in the specification. The sequence was not shown in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human myocardial infarction-associated gene derived protein, SEQ ID 1020.
                                                            Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.2%; Score 55; DB 8; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No. 0.051; ive 0; Mismatches 0; Indels
                                                                                                                                                         Claim 10; SEQ ID NO 1022; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ39357 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-0434778P.
2003US-0453135P.
2003US-0466412P.
2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiant; gene therapy; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
WPI; 2004-533949/51.
                     N-PSDB; ADQ38531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004058052-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-2002; 2
10-MAR-2003; 2
30-APR-2003; 2
23-SEP-2003; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ39357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ39357
ð
```

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acide, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention curticates an isolated nucleic acid molecule comprising at least comprising an amino acid sequence given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification, an antibody that specification and into the pypeptide or its antigen-binding comprising an amino acid sequence given in the specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in cappendia, a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting an variant polypeptide; and a myocardial infarction. The novel detecting an variant polypeptide; and a myocardial infarction. The novel detection method has an increased or method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction. This composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction. This sequence represents the protein of a human myocardial infarction. This sequence represents the protein of a human myocardial infarction. This sequence was not shown in the specification. The sequence has come from a sequence was not shown in the specification. The sequence has come from a electronic sequence listing downloaded from the sequence has come from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclarosis, cancer; myocardial infarction, coronary arterial thrombosis, renal disease; dabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme (ACEV) splice variant protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.2%; Score 55; DB 8; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Core 50,
Pred. No. 0.051;
Pred. no. 0.051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. v.v.
                                                                                                                                                                                                                                                                                                    Claim 10; SEQ ID NO 1020; 145pp; English.
                                                                         Iakoubova O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU02916 standard; protein; 459 AA.
                                                                                                                                                                                                                                                    the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FQGVLQNVRFV 11
                                                                         Cargill M, Devlin JJ,
                       (APPL-) APPLERA CORP.
                                                                                                                           WPI; 2004-533949/51.
                                                                                                                                                N-PSDB; ADQ38529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU02916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                유
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucapon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various of sisoacts including cardiovascular diseases such as artriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                     Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthitic; antiviral; dermatological; autithyroid; antiallergic; antiacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haemacopoletic cell disorder; autoimmune disorder; haemacopoletic cell disorder; autoimmune disorder; haemostetic; cardiovascular disease; organ rejection; haemostetic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.2%; Score 55; DB 4; Length 459; 100.0%; Pred. No. 0.055; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cancer associated protein sequence SEQ ID NO:1047.
                                                                                                                                                                                                                                                                                    Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 0.0 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB43602 standard; protein; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 16; 519pp; English.
                                                                                                                                       17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                             99IL-00132978.
99IL-00133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVLONVRFV 11
                                                                                                                                                                                                                                              (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                    Levine Z, David A,
                                                                                                                                                                                                                                                                                                                           WPI; 2001-336004/35,
N-PSDB; AAS06016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 459 AA;
                                                            WO200136632-A2
                   Homo sapiens.
                                                                                                                                                                                17-NOV-1999;
10-DEC-1999;
                                                                                                  25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB43602
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
```

Gaps

ø

```
AAC77607 to AAC7848 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antialergic; antiacthritic; anticlammatory; antithyroid; antiallergic; antibacterial; antiviral; cermatological; neuroprotective, cardiant; thrombolytic; coagulant; nootropic; antipprotective, cardiant; thrombolytic; coagulant; nootropic; antipprotective, cardiant; thrombolytic; coagulant; nootropic; antipprotective, cardiant; thrombolytic; coagulant; cootropic; antipprotective, and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or meliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating crimume cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, differentiation or mobilisation of cincinn, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to the present invention of the exemplification of the processor invention of the present invention o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acids comprising sequences encoding peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angiotensin converting enzyme (ACEV) splice variant protein #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 55; DB 3; Lengtn acc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 1636-1638; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU02915 standard; protein; 546 AA.
                                                                                                                                                                              08-MAR-2000; 2000WO-US005882.
                                                                                                                                                                                                                                 99US-0124270P
                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 FQGVLQNVRFV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGULONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention
                                                                                                                                                                                                                                                                                                                                     Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC77811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 466 AA;
                                                                           WO200055350-A1.
                          Homo sapiens.
                                                                                                                                                                                                                               12-MAR-1999;
                                                                                                                              21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
AAU02915
ID AAU02915
XX
AC AAU02
XX
XX
DT 12-SE
XX
XX
DE Angio
XX
XM Angio
XM Plate
XM Callu
XM Callu
XM Callu
XM Callu
XM Callu
XM Callu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic caids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various clasorates including cardiovascular diseases such as atteriosclerosis, mycardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenovirus vector; anti-neoplastic; TSF polypeptide; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%; Score 55; DB 4; Length 546; 100.0%; Pred. No. 0.067; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Azar I, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN02474 standard; protein; 548 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 15; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                99IL-00132978
                                                                                                                                                                                                                                                                                                                                                                                                                                                   99IL-00133455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-336004/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS06015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSF polypeptide.
                                                                                                                                                                                                             WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-2004
                                                                                                                                                                                                                                                                             25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CN1401387-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN02474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN02474
          $$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$\times$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

12-MAR-2003

```
AAU02913
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                      mediated anti-neoplastic composition is prepared through cloning the cDNA sequence from the human peripheral blood cell by specific primer and reverse transcription-polymerase chain reaction (RT-PCR) method for coding TSF polypeptide, construction in human embryonic kidney cell 293 by AdEasy system, and packaging and expressing the recombinant adenovirus vector of TSF. It can suppress the growth and transfer of cancer. The present sequence represents the TSF polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; mycoardial infarction; coronary arterial thrombosis; rand disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                              present invention relates to a novel recombinant adenovirus vector
                                                                                                                                                         Tumor suppressing polypeptide TSF and gene therapy vector composition.
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Angiotensin converting enzyme (ACEV) splice variant protein #14.
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 7; Length 548;
Pred. No. 0.067;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            David A, Azar I, Khosravi R, Bernstein J;
                                                               (TAID-) TAIDA LIFE SCI TECH RES CENT HEMATOLOGY.
                                                                                                                                                                                                                                                                                                                                                 93.2%; Sco...
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                  Claim 2; SEQ ID NO 1; 13pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU02914 standard; protein; 555 AA.
            21-AUG-2002; 2002CN-00129408
                                     21-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99IL-00132978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                   208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COMP-) COMPUGEN LTD
                                                                                                                  WPI; 2003-469302/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-336004/35
                                                                                                                                N-PSDB; ADN02475.
                                                                                                                                                                                                                                                                                                                                  Sequence 548 AA;
                                                                                          Han Z, Liu P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU02914;
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                       Matches
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
(MCEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated mucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as mmune compounds cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; multiple sclerosis; immune disorder; sarcoidosis; notatione complex nephritis; deep vein thrombosis; vascular disorder; sarcoidosis; vascular disorder; asbestosis.
                                               Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                  splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiotensin converting enzyme (ACEV) splice variant protein #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.2%; Score 55; DB 4; Length 555;
100.0%; Pred. No. 0.068;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                  The sequence represents an angiotensin converting enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Levine Z, David A, Azar I, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02913 standard; protein; 731 AA.
                                                                                                                                                Claim 4; Fig 14; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99IL-00132978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-336004/35
N-PSDB; AAS06014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
```

N-PSDB; AAS06013. 01-FEB-1999; Region Region Region Matches RESULT 15 à g

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acididate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                  Claim 4; Fig 13; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 731 AA;
```

93.2%; Score 55; DB 4; Length 731; 100.0%; Pred. No. 0.092; ive 0; Mismatches 0; Indels 11; Conservative 208 FQGVLQNVRFV 218 7 1 FQGVLQNVRFV Query Match Best Local Similarity

ö

Gaps

; 0

AAB00042 standard; protein; 1152 AA. Human thrombospondon-1 (TSP-1). 08-NOV-2000 (first entry) AAB00042;

TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection; glaucoma.

Homo sapiens

361. .416 /label= Type 1 repeat region Location/Qualifiers

WO200044908-A2

03-AUG-2000

01-FEB-2000; 2000WO-US002482

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

Lawler JW;

WPI; 2000-514823/46.

```
New nucleic acids are described which encode a protein comprising the second and third type I repeats of human TSP (thrombospondin)-1, but not the TGF (transforming growth factor)-beta acityvation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerase chain reaction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating angiogenesis related diseases such as cancer (by reducing for treating angiogenesis related diseases such as cancer (by reducing for treating human immunodeficiency virus (HIV) infection. Anti-cating human immunodeficiency virus (HIV) infection. Anti-angiogenic therapy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                         Nucleic acids encoding chimeric proteins such as cartilage oligomeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                             matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%; Score 55; DB 3; Length 1152; 100.0%; Pred. No. 0.15; ive 0; Mismatches 0; Indels
                                                                                                                    Disclosure; Fig 1; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 FQGVLQNVRFV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

5, 2006, 22:24:59 completed: June ne : 91.1379 secs Search con Job time

```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

5, 2006, 22:25:22 ; Search time 13.9655 Seconds June Run on:

(without alignments) 82.675 Million cell updates/sec

US-10-030-735-28 59 1 FQGVLQNVRFVA 12 Perfect score: Title:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	thrombospondin 1 -	7	thrombospondin 1 p	æ	H+-transporting tw	Ca2+-transporting	protein envelope C	Ca2+-transporting	Ca2+-transporting	thrombospondin 2 p	thrombospondin 2 p	probable pilin, ty	probable 3-oxoacyl	3-oxoacyl-[acyl-ca	drug-export protei	reverse gyrase (to	polysialic acid tr	kpsT protein - Esc	hypothetical prote	ribosomal protein	hypothetical prote	hypothetical prote	hypothetical prote	neuraminidase, pro	two component resp	probable autotrans	probable transcrip	thrombospondin pre	hypothetical prote
SUMMARIES	ID		TSHUP1	A40558	E72462	D84938	S71168	D86402	T51925	T51926	TSHUP2	A42587	B75421	A64590	B71923	D86793	H69377	B42469	S12237	G84013	E64083	F69113	T34271	B89832	G95153	AE2929	AC0368	A98353	A39804	F96625
	DB	7	٦	7	~	7	7	~	7	~	-1	~	N	-	~	N	N	~	N	N	~	N	N	~	7	7	~	N	Н	~
	Guery Match Length	229	1170	1170	295	467	946	1020	1020	1020	1172	1172	186	247	247	454	1054	218	224	102	163	248	304	498	740	747	759	783	1178	82
d	Query Match	93.2	93.2	93.2	64.4	64.4	62.7	62.7	62.7	62.7	62.7	62.7	61.0	61.0	61.0	61.0	61.0	60.2	60.2	59.3	59.3	59.3	59.3	59.3	59.3	9.	59.3	6	e,	
	Score	55	22	22	38	38	37	37	37	37	37	37	36	36	36	36	36	35.5									35			
	Result No.	1	7	m	4	ស	9	7	80	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

probable imidazole	probable cell surf	NADH oxidase SP146	NADH oxidase (EC 1	probable protein k	zona pellucida gly	rep protein homolo	hypothetical prote	hypothetical prote	surfactin syntheta	laminin alpha-1 ch		hypothetical prote	_	hypothetical prote	mesY protein - Leu		
D81929	G95913	B95171	B98037	A84548	S70397	T02634	T05178	AE1864	I40486	S18253	T31048	B87397	C87403	H83708	\$52206		ALIGNMENTS
7	~	~	~	7	~	N	7	~	~	7	7	7	~	~	7		
212	219	459	459	465	715	1038	1308	1829	3587	3712	93	268	298	417	457		
57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	57.6	55.9	55.9	55.9	55.9	55.9		
34	34	34	34	34	34	34	34	34	34	34	33	33	33	33	33		
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45		

```
Chrombospondin 1 - bovine (fragment)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
Cispecies: 13-Jan-1996
Cispecies: 13-Jan-1996
Cispecies: Sispecies: Sispe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 229;
0.0024;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%; Score 55; DB 100.0%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

190 FQGVLQNVRFV 200 셤

RESULT 2

thrombospondin 1 precursor - human
C;Species: Homo sapiens (man)
C;Accession: A26155; A34274; A30140; A25812; A05172; A42527
R;Lawler, J; Hynes, R.O.
J, C41 Biol. 103, 1635-1648, 1986
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple cs
A;Reference number: A26155; MUID:87057617; PMID:2430973
A;Reference number: A26155; MUID:87057617; PMID:2430973
A;Residues: 1-1170 «LAW»
A;Reference number: A34274; MUID:89291870; PMID:2544587
A;Accession: A34274; MUID:89291870; PMID:2544587
A;Residues: 1-166 «LAM»
A;Residues: 1-160 «

```
Aritie: Characterization of the murine thrombospondin gene.
A; Fittle: Characterization of the murine thrombospondin gene.
A; Reference number: A40558; MUD:92128941; PMID:1774063
A; Reference number: A40558
A; Reference number: A40558
A; Residues: 1-1770 cLAW
A; Residues: 1-1770 cLAW
A; Residues: 1-1770 cLAW
A; Residues: 1-170 cLAW
A; Cross-references: UNIPROT: P35441; UNIPARC:UPI0000028012; GB:M62449; GB:M62450; GB:M62465
B; Bornstein, P.; Affi, D.; Devarayalu, S.; Framson, P.; Li, P.
B; Bornstein, P.; Affi, D.; Devarayalu, S.; Framson, P.; Li, P.
A; Reference number: A37905; MUD:90375546; PMID:2398070
A; Reference number: A37905
A; Accession: A37905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-490 cBOR>
A;Cross-references: UNIPARC;UPI000016D076; GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40;
B;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
B;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell characterization of mouse thrombospondin 2 sequence and expression during cell characterization by Richary: MUD:92147683; PMID:1371115
A;Residues: Dreliminary; not compared with conceptual translation
A;Residues: 1-1152, PV, 1154-1170 cLAH>
A;Residues: 1-1152, PV, 1154-1170 cLAH>
A;Residues: 1-1152, PV, 1154-1170 cLAH>
A;Cross-references: UNIPARC;UPI0000177A96; GB:M87276
A;Residues: 1-1152, PV, 1154-1170 cLAH>
A;Cross-references: UNIPARC;UPI0000177A96; GB:M87276
A;Residues: 1-1152, PV, 1154-1170 cLAH>
A;Cross-references: UNIPARC;UPI0000177A96; GB:M87276
A;Residues: 1-1152, PV, 1154-1170 cLAH>
B;Residues: 1-1152, PV, 1154-1170 cLAH>
A;Residues: 1-1152, PV, 1154-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable lippoic acid synthetase APE2344 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 31-Dec-2004
C;Accession: E72462
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K. NNA Res. 6, 83-101, 1999
A;Reference number: A72450; MuID:99310339; PMID:10382966
A;Accession: E72462
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A;Residues: 19-26,'X',28-37 < CHE>
A;Cross-references: UNIPARC: UP10000177A97
A;Cross-references: UNIPARC: UP10000177A97
C;Complex: homotrimer, disulfide linked
C;Complex: homotrimer, disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type I repeat homotrimer
C;Keywords: calcium binding; glycoprotein; homotrimer
F;19-1170/Product: thrombospondin 1 #status predicted <NAT>
F;19-1170/Product: thrombospondin 1 #status predicted <NAT>
F;378-429/Domain: thrombospondin type I repeat homology <THR1>
F;38-449/Domain: thrombospondin type I repeat homology <THR2>
F;491-547/Domain: EGF homology <EGF>
F;551-586/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9Y9E3; UNIPARC:UPI00005E2E9; DDBJ:AP000064; NID:g5105945; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar A;Reference number: S68787; MUID:96234006; PMID:8654563
A;Accession: S68787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 55; DB 2; Length 1170; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
Les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 FÓGVLÓNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Complex: homotrimer, disulfide linked
C; Function:
C; Function:
C; Function: participates in cell migration and adhesion, and in platelet aggregation
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc
C; Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F; 1-18/Domain: signal sequence #status predicted <AMT>
F; 19-1170/Product: thrombospondin 1 #status predicted <AMT>
F; 317-375/Domain: thrombospondin type 1 repeat homology <THR1>
F; 318-4-490/Domain: thrombospondin type 1 repeat homology <THR2>
F; 431-547/Domain: EGF homology <EGF1>
F; 551-586/Domain: EGF homology <EGF2>
F; 550-586/Domain: EGF homology <EGF2>
F; 520-586/Domain: EGF homology <EGF2>
F; 520-586/Domain: EGF homology <EGF2>
F; 520-586/Domain: EGF homology <EGGT2>
F; 520-586/Domain: EGF homology <EGGT2>
F; 520-7081/Eide bonds: #status predicted
F; 270, 274/Disulfide bonds: #status predicted
F; 200, 274/Disulfide bonds: interchain #status predicted
F; 210, 274/Disulfide bonds: interchain #status predicted
F; 105/Modified site: carbohydrate (Asn) (covalent) #status absent
                                                                              A; Molecule type: mRNA
A; Residues: 1-83, 'A', 85-522, 'A', 524-1170 < HEN>
A; Residues: 1-83, 'A', 85-522, 'A', 524-1170 < HEN>
A; Cross-references: UNTPARC:UPI0000038AB1; EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID
A; Cross-references: Untparc:Upi0000038AB1; EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID
B; Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A; Fitle: Partial amino acid sequence of human thrombospondin as determined by analysis of A; Reference number: A25812; MUID:8715792; PMID:3030396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-83, Ar, 485-397 <KOB>
A;Residues: 1-83, Ar, 485-397 <KOB>
A;Cross-references: UNIPARC:UPI000016B0CA; GB:M25631; NID:G538353; PIDN:AAA36741.1; PID:
R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
R;Dixit, V.M.; Hennessy, S.W.; Bant, G.A.; Rotwein, P.; Frazier, W.A.
A;Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-83, A', 85-374, RC' <DIX>
A; Residues: 1-83, A', 85-374, RC' <DIX>
A; Residues: 1-83, A', 85-374, RC' 
A; Cross-references: UNIPARC:UPIO00016B140; GB:M14326; NID:g340005; PIDN:AA61237.1; PII
A; Note: parts of this sequence, including the amino end of the mature protein, were det
R; Sun, X.; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 119, 691-701, 1992
A; Tille: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A; Reference number: A42927; MUID:92348511; PMID:1379247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787
R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.2%; Score 55; DB 1; Length 1170;
100.0%; Pred. No. 0.014;
iive 0; Mismatches 0; Indels
A; Reference number: A30140; MUID:89139590; PMID:2918029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Note: Cys-992 is shown to have a free sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: GDB:THBS1; TSP1; TSP
A,Cross-references: GDB:120438; OMIM:188060
A,Map position: 15q15-15q15
A,Introns: 23, A,Note: the list of introns may be incomplete C,Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: protein
A,Residues: 987-1003 <SUN>
A,Cross-references: UNIPARC:UP100001742C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111111111
208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A42927
```

원 ò

```
C; Accession: D86402
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, Y.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT:Q37145; UNIPARC:UP10000162EF1; GB:AE005172; NID:g10998927; P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 1
C;Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding dome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T51925
R;Huang, L.; Berkelman, T.; Franklin, A.B.; Hoffman, N.B.
Proc. Natl. Acad. Sci. U.S.A. 90, 10066-10070, 1993
A;Title: Characterization of a gene encoding a Ca(2+)-ATPase-like protein in the plastid A;Reference number: Z25866; MUID:94052104; PMID:8234257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding dome; Keywords: chloroplast; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ca2+-transporting ATPase (EC 3.6.3.8) PEAl [imported] - Arabidopsis thaliana chloroplast N;Alternate names: envelope Ca2+-ATPase C;Species: chloroplast Arabidopsis thaliana (mouse-ear cress) C;Species: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1020 < HUDA
A;Residues: 1-1020 < HUDA
A;Cross-references: UNIPROT:Q37145; UNIPARC:UP1000016D30B; EMBL:L08468; PIDN:AAD10211.1
A;Experimental source: cultivar Columbia
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                           protein envelope Ca2+-ATPase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                Gaps
                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 2; Length 1020; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 1020;
      DB 2; Length 946;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.7%; Score 37; DB
58.3%; Pred. No. 51;
tive 3; Mismatches
                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
      Score 37;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.7%;
58.3%;
      62.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|:|:|
954 FKGILKNYVFVA 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.7
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                     |:|:|:|
880 FKGILKNYVFVA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQGVLQNVRFVA 12
|:|:|:| ||
                                                                                                                       1 FQGVLQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGULQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1020 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Genome: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: T51925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: PEA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S71168
S71168
N.alternate names: envelope C23.6.3.8) ACA1 precursor - Arabidopsis thaliana
N.alternate names: envelope C32-ATPase
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
C; Accession: S71168; S71167
B; Hundi, L.; Berkelman, T.; Franklin, A.E.; Hoffman, N.E.
submitted to the EMBL Data Library, December 1992
A; Description: Molecular cloning and characterization of a chloroplast envelope Ca2+-ATE
A; Reference number: S71167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H+-transporting two-sector ATPase (EC 3.6.3.14), flagellum-specific [imported] - Buchner C; Species: Buchnera sp. C; Species: Buchnera sp. C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004 C; Accession: B4938 R; Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H. Nature 407, 81-86, 2000 A; Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A; Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       펍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: fli1; BU076
C,Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. Reference number: A84930; MUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .Molecule type: mRNA
.Residues: 1-87,'S',89-726,'I',728-946 <HUZ>
.Cross-references: UNIPARC:UPI000016DBCE; EMBL:D13983; NID:g493621; PIDN:BAA03090.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-946 <HUA>
A;Cross-references: UNIPARC:UPI000016DAFA; EMBL:D13984; NID:g471088; PIDN:BAA03091.1;
A;Accession: S71167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 59/3; 78/1; 654/3; 707/3; 765/1; 864/3
C;Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding
C;Keywords: chloroplast; hydrolase
F;12-71/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;12-946/Product: Ca2+-transporting ATPase #status predicted <MAT>
F;55-750/Domain: ATPase nucleotide-binding domain homology <ATN>
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-467 <STO>
A;Cross-references: UNIPARC:UPI000005E44F; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 467;
                                                                                                                                                  Score 38; DB 2; Length 295;
Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 2;
Pred. No. 14;
3; Mismatches
                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                     64.4%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.4%;
60.0%;
      Experimental source: strain K1
                                                             A;Gene: APE2344
C;Superfamily: lipoyl synthase
                                                                                                                                                                                                                                                                                                        138 FQGVEEHVRLVA 149
                                                                                                                                                                              Best Local Similarity 66.7
Matches 8, Conservative
                                                                                                                                                                                                                                                                       1 FQGVLQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|:| |:||
10 FRGILMNLRF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLONVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Reference number: A(A,Accession: D84938
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S71168
                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: ACA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
                                    C,Genetics
                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

염

```
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;435-5498/Domain: thrombospondin type 1 repeat homology <THR3>
F;535-588/Domain: BGF homology <BGFF1>
F;552-691/Domain: BGF homology <BGFP3-
F;52-691/Domain: BGF homology <BGF>
F;52-691/Domain: BGF homology <BGF>
F;52-691/Domain: BGF homology <BGF>
F;52-691/Domain: BGF homology care
F;52-691/Domain: BGF homology care
F;52-691/Domain: BGF homology care
F;52-691/Bomain: BGF homology care
F;56-70/Disulfide bonds: #status predicted
F;26-70/Disulfide bonds: interchain #status predicted
F;26-70/Disulfide bonds: homology care
F;26-70/Disulf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Status: preliminary, not compared with conceptual translation
A/Status: preliminary, not compared with conceptual translation
A/Status: preliminary,
Nolecule type: nucleic acid
A/Rolecule type: W.; MYESTCOM, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
J. Biol. Chem. 266, 12821-12824, 1991
A/Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
A/Rocession. A39851
A/Accession. A39851
A/Acces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable pilin, type IV - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B75421
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F.White, O.; Eisen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maß. Simith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A42587

Librombospondin 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 04-Mar-1993 #sequence_revision: Wi; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
A; Diol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell A;Reference number: A42587; Mull: 91311115
A;Accession: A42587, Mull: A42587; Mull: 91311115
A;Accession: A42587, Mull: A42587; Mull: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.7%; Score 37; DB 2; Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 59;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.7%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|:|||| |
202 FRGLLQNVHLV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 FRGLLÓNVHLV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
B75421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                            Ca2+-transporting ATPase (EC 3.6.3.8) PEAL [imported] - Arabidopsis thaliana chloroplast NyAlternate names: envelope Ca2+-ATPase CiSpecies: chloroplast Arabidopsis thaliana (mouse-ear cress) CiSpecies: chloroplast Arabidopsis thaliana (mouse-ear cress) CiDate: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 31-Dec-2004 CiAccession: T51926 RiHuang, L.; Berkelman, T.; Franklin, A.B.; Hoffman, N.E. Proc. Natl. Acad. Sci. U.S.A. 90, 10066-10070, 1993 A; Title: Characterization of a gene encoding a Ca(2+)-ATPase-like protein in the plastid A; Accession: T51926 A; Accession: T51926 A; A; Accession: T51926 A; Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cipecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Ciscesion: A47379; A42173
RilaBell, T.L.; Byers, P.H.
Genomics 17, 225-229; 1993
Airtle: Sequence and characterization of the complete human thrombospondin 2 cDNA: pote A; Reference number: A47379; MUID:94010892; PMID:8406456
A; Residues: 1-1172 < LAB>
A; Residues: 1-1172 < LAB>
A; Residues: 1-1172 < LAB>
A; Residues: 1-172 < LAB>
A; Residues: 1-172 < LAB>
A; Residues: 1-1429; 1992
A; Trile: Thrombospondin II: partial cDNA sequence, chromosome location, and expression characterior number: A42173; MUID:92217961; PMID:1559694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Genec: GDB:THBS2; TSP2
A;Cross-references: GDB:128789; OMIM:188061
A;Cross-references: GDB:128789; OMIM:188061
A;Cross-references: GDB:128789; OMIM:188061
C;Complex: homorrimer, disulfide linked
C;Function:
C;Function:
C;Function: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Genome: chloroplast
A;Introna: 59/3; 78/1, 728/3; 781/3; 839/1; 938/3
C;Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding dom
C;Keywords: chloroplast; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1020 <HUA>
A;Cross-references: UNIPROT:Q37145; UNIPARC:UPI0000125171; EMBL:L08469; PIDN:AAD10212.1
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 560-1172 - CLA2>
A;Cross-references: WNIPARC:UPI00001742C1; GB:M81339
A;Experimental source: fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.7%; Score 37; DB 2;
58.3%; Pred. No. 51;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         954 FKGILKNYVFVA 965
                               FKGILKNYVFVA 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.7
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQGVLQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: PEA1
```

C,Genetics:

8

Gaps

ö

DB 2;

```
Ribolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg. A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT:Q9CFW6; UNIPARC:UPI00000C6A19; GB:AE005176; PID:g12724331; P
A,Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug-export protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
                       F;6-186/Domain: short-chain alcohol dehydrogenase homology <SAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2; Length 454;
Pred. No. 34;
2; Mismatches 1; Indels
                                                                                                                                                                                       Pred. No. 17;
4; Mismatches
                                                                                                                                       Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: yniG
C;Superfamily: multidrug-efflux transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: June 5, 2006, 22:45:02
Job time: 14.9655 secs
                                                                                                                                 Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         171 YEGALRNIRF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 GILKNHRFVA 260
                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GVLQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: D86793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75421
A;Status: preliminary
A;Retus: preliminary
A;Residues: 1-186 < WHI>
A;Residues: 1-186 < WHI>
A;Cross-references: UNIPROT:Q9RUZ7; UNIPARC:UPI0000D3E03; GB:AE001971; GB:AE000513; NIC G;Genetics: strain R1
A;Genetics: A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loffus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A.Authors: Wallin, B.; Hayes, W.S.; Boxodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A.Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A.Reference number: A64520; MuID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-247 <TOM>
A;Residues: 1-247 <TOM>
A;Cross-references: UNIPROT:025286; UNIPARC:UPI00000D3178; GB:AE000570; GB:AE000511; NID
C;Cusperfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: fatty acid biosynthesis; NAD; oxidoreductase
F;6-186/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable 3-oxoacyl-{acyl-carrier-protein} reductase (EC 1.1.1.100) - Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - Helicobacter pylori (strain C; Species: Helicobacter pylori (strain C; Species: Helicobacter pylori (strain J) A; Variety: strain J99 (c; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004 (c; Accession: B71923 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004 (c; Accession: B71923 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004 (c; Accession: B7192) #text_change 05-Oct-2004 (c; Accession: B7192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: B71923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:09ZLSO; UNIPARC:UPI0000003648; GB:AE001484; GB:AE001439; NII
A,Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology C;Reywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.0%; Score 36; DB 1; Length 247; 50.0%; Pred. No. 17; 1:ve 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 YEGALRNIRF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLONVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 OGVLENVR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 QGVLQNVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-247 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
```

ö

Gaps



```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

	1 Seconds ts) ell updates/sec
OM protein - protein search, using sw model	June 5, 2006, 22:09:41; Search time 108.931 Seconds (without alignments) 101.901 Million cell updates/sec
OM protein	Run on:

1 FQGVLQNVRFVA 12 US-10-030-735-28 59 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2849598 segs, 925015592 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q28194 bos taurus	Q7sy84 xenopus lae	Q28178 bos taurus	P07996 homo sapien	P35441 mus musculu	Q3tr40 mus musculu	Q71sa3 rattus norv	Q80yq1 mus musculu	Q8cgb2 mus musculu	P35448 xenopus lae			Q48758 tetraodon n	Q5u903 sus scrofa			Q4p665 ustilago ma		Q467v1 methanosarc	Q8tlx6 methanosarc	_	_	_	Q411m8 burkholderi	Q5vh52 ciona intes	Q2xgs4 pseudomonas	Q88qb0 pseudomonas	_	_	_	Q5fa21 neisseria g
QI	Q28194_BOVIN	Q7SY84_XENLA	TSP1 BOVIN	TSP1 HUMAN	TSP1 MOUSE	Q3TR40 MOUSE	Q71SA3_RAT	Q80YQ1 MOUSE	Q8CGB2 MOUSE	TSP1 XENLA	Q59E99 HUMAN	Q5SPG5_BRARE	Q4S758_TETNG	Q5U903_PIG	Q4RLR5_TETNG	Q4RQ74_TETNG	Q4P665 USTMA	QBPRY3_METMA	Q467V1 METBA	Q8TLX6 METAC	Q3CJK9 THEET	Q3F1U8_9BURK	Q44XL2_9BURK	Q4LLM8_9BURK	QSVH52_CIOIN	Q2XGS4_PSEPU	Q88QB0 PSEPK	Q2LZ43_DROPS	RL10_HAEDU	Q31IL6_THICR	Q5FA21_NEIG1
08	7	7							~								~	~	~	~							~	~	-	~	7
Length	229	496	1170	1170	1170	1170	1170	1171	1171	1173	1225	1090	1193	249	1171	1034	704	727	730	733	1549	713	713	713	1168	647	647	695	163	189	212
* Query Match	93.2	ë.	٠	93.2	93.2	93.2	٠	٠	93.2	•	93.2	•	84.7	83.1	83.1	76.3	71.2	71.2	71.2	71.2	71.2		6.		69.5	•			66.1	66.1	66.1
Score	55	55	25	55	55	55	55	55	52	55	55	20	20	49	49	45	42	42	42	42	42	41	41	41	41	40	40	40	39	39	39
Result No.	7	8	٣	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21		23	24	25	26	27	28	59	30	31

Q8isi2 oxytricha Q3vhw7 pelodictyon Q51310 geobacillus Q5avq8 aspergillus Q86nr6 drosophila Q42ua9 pseudomonas Q813C0 pseudomonas Q9vth0 drosophila Q4dwh6 trypanosoma Q722b9 trypanosoma Q722b9 trypanosoma Q722b9 trypanosoma Q6fxf4 candida g1a Q2ty18 aspergillus
Q81512_9STIC Q3VHW7_9CHLB Q5L310_GEOKA Q5AVQ8_EMENI Q86NR6_DROME Q4BH16_PSE14 Q4ZUA9_PSEU2 Q9VTHO_DROME Q4DWH6_TRYCR Q7ZZB9_TRYCR Q7ZZB9_TRYCR Q7ZZB9_TRYCR Q6FXF4_CANGA Q2TY18_ASPOR
0000000000000
232 3232 327 494 694 646 646 646 1034 1172 1172 1172
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
66666666666666666666666666666666666666

ALIGNMENTS

```
ö
                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                  Peige J.J.;
"Opposite regulation of thrombospondin-1 and corticotropin-induced secreted protein/thrombospondin-2 expression by adrenocorticotropic hormone in adrenocortical cells.";
J. Cell. Physiol. 167:164-172(1996).
                                                                                                                                                             Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia;
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 AA; 25015 MW; 90D9EBCE4E6B669C CRC64;
                                                                                                                                                                                                                                                                                                                                                            EMBL, X89511; CAA61682.1; -; mRNA.
PIR; S57957; S57957.
GO; GO:0005198; F:serructural molecule activity; IEA.
GO; GO:000155; F:cell addesion; IEA.
InterPro; IPR013320; ConA like subgrp.
InterPro; IPR03329; Laminin_G_TSP_N.
                               01-NOV-1996, integrated into UniProtKB/TrEMBL. 01-NOV-1996, sequence veraion 1. 07-FEB-2006, entry version 24. Thrombospondin-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%; Score 55; DB 2;
100.0%; Pred. No. 0.03;
iive 0; Mismatches
    229 AA.
    PRT;
QZ8194_BOVIN PRELIMINARY;
Q28194;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00210; TSPN; 1.

NON TER 1 1

NON TER 229 229

SEQUENCE 229 AA; 25015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.2
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGVLONVRFV 11
                                                                                                                                                 NCBI_TaxID=9913;
       ઠ
```

496 AA. Q7SY84 XENLA PRELIMINARY; PRT; 190 FQGVLQNVRFV 200 O7SY84 ID O77 AC O77 DT 01 DT 01 g

01-071-2003, integrated into UniProtKB/TrEMBL. 01-0CT-2003, sequence version 1. 07-FEB-2006, entry version 12.

```
셤
                                                                                                                                                                                                                                                                                                Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A physins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A paleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garca A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley B. W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C. Gnimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C. Gnimcoch A., Schehn J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                         Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 496; 0.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BCO34970; AAB19470.1.1; "IRLNA.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100.1.100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50184; VWFC 2; 1.
496 AA; 54843 MW; E4FD2F07CB7EF51B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.2%; Score 55; DB 100.0%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC054970; AAH54970.1; -; mRNA.
                                                                                                                   Xenopodinae; Xenopus; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
108 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
protein.
                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Whole;
   MGC64438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

```
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, fibronectin, fibronectin, chaminin, type V collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-IIb/beta-3. May play a role in dentinogenesis and/or maintenance of dentin and dental pulp.

C -- SUBUNIT: Homotrimer; disulfide-linked.

C -- SIMILARITY: Contains 3 EGF-like domains.

C -- SIMILARITY: Contains 1 TSP C-terminal (TSPC) domain.

C -- SIMILARITY: Contains 3 TSP type-1 domains.

C -- SIMILARITY: Contains 7 TSP type-1 domains.

C -- SIMILARITY: Contains 7 TSP type-1 domains.

C -- SIMILARITY: Contains 7 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Aortic endothelium;
Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin stimulatory effect of
                                                                                                                                                                                                                                                                                                                                                      STRAIN=Holstein; TISSUE=Tooth; MEDLINE=98173773; PubMed=9507054; DOI=10.1016/S0167-4838(97)00188-X; Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                              Inoue H.; "cDNA cloning of bovine thrombospondin 1 and its expression in odontoblasts and predentin.";
                                                                                       TSP1_BOVIN STANDARD; PRT; 1170 AA. 028178; 028179; 0210V-1997, integrated into UniProtKB/Swiss-Prot. 01-DEC-2000, sequence version 2. 07-MAR-2006, entry version 56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA] OF 1-18 AND 710-1170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X87618; CAA60950.1; -; mRNA.
EMBL; X87619; CAA60951.1; -; mRNA.
FIR; S5561; S55501.
FIR; S5561; S55501.
SMR; Q28178; 549-1169.
GlycoSulteDB, Q28178; -.
InterPro; IPR013320; Cona_like_subgrp.
InterPro; IPR06210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 odontoblasts and predentin.";
Biochim. Biophys. Acta 1382:17-22(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000742; EGF_3.
InterPro; IPR001881; EGF_Ca_bd.
InterPro; IPR00509; EGF_like_reg.
InterPro; IPR013012; EGF_like_reg.
InterPro; IPR013129; LamInin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB005287; BAA21115.1; -; mRNA.
                                                                                                                                                                               Thrombospondin-1 precursor.
Name=THBS1, Synonyms=TSP-1, TSP1;
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP1.
InterPro; IPR003367; tsp-3.
InterPro; IPR001007; VWF_C.
InterPro; IPR001007; VWF_C.
Pfam; PF00009; EGF; 1.
Pfam; PF002412; TSP 13.
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [MRNA]
214 FQGVLQNVRFV 224
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGF-beta
                                                    RESULT 3
TSP1_BOVIN
```

Gaps

ö

Indels

. 0

1 FOGVLONVRFV 11

ò

Best Loc Matches

```
11; Conservative
                                              1 FOGVLONVRFV 11
                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
Query Match
Best Local Similarity
                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                    208
                        Matches
                                                                                                                                                                                                                                      Homo,
                                                                  셤
                                               ਨੇ
                                                                                                                         TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2; calcium-binding (Potential).
EGF-like 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 3.
TSP type-3 4.
TSP type-3 4.
TSP type-3 5.
TSP type-3 6.
TSP type-3 7.
TSP typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ODD6ADF3E5FA031A CRC64;
                                                                         PROSITE: PS00022; EGF 1; FALSE_NEG.
PROSITE: PS00186; EGF 2; 1.
PROSITE: PS00026; EGF 3; 2.
PROSITE: PS01208; VWFC_1; 1.
PROSITE: PS01208; VWFC_1; 1.
PROSITE: PS50184; VWFC_2; 1.
Calcium; Cell adhesion; EGF-like domain; Glycoprotein; Heparin-binding; Repeat; Signal.
SIGNAL
                                                                                                                                                           By similarity.
Thrombospondin-1.
/FTIGE-PRO 0000035841.
TSP N-terminal.
                    PRINTS; PRO1705; TGPIREPEAT.
SWART; SM0101; EGF; 3.
SWART; SM00209; TSP1, 3.
SWART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129534
  TSP_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     248
360
708
1067
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                REGION
                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                DOMAIN
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Endothelial cell;
MEDLINE=87057617; PubMed=2430973; DOI=10.1083/jcb.103.5.1635;
Lawler J., Hynes R.O.;
"The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLECTIDE SEQUENCE OF 1-374.

MEDLINE=86287276; PubMed=3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
Dixit V.B., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
Characterization of a CDNA encoding the heparin and collagen binding domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE OF 1-397.
MEDLINE=87157592; PubMed=3030396;
Kobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.;
"Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLECTIDE SEQUENCE OF 1-166, MEDLINES 92219870; MEDLINES 92919870; Dubmed=254587; MEDLINES 92919870; Dixit V.M.; Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription."; J. Biol. Chem. 264:11222-11227(1989).
                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89139550; PubMed=2918029; DOI=10.1083/jcb.108.2.729; Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L., Baumgartel D.M., Rotwein P., Frazier W.A.; "Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region."; J. Cell Biol. 108:729-736 [1989].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLECTIDE SEQUENCE OF 1028-1170.

La Fleur M., Jobin C., Gauthier J., Kreis C.G.;

La Expression of thrombospondin in chronic inflammation: neutrophils from synovial fluids synthesize a novel 3.9 kb TSP mRNA.";

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441; THR-460; TRP-498 AND THR-507. TRISUBE-Platelet; TSUBE-Platelet; MEDLINE=21125860; Pubmed=11067851; DOI=10.1074/jbc.M008073200;
Length 1170;
                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                        TSP1 HUMAN STANDARD; PRT; 1170 AA.
TSP2 HUMAN STANDARD; PRT; 1170 AA.
TSP2 HUMAN STANDARD; PRT; 1170 AA.
TSP3 HUMAN STANDARD; DT 01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1988, sequence version 1.
DT 07-MAR-2006, entry version 78.
DE Thrombospondin-1 precursor.
GN Name=THBS1; Synonyme=TSP, TSP1;
                                               0.18;
                           100.0%; Prec. ....
       Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell Biol. 103:1635-1648(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 25:8418-8425(1986).
```

```
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGION
MOTIF
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                       CHAIN
  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITES ASN-248 AND ASN-1067.

PubMed=16335952; DOI=10.1021/pr0502065;
Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
Moore R.J., Smith R.D.;
"Human plasma N-glycoproteome analysis by immunoaffinity subtraction,
Tydrazide chemistry, and mass spectrometry.";
J. Proteome Res. 4:2070-2080(2005).
L.J. Proteome Res. 4:2070-2080(2005).
C.I. PUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
cell-to-matrix interactions. Can bind to fibrinogen, fibromectin,
laminin, type V collagen and integrins alpha-V/beta-1, alpha-
V/beta-3 and alpha-IIb/Peta-3.
C.I. SUBUNIT: Homotrimer; disulfide-linked.
C.I. SUBUNIT: Belongs to the thrombospondin family.
C.I. SIMILARITY: Contains 3 ESP-like domains.
C.I. SIMILARITY: Contains 3 TSP C-terminal (TSPN) domain.
C.I. SIMILARITY: Contains 3 TSP type-1 domains.
C.I. SIMILARITY: Contains 3 TSP type-1 domains.
C.I. SIMILARITY: Contains 7 TSP type-3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                 THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES.

MEDLINE=22338361; PubMed=12450399; DOI=10.1021/bi026463u;

Huwiler K.G., Veefling M.M., Annis D.S., Mosher D.F.;

"Biophysical characterization, including disulfide bond assignments, of the anti-angiogenic type 1 domains of human thrombospondin-1.";

Biochemistry 41:14329-14339(2002).
Hofeteenge J., Huwiler K.G., Macek B., Hess D., Lawler J., Mosher D.F., Peter-Katalinic J.; "C-mannosylation and O-fucosylation of the thrombospondin type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC; HGNC:11785; THBS1.

MIM; 188060; gene.

Reactome; P0796; C:extracellular region; NAS.

GO; GO:0004866; F:endopeptidase inhibitor activity; TAS.

GO; GO:0004871; F:signal transducer activity; TAS.

GO; GO:0007275; P:edevelopment; TAS.

InterPro; IPR013120; ConA_like_subgrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M25631; AAA36741.11; -; mRNA.
EMBL; X14787; CAA28370.1; -; mRNA.
EMBL; X14787; CAA28370.1; -; mRNA.
EMBL; X14787; CAA28399.1; -; mRNA.
EMBL; M14226; AAA61270.1; -; mRNA.
EMBL; J04835; AAA61270.1; -; mRNA.
EMBL; M99425; AAA61178.1; -; GENOMIC_DNA.
EMBL; M99425; AAB59366.1; -; mRNA.
PDB; 1LSL; X-ray; A=434-546.
PDB; 1LX6; X-ray; A=434-1170.
PDB; 1Z78; X-ray; A=19-233.
PDB; 1ZA4; X-ray; A=19-257.
PDB; 2ERF; X-ray; A=19-257.
PDB; 2ERF; X-ray; A=25-233.
GLYCSUITEDB; P07996; -.
GGP; P07996; -.
GGP; P07996; -.
GGP; P07996; -.
GRPSEMD1; ENSGOUOUT37801; HOMO Sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000742; EGF 3.
InterPro; IPR00181; EGF Ca bd.
InterPro; IPR001801; EGF like reg.
InterPro; IPR013032; EGF like reg.
InterPro; IPR003129; Laminin_G_TSP_N.
InterPro; IPR00884; TSP1.
InterPro; IPR008865; TSP1.
InterPro; IPR008855; TSP 7.
InterPro; IPR008859; TSP C.
InterPro; IPR001007; VWF_C.
Pfam; PP00008; EGF; 2.
Pfam; PP00009; EGF; 2.
                                                       J. Biol. Chem. 276:6485-6498(2001).
```

```
R Pfam; PF02412; TSP_3; 12.

R Pfam; PF0093; VWC; 1.

R PRINTS; PR01705; TSP_C; 1.

R PRINTS; PR01705; TSPLEBAT.

R MART; SM00181; EGF; 3.

R SMART; SM00210; TSP1; 3.

R MART; SM00210; TSP1; 3.

R MART; SM00210; TSP1; 3.

R PROSITE; PS00022; EGF_1; PALSE_NEG.

R PROSITE; PS0008; EGF_2; 1.

R PROSITE; PS01080; TSP1; 3.

R PROSITE; PS01080; VWC_2; 1.

R PROSITE; PS0104; VWC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 3.
TSP type-3 4.
TSP type-3 5.
TSP type-3 6.
TSP type-3 7.
TSP ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTIGHCAR 000210.
O-linked (Fuc. ..).
/FTIGHCAR 000211.
N-linked (GlCNAC. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-linked (GlCNAC. . .
Interchain (Probable)
Interchain (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombospondin-1.
/FTId=PRO_000035842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=CAR 000205.
0-linked (Fuc. ..)
/FTId=CAR 000206.
C-linked (Man).
/FTId=CAR_000207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-linked (Man).
/FIId=CAR 000208.
O-linked (Puc. .)
/FIId=CAR 000209.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FIId=CAR_000zv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VWFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.2%; Scu-
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                           3D-structure; Calcium; Cell adh
Heparin-binding; Repeat; Signal
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100 es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1067
270
274
423
428
413
484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507
                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                915
951
19
926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507
```

```
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                         01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
01-JUN-1994, sequence version 1.
01-JUN-1994, se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90375546; PubMed-2298070;
Bornstein P., Alfi D., Devarayalu S., Framson P., Li P.;
"Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";
J. Biol. Chem. 265:16691-16698(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development."; J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
MEDINE-21128941, PubMed=1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
Jenkins N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
BEDLINE=92147683; PubMed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of the murine thrombospondin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L; M62470; AAA50611.1; -; Genomic_DNA.
L; M62451; AAA50611.1; JOINED; Genomic_DNA.
L; M62451; AAA50611.1; JOINED; Genomic_DNA.
L; M62453; AAA50611.1; JOINED; Genomic_DNA.
L; M62453; AAA50611.1; JOINED; Genomic_DNA.
L; M62454; AAA50611.1; JOINED; Genomic_DNA.
L; M62455; AAA50611.1; JOINED; Genomic_DNA.
L; M62456; AAA50611.1; JOINED; Genomic_DNA.
L; M62458; AAA50611.1; JOINED; Genomic_DNA.
L; M62458; AAA50611.1; JOINED; Genomic_DNA.
L; M62459; AAA50611.1; JOINED; Genomic_DNA.
L; M62459; AAA50611.1; JOINED; Genomic_DNA.
L; M62450; AAA50611.1; JOINED; Genomic_DNA.
L; M62460; AAA50611.1; JOINED; Genomic_DNA.
L; M62460; AAA50611.1; JOINED; Genomic_DNA.
                                                                                               PRT; 1170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 1-490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE OF 19-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 11:587-600(1991)
                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                               TSP1 MOUSE P35441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                         DER PER PRESENTATION OF THE PROPERTY OF THE PR
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUB=Aorta and vein;
PubMed=16141072; DOI=10.1126/science.1112014;
PubMed=16141072; DOI=10.1126/science.112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V. W.B., Brenner S. B., Batalov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CSTBL/60; TISSUE-Aorta and vein;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530055N06 product:thrombospondin 1, full insert sequence.
.) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1170;
0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0443E493615E7F06 CRC64;
            Interchain (Probable).
Interchain (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1170 AA.
                                                           similarity.
similarity.
                                                                                           similarity.
                                                                                                                         similarity.
                                                                                                                                        similarity.
                                                                                                                                                     similarity.
Similarity.
                                                                                                                                                                                                                                                similarity.
                                                                                                                                                                                                                                                                                                                           similarity.
                                                                                                                                                                                                                                                                                                                                        similarity.
                                                                                                                                                                                                                                                                                                                                                          similarity.
                                                                                                                                                                                                                                                                                                                                                                                                     similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                         similarity
                                                                                                                                                                                   similarity
                                                                                                                                                                                                     similarity.
                                                                                                                                                                                                                                similarity
                                                                                                                                                                                                                                                              similarity
                                                                                                                                                                                                                                                                              similarity.
                                                                                                                                                                                                                                                                                             similarity.
                                                                                                                                                                                                                                                                                                              similarity
                                                                                                                                                                                                                                                                                                                                                                        similarity
                                                                                                                                                                                                                                                                                                                                                                                        similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       similarity
                                                                                                                                                                                                                 similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%; Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129647 MW;
                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q3TR40 MOUSE PRELIMINARY;
Q3TR40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FOCVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1025 102
1170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Thbs1;
                                            DISULFID
                                                                                           DISULFID
                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                           DISULFID
                                                                                                                           DISULFID
                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A CONTRACT REPORTS TO STAND IN THE PROPERTY OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
   ð
```

Chief W. Parter L. Belder R.W. Person T. Sono H. Chalk A.M.

Chief W.L. Dilla E. Dalrymolic B. Per de Bono B. Della Getta G.,

A Georgi-Hemming P. Gingeres T. Pernon W. Flutski S. Garboldt M.,

Goorgi-Hemming P. Gingeres T.R. Golobori T. Green R.E.,

B. Mills D. Bennick S. Jackson W. Branks S. Garboldt M.,

B. Hill D. Bennick S. Habere M. Hayasin Y. Renap T.K. Harokawa M.,

B. Hill D. Bennick S. Jackson W. Jaco K. Wenner J. Kithakawa M.,

B. Hill D. Bennick S. Malder H. Hayasin Y. Renap T.K. Harokawa M.,

B. Hill D. Bennick S. Malder M. Hayasin Y. Renap T.K. Harokawa M.,

B. Hill D. Bennick S. Malder M. Hayasin Y. Renap T.K. Harokawa M.,

B. Hill D. Bennick S. Malder M. Hayasin Y. Kamerfeld S. M.

Rarochal H. Waterawa S. Miki H. Mignone P. Miyake S. Morris K.,

B. Matchall T. V. Lareau L.F., Larono W., Ikee K., Sengle C., Morris K.,

B. Misson B. M. Matchala S. Malder M. Nakand M. Mactan M. Mactin M. Bactin M.

M. Misson B. M. Matchala S. Malder M. Nakand M. Sakandi H. Mgt.

B. Milsen B. M. M. Readels S. M. Sandler M. Sakandi H. Mgt.

B. Milsen B. M. M. Readels S. L. Sengle J. S. Sessa L. Sheng Y.,

B. Milsen M. W. Charles S. Sulva D. Sinclair B. Treatawa T. Richark M. Mactan M. Mactan M. Mactan M.

B. Milsen M. M. Readels S. L. Hane D. M. Scholar S. Messal D. Sinclair B.

B. Mandleredd C. Mattick J. S. Hane D. M. Kai C. Treatawa T. S. Mandleredd C. Mattick J. S. Hane D. M. Kai C. T. Readels D. Sinclair B. M. Radels M. Packer M. M. Machal M. Machal M. M. Kandleredd C. Mattick J. St. Hane D. M. Kai C. T. Mackawa T. M.

M. Mahleredd C. Mattick J. S. Hane D. M. Kai C. T. Kawaji H. W. Kawashina T. M. Makanda T. W. Matchala M. Packer M. M. Machala M. M. Machala M. Packer M. M. Machala M. M. Machala M. Machala M. Machala M. Machala M. M. Machala M. M. Machala M. M. Machala M. Machala M. M. Machala M. M. Machala M. M. Machala M. Machala M. Machala M. M.

us-10-030-735-28.rup

```
Name=Tsp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q71SA3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
   SO DE RESERVADO DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/64; TISSUB-Aorta and vein;

NEALINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

A REDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

A Arawa J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rushi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

B., Washahia-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUB=Aorta and vein;
MEDLINE=27BL/6J; TISSUB=Aorta and vein;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mornalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20510913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CSTBL/6J; TISSUE-Aorta and vein;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Niomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.,
Submitted (APR-2004) to the EMBL/GenBank/DD9J databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0016525; C:extracellular space; RCA.
GO; GO:0016525; C:extracellular space; RCA.
InterPro; IPR006210; EGF.
InterPro; IPR00742; EGF.
InterPro; IPR001881; EGF.
InterPro; IPR00180209; EGF.
InterPro; IPR013032; EGF.like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK163092; BAE37190.1; -; mRNA.
MGI; MGI:98737; Thbs1.
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                        NUCLEOTIDE SEQUENCE
   HERE THE SECOND SEED OF SECOND SEED OF SECOND SEED OF SECOND SECO
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.2%; Score 55; DB 2; Length 1170; 100.0%; Pred. No. 0.18; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; Iwabu A., Hirohata S., Kusachi S., Nakamura K., Murakami Ninomiya Y., Tsuji T.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1170 AA; 129619 MW; 55BF04A20D91B194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMR; Q715A3; 834-1169.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005198; F:extractural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR013320; Cond_like_subgrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY; PRT; 1170 AA.
                                                                             InterPro; Irro08085; TSP 1.
InterPro; IPR003867; TSP 1.
InterPro; IPR003867; TSP 1.
InterPro; IPR003867; TSP 1.
InterPro; IPR001007; VWF C.
InterPro; IPR001007; VWF C.
InterPro; IPR001007; VWF C.
InterPro; IPR001007; TSP 1.
INTERPRO; IPR011007; IPRN; INTERPRO; IPR001107; IPRN; INTERPRO; IPR001107; IPRN; INTERPRO; IPR001107; IPRN; INTERPRO; IPR001107; IP
Laminin G TSP N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF309630; AAQ14549.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000742; BGF_3.
InterPro; IPR018B1; EGF_Ca_bd.
InterPro; IPR016209; BGF_like.
InterPro; IPR013032; EGF_like reg.
InterPro; IPR03129; Laminin_G_TSP_InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008085; TSP 1.
InterPro; IPR003367; tsp 3.
InterPro; IPR008859; TSP C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
1es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FÓGVLÓNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGULQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q71SA3_RAT
Q71SA3;
```

```
Name=Thbs1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NECLEGIBLE SEQUENCE.

ON TREATING SEQUENCE.

ON TRAINECSTBL/6; TISSUEBRIAI;

NEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

A Distribution N.A., Farmer A.A., Rubin G.M., Hong L.,

B Carailla D. M., Hodin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rachards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.B.N., Marra M.A.,

Butterfield Y.S.N., Marra M.A.,

Butterfi
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                      Score 55; DB 2; Length 1170;
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                   AA; 129671 MW; 6F38D3DCE733060F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CC7BL/6; TISSUE-Brain;
Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1171 AA
                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0%; Pred. No. 0.1 les 11; Conservative 0; Mismatches
                                                                                                                                                                               PROSITE; PS01186, EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50092, TSPP, 3.
PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
InterPro; IPR001007; VWF_C. Pfam; PP00008; EGF; 2. Pfam; PP00090; TSP_1; 3. Pfam; PP02412; TSP_2; 12. Pfam; PP05735; TSP_C; 1. Pfam; PP00093; VWC; 1.
                                                                                                                                                                                                                                                                                                       93.2%;
                                                                                                   PRINTS; PR01705; TSP1REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."
                                                                                                                                  SMART; SM00209; TSP1; 3.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  208 FQGVLQNVRFV 218
                                                                                                                    SMART; SM00181; EGF; 3.
SMART; SM00209; TSP1; 3
SMART; SM00210; TSPN; 1
                                                                                                                                                                                                                                                                                                                                                                          1 FOGULONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombospondin 1.
                                                                                                                                                                                                                                                                          1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBOYO1 MOUSE
QBOYO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Thbs1;
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc.
                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 22.
Thrombospondin 1 (Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library, clone:G930018021 product:thrombospondin 1, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arose spontaneously;
MEDLINE_2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE_2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhate N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor
                                                R MSSK; (200790; 1452).

R MSSK; (200700; 1452).

R MGI: 98737; Thbs1.

R GO; GO:0005615; C:extracellular space; RCA.

GO; GO:0005615; C:extracellular space; IDA.

R GO; GO:0005615; C:extracellular space; IDA.

GO; GO:0005615; C:extracellular space; IDA.

R InterPro; IPR001320; ConA like_subgrp.

R InterPro; IPR00181; EGF Ca bd.

R InterPro; IPR00181; EGF Ca bd.

R InterPro; IPR00181; EGF Laminin G TSP_N.

InterPro; IPR001829; EdF like reg.

R InterPro; IPR00189; TSP_1.

R InterPro; IPR001895; TSP_1.

R InterPro; IPR001895; TSP_2.

R InterPro; IPR001805; TSP_2.

R InterPro; IPR001805; TSP_2.

R Pfam; PF00010; TSP_1; 3.

R Pfam; PF0010; TSP_1; 3.

R Pfam; PF00100; TSP_1; 3.

R Pfam; PF00112; TSP_2: 1.

R Pfam; PF00112; TSP_2: 1.

R Pfam; PF00113; VWF_C: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1171 AA; 129690 MW; 12E077B50C64E2D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%; Score 55; DB 2;
100.0%; Pred. No. 0.18;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SW00181; EGF; 3.
SWART; SW00209; TSP1; 3.
SWART; SW00210; TSP1; 1.
SWART; SW00214; VWC; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS50026; TSP1; 3.
PROSITE; PS501208; VWFC_1; UNKNOWN_1.
EMBL; BC050917; AAH50917.1; -; mRNA.
HSSP; P07996; 1LSL.
SMR; Q80YQ1; 835-1170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBCGB2_MOUSE PRELIMINARY;
Q8CGB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01705; TSPIREPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=10090;
```

```
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Gyama R., Rasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Gyama R., Rasukawa T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Shimokawa K., Davis M.J., Wilming L.G., Aldinis V., Allen J.E.,

Annbesi-Impionbato A., Apweiler R., Aturaliya R.N., Bailey T.L.,

Annbesi-Impionbato A., Apweiler R., Aturaliya R.N., Bailey T.L.,

Annbesi-Impionbato A., Apweiler R., Aturaliya R.N., Bailey T.L.,

RA Annbesi-Impionbato A., Dalrymple B.P., de Bono B., Della Gatta G.,

Grow M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

A di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,

RA Fletcher C.F., Fukushima T., Furuno M., Fredxi S., Gariboldi M.,

Georgii-Hemming P., Gingeras T.R., Golobori T., Green R.E.,

A Hill D., Humininecki L., Iacono M., Ikee G., Iarikawa T.,

Att M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

A Kanapin A., Katoh M., Kawasawa Y., Kalso J., Kitamura H.,

Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,

Luni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,

Mutsuawa S., Milder N., Nakano N., Nakauchi H., Ng P.,

Mutson R., Mishiguchi S., Nishikawa S., Nori F., Ohara O.,

RA Agazki Y., Orlando V., Pang K.C., Pavan M. J., Pavesi G., Penge C.,

RA Rost B., Ruan Y., Salzberg S., Reed J.F., Send S., Sessa L., Sheng Y.,

Rost B., Ruan Y., Stubka B., Shimada K., Silva D., Sinclair B.,

Rost B., Ruan Y., Salzberg S., Reed J., Fegner J., Techneider C.,

Rost B., Ruan Y., Salzberg S., Reed J., Seno S., Sessa L., Brusic V., Quackenbush J.,

Rammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teknaka Y.,

Rammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teknaka S., Ramanishi H., Zabarowsky E., Zhu K., Wei C.L., Yagi K.,

Ramanja H.R., van Nimwegen B., Attuka K., Shiraki K., Bukashima T., Shima M., Kato T., Kawashima T., Shimah M., Rondo S., Konnoni-Ya, Shiraki K., Bukashima T., Shimah M., Rayashi J., H
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schwitz J., Myers R.M., Schmitz J., Schmitz J., Myers R.M., Schmitz J., Schmitz J., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schmitz J., Schmitz J., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schill-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CZECH II; TISSUB=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Mammary gland;
PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg
```

Science 309:1559-1563(2005)

NUCLEOTIDE SEQUENCE

```
RESULEMENTES SEQUENCE.

RESULEMENTARY Gland;

RESULEMENTES 25354683; PubMed=12466851; DOI=10.1038/nature01266;

REDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA OKAZAKI Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Mikaido I., Osato N., Saito R., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Gontim L.M., Kanapin A., Matsuda H., Bataloo S., Beisel K.W.,

RA Balake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,

RA Gasterland T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Anai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lehhard B., Lyons P.A.,

RA Magashima T., Mantais L., Marchinoni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Okido T., Pavan W.J., Perrea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Kingwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takennaka Y., Taylor M.S., Teasdala R.D., Tomita M.,

RA Verardo R., Wangner L., Wahlbestett C., Wang Y., Watanabe Y., Walls C.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I., Yang I.,

RA Minazaki A., Sakai K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hirozane-Kishikawa T., Konno H., Nakauura M., Sakazume N., Sakai K.,

RA Mayazaki A., Sakai K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

Baniney E., Hayahizaki Y.,

RH Mayazaki A., Sakai K., Sasasi D., Raidara K., Shinagawa A.,

Baniney E., Hayahizaki Y.,

RH Malaysis of the mouse transcriptome based on functional annotation of R. Mature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Azakaa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azakaa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fluichlamm W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Mammary gland;
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
TISSUE=Mammary gland;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Mammary gland;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
                                                                                                                                                                                        NUCLEOTIDE SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 2.
EGF-like 3.
TSP type-3 1.
TSP type-3 4.
TSP type-3 4.
TSP type-3 5.
TSP type-3 6.
TSP type-3 7.
TSP type-1 7.
TSP type-1 7.
TSP type-3 7.
TSP type
                                                                                                              R SMR; P3548; 552-11/2.

R InterPro; 1PR006210; EGF.

InterPro; 1PR006210; EGF.

R InterPro; 1PR006209; EGF-Ca ab.

R InterPro; 1PR006209; EGF-Ca ab.

R InterPro; 1PR006209; EGF-Like.

R InterPro; 1PR0013129; EGF-Like.

R InterPro; 1PR001009; TSP-1.

R InterPro; 1PR001007; VWF-C.

R Pfam; PP00009; TSP-1.

R PFam; PP00099; TSP-1.

R PRNO175; PR01705; TSP-1.

R SMART; SW00181; EGF; 2.

R SMART; SW00181; EGF; 2.

R SMART; SW00181; EGF; 2.

R SMART; SW00181; EGF; 3.

R SMART; SW00181; EGF; 2.

R PROSITE; PS00022; TSP1; 3.

R PROSITE; PS00189; WPC-L; 1.

R PROSITE; PS0189; WPC-L; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombospondin-1.
/FTId=PRO_0000035844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GlcNAc.
(GlcNAc.
(GlcNAc.
(GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
                                          EMBL; L04278; -; NOT ANNOTATED_CDS; MENA.
HSSP; P07996; 1LSL.
SMR; P35448; 552-1172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-linked
N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9173
953
11173
235
931
158
158
158
705
711
1070
426
431
492
492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heparin-binding;
SIGNAL 1
CHAIN 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

TISSUE=Mammary gland;

Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,

Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,

Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,

Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,

Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,

Muramatsu M., Hayashizaki Y.;

Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                     TISSUE=Mammary gland;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Sumino K., Mateunoto H., Sakaguchi S., Ikegami T., Kaabhiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Kokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
**REN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994, sequence version 1.
07-MAR-2006, entry version 54.
Thrombospondin-1 precursor.
Name=thbal; Synonyms=tspl;
Kenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Urry L.A., Ramos J., Duquette M., Desimone D.W., Lawler J.; "Cloning, characterization and expression of thrombospondin-1 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 1171; 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.2%; Score 55;
100.0%; Pred. No.
ive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC042422; AAH42422.1; -; mRNA.
EMBL; AK145202; BAE26293.1; -; mRNA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLONVRFV 11
      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSP1 XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P35448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
TSP1_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
```

요

ð

(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).

us-10-030-735-28.rup

셤 ઠ

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barker D.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
-!- FUNCTION: Anteractions. Can bind to fibrinogen, fibronectin,
laminin and type V collagen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-2004, integrated into UniProtKB/TrEMBL.
21-DEC-2004, sequence version 1.
21-FEB-2006, entry version 12.
Novel protein similar to vertebrate thrombospondin 1.\n\ (Fragment).
ORFNames=DKEY-11E23.1-001;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
              R Pfam; PF00008; TSP_1; 3.

R Pfam; PF001008; TSP_1; 3.

R Pfam; PF00135; TSP_2; 1.2.

R Pfam; PF00735; TSP_C; 1.

R Pfam; PF00735; TSP_C; 1.

R Pfam; PF00735; TSP_C; 1.

R SMART; SM00108; ESF; 3.

R SMART; SM00210; TSP1; 3.

R PROSITE; PS50026; EGF_2; 1.

R PROSITE; PS50026; EGF_2; 1.

R PROSITE; PS50184; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 Length 1225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL928866; CAI20599.1; -; Genomic_DNA.
SMR: QSSPG5; 751-804, 754-1089.
Ensembl; ENSDAGG00000100785; Danio rerio.
GO; GO:0005509; E:calcium ion binding; IEA.
GO; GO:0008201; F:heparin binding; IEA.
GO; GO:0008151; F:protein binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR013120; ConA_like_subgrp.
InterPro; IPR002048; EF hand_Ca_bd.
InterPro; IPR002010; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 2;
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Scor.
100.0%; Pred. No. v.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1090 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000142; EGF 3.
InterPro; IPR001881; EGF Ca bd.
InterPro; IPR001809; EGF like.
InterPro; IPR013012; EGF like reg.
InterPro; IPR03129; Laminin G TSP N.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR008085; TSP_1
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 FQGVLQNVRFV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSSPGS_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q5SPG5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
COSSPGS BRA
DOSSPGS BRA
DOSSPGS
DT 21-DB
DT 21-
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution.NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĸ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Aorta endothelial cell;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama
Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1173;
0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                         By similarity.
MW; A9F036D6516C0F24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB209912; BAD93149.1; -; mRNA.
SMR; Q59E99; B86-939, B89-1225.
BASGO0000137801; Homo sapiens.
G0; G0: 0005576; C:extracellular region; IEA.
G0; G0: 0005509; F:calcium ion binding; IEA.
G0; G0: 000515; F:peparin binding; IEA.
G0; G0: 000515; F:percein binding; IEA.
G0; G0: 000515; F:structural molecule activity; IEA.
G0; G0: 0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2005, integrated into UniProtKB/TrEMBL
                                                                                                 similarity.
similarity.
similarity.
similarity.
similarity.
                                         similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1225 AA
                                                                                                                                                                                                                                            similarity.
                                                                                                                                                                                                                                                            similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                    Bimilarity
                                                                                                                                                                                                                                                                                 similarity
                                                                                                                                                                                                                                                                                                                          Bimilarity
                                                                                                                                                                                                                                                                                                                                                                                                   Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR013320; ConA_like_subgrp.
InterPro; IPR006420; BGF.
InterPro; IPR000742; BGF 3.
InterPro; IPR001881; BGF_Ca_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF 3.
EGF Ca bd.
EGF like.
EGF like reg.
Laminin G TSP N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombospondin 1 variant (Fragment) Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-2005, sequence version 1. 21-FEB-2006, entry version 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
    93.2%; 8
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q59E99_HUMAN PRELIMINARY;
Q59E99;
                                                                                                                                                                                                                                                                                                                                                              130020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro, IPR008085; TSP 1.
Interpro, IPR003367; tsp 3.
Interpro, IPR008859; TSP C.
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Marches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 FÓGVLÓNVRFV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLONVRFV 11
                                                                                                                                                                                                  741
777
800
836
859
897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR013032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR008859;
                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                           1173
DISULFID
DISULFID
DISULFID
DISULFID
                                                                          DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang K., Mauco G., Hauet T., Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1193 AA; 133256 MW; 6E8781648FCEC7F2 CRC64;
                                                                                                                                         R GO; GO:0005509; P:calcium ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
R GO; GO:000515; F:protein binding; IEA.
GO; GO:000515; F:protein binding; IEA.
R GO; GO:000518; F:erructural molecule activity; IEA.
R InterPro; IPR006210; EGF.
R InterPro; IPR00042; EGF.
R InterPro; IPR00042; EGF.
R InterPro; IPR001801; EGF.
R InterPro; IPR001801; EGF.
R InterPro; IPR001803; EGF.
R InterPro; IPR001804; TSP1.
R InterPro; IPR001007; VW.—C.
R InterPro; IPR001007; VW.—C.
R Ffam; PP00008; EGF; 2.
R Ffam; PP00008; EGF; 2.
R Pfam; PP00135; TSP 1.
R PFam; PP00135; TSP 1.
R PFam; PP00135; TSP 1.
R PFam; PP00135; TSP 2.
                                      EMBL, CAAE01014723; CAG03524.1; -; Genomic_DNA.
SWR; Q4S758; 811-114A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 2;
Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SW00181; EGF; 2.
SWART; SW00181; EGF; 2.
SWART; SW00210; TSP1, 3.
SWART; SW00214; VWC; 1.
PROSITE; PS01186; EGF 2; UNKNOWN_1.
PROSITE; PS50026; EGF 2; 2.
PROSITE; PS50092; TSP1; 3.
PROSITE; PS501208; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AY773342; AAV38110.1; -; mRNA.
InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP_1.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-2004, sequence version 1. 07-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombospondin 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01705; TSP1REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.5 es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 FMGVLQNVRFV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03 PIG
Q5U903 PIG
Q5U903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
050903 PIG
1D 075090
AC 05090
AC 05090
DT 07-DE
DT 07-DE
DT 07-PE
DT 07-PE
DT 07-PE
DT 07-DE
         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pubmed-15496914; DOI=10.1038/nature03025;

Nauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Sequrens B.,

Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,

Nathouard V., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,

Remont C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

Relis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Linddet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Honder P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Honder P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Honder P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Honder P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Honder P., Lander E.S., Weissenbach J., Roest Crollius H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
19-JUL-2006, entry version 8.
Chromosome 14 SCRF1473, whole genome shotgun sequence. (Fragment) ORFNames=GSTENG00022976001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis (Green puffer).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.7%; Score 50; DB 2; Length 1090; 90.9%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1090 AA; 120978 MW; 5A9320504A22D836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00018; EF HAND 1; UNKNOWN_1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50029; TSP1; 2.
PROSITE; PS501208; VWFC_1; 1.
PROSITE; PS501304; VWFC_2; 1.
Cell adhesion; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
0465786 TERING
010 0465788 TETING PRELIMINARY;
AC 046758;
                                                                                                                                                                                                                                                      PRINTS; PRO1705; TSPIREPEAT.
SWART; SM00181; EGF; 2.
SWART; SM00209; TSP1; 2.
SWART; SM00210; TSPN; 1.
SWART; SM00210; TSPN; 1.
                                                                                                Pfam; PF00008; EGF; 1.
Pfam; PF00090; TSP 1; 2.
Pfam; PF05412; TSP 3; 12.
Pfam; PF05735; TSP C; 1.
Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 FMGVLQNVRFV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
```

g

ò

HERE THE PROPERTY OF THE PROPE

```
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wheded15496914; DOI=10.1038/nature03025;
While Doi, Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., Jaillon O., Aury J.-M., Brunet C., Ozouf-Costaz C., Bernot A., Manuceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Mancaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Cattollaro L., Poulain J., De Berardinis V., Anthouard V., Salili Z., Cattollaro L., Poulain J., De Berardinis V., Anthouard C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., A. Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lander P., Lander E.S., Weissenbach J., Roest Crollius H.;
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2005, sequence version 1.
21-FPB-2006, entry version 8.
Chromosome 10 SCAF15G19, whole genome shotgun sequence. (Fragment)
ORFNames=GSTENG0032374901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope, Whitehead Institute Centre for Genome Research,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                  83.1%; Score 49; DB 2; Length 249; 100.0%; Pred. No. 0.52; cive 0; Mismatches 0; Indels
                                                                                                                                                                  249 AA; 27560 MW; 465D664BE0329C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 Q4RLR5; 834-887, 837-1171, CO. 0005576; Cextracellular region; IEA. GO:0005570; F:calcium ion binding; IEA. GO:0008201; F:heparim binding; IEA. GO:0005195; F:protein binding; IEA. GO:0005195; F:structural molecule activity; IEA. GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; CAAE01015019; CAG10667.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                        QARLES TETNG PRELIMINARY; PRT; 1171 AA. Q4RLES; 19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                             PRINTS; PRO1705; TSPIREPEAT.
SMART; SM00209; TSP1; 1
RNOSTTE; SR00209; TSP1; 1
PROSTTE; PSS0092; TSP1; 1.
PROSTTE; PS01208; VWFC_1; 1.
                                                                                                                                                                                Pfam; PF00090; TSP_1; 2.
                                                                                                                                                                                                                                                                      2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                      1 QGVLQNVRFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                   NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       80 88 88 8 8 F F S
                                                                                                                                                                                                                                                                                                      쉽
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 2; Length 1171;
Pred. No. 2.8;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1171 1171
1171 AA; 129304 MW; 865F3749693F7FCE CRC64;
InterPro; IPR000742; EGF 3.
InterPro; IPR00181; EGF Ca bd.
InterPro; IPR01812; EGF Like reg.
InterPro; IPR013129; Laminin_G_TSP_N.
InterPro; IPR000884; TSP1.
InterPro; IPR0008089; TSP 1.
InterPro; IPR0008089; TSP 1.
InterPro; IPR001007; VWF_C.
Pfam; PP00008; EGF; 1.
Pfam; PP00412; TSP_3; 12.
Pfam; PP02412; TSP_3; 12.
Pfam; PP05735; TSP_3; 12.
Pfam; PP05735; TSP_3; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: June 5, 2006, 22:42:43
                                                                                                                                                                                                                                                                                                                                        PROSITE, PSO1186; EGP 2; UNKNOWN 1. PROSITE; PSC0026; EGP 3; 2. PROSITE; PSC0092; TSPI; 3. PROSITE; PSC12098; WWFC 1; 1. PROSITE; PSS0184; WWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.1%;
90.9%;
                                                                                                                                                                                                                                             TSP1REPEAT
                                                                                                                                                                                                                                         PRINTS; PRO1705; TSPIREPEA:
SWART; SW00181; EGF; 2.
SWART; SW00209; TSP1; 3.
SWART; SW00210; TSP1; 1.
SWART; SW00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 FTGVLQNVRFV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Job time : 110.931 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
```



```
RESULT 1
US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 482, App
Sequence 97, Appl
Sequence 20, Appl
Sequence 2, Appli
Sequence 350, Appl
Sequence 11112, A
Sequence 11112, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6333, Ap
527, App
10457, A
164, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3511, Ap
3429, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10, Appi
10, Appi
10, Appi
10, Appi
10, Appi
5578, Ap
                                                         5, 2006, 22:43:07; Search time 23.8966 Seconds (without alignments) 43.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                            /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-002-482
US-09-939-853A-97
US-09-939-853A-98
US-08-313-288B-20
US-09-657-472-2
US-09-67-472-2
US-09-270-767-42057
US-09-949-016-6133
US-09-949-016-6133
US-09-949-016-633
US-09-782-210-527
US-09-782-210-527
US-09-134-000C-3511
US-09-134-00C-3511
US-09-134-00C-3511
US-09-134-00C-3511
US-09-134-00C-3511
US-08-484-158B-10
US-08-484-158B-10
US-08-484-158B-10
US-08-484-158-10
US-08-484-158-10
US-08-484-158-10
US-08-484-158-10
US-08-134-000C-5578
US-09-134-000C-5578
US-10-037-417-48
US-10-037-417-51
                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                        650591 segs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         OM protein - protein search, using sw model
                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                       Patents AA:*
                                                                                                 US-10-030-735-28
59
1 FQGVLQNVRFVA 12
                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                 %
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        June
                                                                                                                                                                                                                                                                                                ..........
                                                                                                             Perfect score:
                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                       Database
                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
```

```
Sequence 482, Application US/09949002

Sequence 482, Application US/09949002

Batent No. 690016

GENERAL INFORMATION:

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION OF SECTION O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 97, Application US/09939853A

Sequence 97, Application US/09939853A

Patent No. 6989232

GENERAL INFORMATION:

APPLICANT: BURGERATION:

TITLE OF INVENTION: No. 6989232e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-099

CURRENT PAPLICATION NUMBER: US/09/939,853A

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                          Sequence 20800, A Sequence 267, App Sequence 16180, A Sequence 4331, App Sequence 6791, App Sequence 6792, App Sequence 6792, App Sequence 9533, App Sequence 9533, App Sequence 9533, App Sequence 9533, App Sequence 9534, App Sequence 9536, App Sequence 9539, A
Appli
                                            4891, A
20800,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-20800
US-09-199-677A-267
US-09-134-000C-4331
US-09-134-000C-4331
US-09-992-11
US-09-949-016-6791
US-09-949-016-6792
US-09-949-016-6793
US-09-948-429C-63
US-09-948-429C-63
US-09-948-429C-63
US-09-949-016-9534
US-09-949-016-9535
US-09-949-016-9536
US-09-949-016-9536
US-09-949-016-9537
US-09-949-016-9537
                              -09-328-352-4891
-09-252-991A-20800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-9539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 FOGVLONVRFV 318
1 FQGVLQNVRFV 11
TYPE: PRT
ORGANISM: Human
```

```
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                            US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Burgess et al.
TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099
FILE REFERENCE: 21402-099
CURRENT APPLICATION NUMBER: US/09/939,853A
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 60/228,191
PRIOR APPLICATION NUMBER: 60/228,191
PRIOR APPLICATION NUMBER: 60/269,961
PRIOR APPLICATION NUMBER: 60/269,961
PRIOR PELING DATE: 2001-02-08
PRIOR PELING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 159
SOFTWARE: Patentin Ver. 2.1
LENGTH: 831
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                        Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.2%; Score 55; DB 2; Length 831; 100.0%; Pred. No. 0.027; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTR: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                        Score 55; DB 2;
Pred. No. 0.027;
                                                                                                                                          93.2%; bcc.
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prec. ...
100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 98, Application US/09939853A; Patent No. 6989232; GENERAL INFORMATION:
              SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 97
LENGTH: 831
                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                          208 FÓGVLÓNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                    1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVLONVRFV 11
NUMBER OF SEQ ID NOS: 159
                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                      US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Cargill, Michele
APPLICANT: Teland, James S.
APPLICANT: Teland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Daley, George Q.
APPLICANT: Daley, George Q.
APPLICANT: McCarthy, Jeenstete J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US 60/153,357
FRIOR FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR APPLICATION NUMBER: US 60/225,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.2%; Score 55; DB 1; Length 1170; 100.0%; Pred. No. 0.039; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 2;
Pred. No. 0.039;
                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECHONE: (212) 278-0400
TELEFONE: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. ....
US/08/313,288B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-949-002-350
; Sequence 350, Application US/09949002
; Patent No. 6900016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09657472
Patent No. 6727063
                             January 5, 1995
                                                                                                                                                                                                                                                                                                             20:
                                                                                                                                                                                                                                                                             TELEX:
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
```

Gaps

```
Score 37; DB 2; Length 1045;
Pred. No. 1.1e+02;
2; Mismatches 2; Indels
  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11112
LENGTH: 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6333, Application US/09949016;
Parent No. 6812339
Parent No. PRORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-08-131-288B-19
; Sequence 19, Application US/08313288B
; Patent No. 5750502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 40021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
                                                                                                                                                       62.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 1172 amino acids
                                                                                                                                                         Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                        |:|:|||| |
281 FRGLLQNVHLV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:|||| |
202 FRGLLQNVHLV 212
                                                                                                                                                                                                                                               1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: USA
                                                                      ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-313-288B-19
                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11112, Application US/09949016

Sequence 11112, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT PILING DATE: 2000-01-28
FILE PRICA PLICATION NUMBER: 60/231,401
PRIOR PELICATION DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
CURRENT FILLS REFERENCE: File Reference: 7326-094
CURRENT FILLNG DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                            93.2%; Score 55; DB 2; Length 1170; 100.0%; Pred. No. 0.039; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 2;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa means any amino acid US-09-270-767-42057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 42057, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.1%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 QGVLQNVDFM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 OGVLONVRFV 11
                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Human
US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-270-767-42057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 42057
LENGTH: 731
                                                                                                                                                                                                                                             SEQ ID NO 350
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.7%; Score 37; DB 1; Length 1172; 63.6%; Pred. No. 1.38+02; ive 2; Mismatches 2; Indels
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     ZIP: 10036

COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40028-A-PCT-US
```

```
PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3511
LENGTH: 169
                                                      1999-01-29
                                                  PRIOR FILING DATE: 1999-01-X
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10457
LENGTH: 415
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 59.3
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 FNGTLENIKF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLONVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 VLKNLRFVA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VLQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC FEATURE LOCATION: (29)...(70)
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-134-000C-3511
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/109/489, 039A
CURRENT FILING DATE: 2000-01-27
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT PERERENCE: CLOO1307
CURRENT PAPLICATION UNMBER: US/09/949,016
CURRENT PAPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PAPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PAPLICATION NUMBER: 60/231,498
PRIOR PELING DATE: 2000-09-8
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Way Yonnie S.
TITLE OF INVENTION: ALL'i-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15.05) B.
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR PELING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SED ID NO 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.7%; Score 37; DB 2; Length 1172; 63.6%; Pred. No. 1.3e+02; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.3%; Score 35; DB 2; Length 162; 50.0%; Pred. No. 36; 7ative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-489-039A-10457
; Sequence 10457, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 527, Application US/09732210; Patent No. 6573361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| :|:| 1:| 1:| 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|:|||| |
202 FRGLLQNVHLV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLONVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-732-210-527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-732-210-527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lyan Doucette-Stamm et al
APPLICANT: Lyan Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-08-15
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                           ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                       59.3%; Score 35; DB 2; Length 415; llarity 77.8%; Pred. No. 1e+02; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.3%; Score 35; DB 2; Length 465; 50.0%; Pred. No. 1.1e+02; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        CARREAL INFOCRATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro. Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129W0
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 1998-03.27
PRIOR FILING DATE: 1998-03.27
PRIOR FILING DATE: 1998-03.19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
SENGTH: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3511, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                 RESULT 13
US-09-769-787-164
; Sequence 164, Application US/09769787
; Patent No. 6936252
; GENERAL NO. MinoRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-164
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Enterococcus faecalis
```

```
RESULT 15
US-09-583-110-3429
US-09-583-110-3429
Sequence 3429, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus;
TITLE OF INVENTION: PRHUMO-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT PILING DATE: 2000-05-26
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR PILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/081,553
PRIOR PILING DATE: 1998-05-12
PRIOR SEQ ID NOS: 5322
SEQ ID NO 3429
LENGTH: 459
; OTHER INFORMATION: Amino acids 29, 30, 59 & 70 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-3511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                         ö
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 2; Length 459;
Pred. No. 1.8e+02;
3; Mismatches 2; Indels
                                                           Query Match

57.6%; Score 34; DB 2; Length 169;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: June 5, 2006, 22:48:55 Job time: 24.8966 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 57.6%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: |:||:||
132 FKATLENVQFV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLONVRFV 11
                                                                                                                                                                      |||||::|
76 FQGVLRQIR 84
                                                                                                                                              1 FOGVLONVR 9
                                                                                                                                                δ
                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
```

THIS PAGE BLANK (USPTO)

Jun

Tue

```
Similarity
                                                                                                                                                                                                                                                                              US-10-474-213-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Appl
Sequence 40, Appl
Sequence 1020, Appl
Sequence 1022, Appl
Sequence 1047, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 455, Appl
Sequence 453, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 455, Appl
Sequence 455, Appl
Sequence 455, Appl
Sequence 455, Appl
Sequence 456, Appl
Sequence 456, Appl
Sequence 456, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 12, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1170, Ap
Sequence 1170, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 114, App
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 482, App
                                                                                                                                                                                                                                                                                                                                     Published Applications AA Main: *

| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep: *
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep: *
| FMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep: *
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                (without alignments)
70.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                      5, 2006, 23:46:43 ; Search time 78.6207 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-474-213-28

US-10-419-462-40

US-10-741-600-1020

US-10-741-600-1022

US-11-043-806-454

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-455

US-11-043-806-451

US-11-12-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-295-027-1170
US-10-211-462-38
US-10-231-956A-482
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                      2097797 seqs, 463214858 residues
                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              protein search, using sw model
                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                          1 FQGVLQNVRFVA 12
                                                                                                                   US-10-030-735-28
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459
466
685
685
685
831
831
1100
11150
11150
11170
11170
11170
11170
11170
11170
11170
11170
11170
                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              June
                                                                                                                                                                                                                                                                                                                                                               .......
                                                                                                                                  Perfect score:
                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein -
                                                                                                                                             Sequence:
                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
```

```
Sequence 28, Application US/10474213

Fublication No. US20040214248A1

Fublication No. US20040214248A1

GENERAL INPORMATION:

APPLICANT: ROBERTS, Henry C

TITLE OF INVENTION: USE OF SEMENOGELIN IN THE DIAGNOSIS, PROGNOSIS AND TREATMENT OF

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: 2002-10-06

FILE REFERENCE: 224329

CURRENT FILING DATE: 2002-10-06

FRIOR APPLICATION NUMBER: CT/US02/10535

PRIOR APPLICATION NUMBER: 60/281,994

FRIOR APPLICATION NUMBER: 60/281,994

FRIOR APPLICATION NUMBER: 02010-04-06

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.2

SEC ID NO 28

TENNING DATE

SEC ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-10-419-462-40
US-10-419-462-40
Sequence 40, Application US/10419462
Publication No. US20040053392A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
TITLE REFERENCE: WIll07-20005
CURRENT APPLICATION NUMBER: US/10/419,462
CURRENT FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                               Sequence 594, App
Sequence 596, App
Sequence 51, App
Sequence 21, Appl
Sequence 28, Appl
Sequence 123, App
Sequence 2428, App
Sequence 2428, App
                                                              44, Appl
548, App
1376, Ap
2, Appli
594, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                          Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%; Score 55; DB 4; Length 12; 100.0%; Pred. No. 0.0012; cive 0; Mismatches 0; Indels
            US-10-741-600-1018

US-10-741-600-1019

US-10-741-600-1021

US-10-782-968-38

US-10-849-989-44

US-10-631-467-1346

US-10-631-467-1376

US-10-995-561-594

US-10-995-561-595

US-10-995-561-595

US-11-046-644-28

US-11-046-644-28
                                                                                                                                                                                                                      US-10-425-114-49331
                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic peptide US-10-474-213-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
            1170
11170
11170
11170
11170
11170
11170
11170
11170
11170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial
\alpha
```

us-10-030-735-28.rapbm

```
RESULT 6
US-11-043-806-462
Squence 462, Application US/11043806
Squence 462, Application WS/11043806
Squence 462, Application Wo. US20060051774A1
GENERAL INFORMATION:
TILLE OF INVENTION: Chapten Lerof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: Lhereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT PILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 462
LENGTH: 459
                                                                                                                                                                                                                                                             APPLICAT: CARGILL, Michele et al.
APPLICAT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASLESQ for Windows Version 4.0
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 459;
100.0%; Pred. No. 0.06;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.2%; Score 55; DB 6;
100.0%; Pred. No. 0.064;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.2%; Score 55; DB 5;
100.0%; Pred. No. 0.06;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
COCATION: (1)...(432)
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-741-600-1022
                                                                                                                                                                                                                Sequence 1022, Application US/10741600 Publication No. US20050026169A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1047, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
  Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.2
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                         208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FOGVLONVRFV 218
                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-11-043-806-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
                                                                 1 FQGVLQNVRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                   US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
                                                                     ò
                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kevin J. Williams
APPLICANT: Kevin J. Williams
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents FILE REFERENCE: W1107-2005
CURRENT APPLICATION NUMBER: US/10/782,968
CURRENT APPLICATION NUMBER: US/10/419,462
PRIOR FILING DATE: 2004-02-20
PRIOR FILING DATE: 2003-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1020, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001499
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 1020
                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                     ; OTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-419-462-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-782-968-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 432;
                                                                                                                                                    DB 4; Length 240; 0.032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 93.2%; Score 55; DB 5; Length 240
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                   0; Indels
                                                                                                                                                    Query Match
93.2%; Score 55; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.2%; Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)...(432)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 40, Application US/10782968
; Publication No. US20050065324A1
                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin version 3.2
SEQ ID NO 40
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                               190 FOGVLONVRFV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 FOGVLONVRFV 200
                                                                                                                                                                                                                                           1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                       US-10-782-968-40
  LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

```
Sequence 452, Application US/11043806
Publication No. US20060051774A1
APPLICATION TO US20060051774A1
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Hereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
LENGTH: 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-043-066-453
US-11-043-066-453
US-11-043-066-453
Jepplication US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
TITLE OF INVENTION: Ltd
TITLE OF INVENTION: Ltd
TITLE OF INVENTION: Ltd
TITLE OF INVENTION: Ltd
CURRENT APPLICATION UNMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
SEQ ID NO 453
LEMETH 804
LEMETH 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78-11-043-806-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-455
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-45
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-46
78-20-06-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.2%; Score 55; DB 6; Length 685; 100.0%; Pred. No. 0.099; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.2%; Score 55; DB 6; Length 804; 100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 0.1 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 11; Conservative
                                                                                 208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLONVRFV 11
                                             1 FOGULONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                RESULT 10
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                             ઠે
                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-043-806-456
Sequence 456, Application US/11043806
Sequence 456, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methode
TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847-1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT PILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 454, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
APPLICAMT: Compugen Lich
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION UNDER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%; Score 55; DB 6; Length 578; 100.0%; Pred. No. 0.082; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%; Score 55; DB 3; Length 466; 100.0%; Pred. No. 0.065; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 93.2%; Score 55; DB 6; Length 555 Best Local Similarity 100.0%; Pred. No. 0.079; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 FQGVLQNVRFV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FÓGVLÓNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Homo sapiens
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 11, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-043-806-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
```

```
208 FQGVLQNVRFV 218
                                                                                                                                                                                     1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 11; Conserva
   US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-043-806-461
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                              q
                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 97, Application US/09939853A

| Sequence 97, Application US/09939853A
| Publication No. US20040039163A1
| GENERAL INFORMATION:
| APPLICANT: Burgess et al.
| TITLE OF INVENTION: NO. US20040039163A1el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099
| CURRENT APPLICATION NUMBER: US/09/939,853A
| CURRENT FILING DATE: 2001-08-27
| FRIOR APPLICATION NUMBER: 60/229,191
| FRIOR APPLICATION NUMBER: 60/267,300
| FRIOR FILING DATE: 2001-02-08
| FRIOR FILING DATE: 2001-02-20
| FRIOR FILING DATE: 2001-03-20
| FRIOR FILING DATE: 2001-03-20
| FRIOR APPLICATION NUMBER: 60/277,337
| FRIOR APPLICATION NUMBER: 60/277,337
| FRIOR SEQ ID NOS: 159
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 98, Application US/09939853A

Sequence 98, Application US/09939853A

Publication No. US20040039163A1

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: No. US20040039163A1e1 Proteins and Nucleic Acids Encoding Same;

FILE REFERENCE: 21402-099

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/264,191

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

SOFTWARE PRIOR FILING DATE: 2001-03-20

EDROFTH SAFT PRIOR FILING DATE: 2001-03-20

SOFTWARE PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                  Query Match
93.2%; Score 55; DB 6; Length 828;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.2%; Score 55; DB 3; Length 831; 100.0%; Pred. No. 0.12; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                    208 FÓGVLÓNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                        1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLQNVRFV 11
                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-939-853A-97
LENGTH: 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
RESULT 15
US-11-043-806-461

i Sequence 461, Application US/11043806

j Sequence 461, Application No. US20060051774A1

j GENERAL INFORMATION:
 APPLICANT: Compugen Ltd

j TILLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
 TILLE OF INVENTION: Lhereof for Diagnosis of Prostate Cancer
 FILE REFERENCE: 1847.1003
 CURRENT PPLICATION NUMBER: US/11/043,806
 CURRENT FILING DATE: 2005-01-27
 NUMBER OF SEQ ID NOS: 575
 SEQ ID NO 461
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
93.2%; Score 55; DB 3; Length 831; 100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.2%; Score 55; DB 6; Length 855; 100.0%; Pred. No. 0.13;
                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: June 6, 2006, 00:00:10 Job time: 78.6207 secs
                   Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                      208 FÓGVLÓNVRFV 218
```

```
57.6%; Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-953-349-39312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-953-349-9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33312, A Sequence 3347, Ap Sequence 34674, A Sequence 34672, A Sequence 2413, Ap Sequence 27518, A Sequence 27517, A Sequence 16526, A Sequence 16526, A Sequence 16526, A Sequence 19574, A Sequence 28462, A Sequence 28461, A Sequence 28462, A Sequence 28461, A Sequence 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2816, Ap
5, Appli
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3713, Ap
39138, A
3586, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          blished Applications AA New:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                                                                                                                                                                                   (without alignments)
37.266 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seduence sed
                                                                                                                                                          6, 2006, 00:00:38 ; Search time 3.72414 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
Sequence
Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-953-349-39312
US-10-953-349-3447
US-10-953-349-34673
US-10-953-349-34672
US-10-953-349-34672
US-10-953-349-34672
US-10-953-349-27518
US-10-953-349-27516
US-10-953-349-16526
US-10-953-349-16526
US-10-953-349-16526
US-10-953-349-19576
US-11-203-3697-2816
US-11-203-3697-2816
US-11-203-3697-3818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   58871 seqs, 11565156 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                             US-10-030-735-28
59
1 FQGVLQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published
                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22222101111111109876543
22221098765432110
```

```
Sequence 39312, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT APPLICATION
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 39312
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3437, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATOMETER PATOM
Sequence 2388, Ap Sequence 39137, A Sequence 39136, A Sequence 24680, A Sequence 24680, A Sequence 26200, A Sequence 26200, A Sequence 26899, A Sequence 28999, A Sequence 22951, A Sequence 28989, A Sequence 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 6; Length 132;
Pred. No. 4.7;
3; Mismatches 3; Indels
                            US-10-953-349-3913
US-10-953-349-3913
US-10-953-349-2913
US-10-953-349-24690
US-10-953-349-24689
US-10-953-349-24689
US-10-953-349-26200
US-11-293-697-3263
US-11-293-697-3263
US-11-293-697-3263
US-10-953-349-28990
US-10-953-349-289990
US-10-953-349-289990
US-10-953-349-289990
US-10-953-349-289990
US-10-953-349-289990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-1066
US-10-504-120-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Zea mays subsp. mays
US-10-953-349-39312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVLONVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|:| | |:|
66 FEGILNNNVFIA 77
         2222EEEEEEEEEEE
```

DB 6; Length 298;

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Moddward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: MacDonald
APPLICANT: Moschberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT FILING DATE: 2004-10-19
FRIOR APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2003-04-24
FRIOR APPLICATION NUMBER: US 10/131,831
FRIOR APPLICATION NUMBER: US 10/325,899
FRIOR RILING DATE: 2002-04-24
FRIOR APPLICATION NUMBER: US 10/325,899
FRIOR FILING DATE: 2002-12-20
FRIOR PILING DATE: 2002-12-20
FRIOR FILING DATE: 2002-12-20
                                                                                                                                                                                             Score 34; DB 6; Length 382;
Pred. No. 15;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 6; Length 750;
Pred. No. 51;
3; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/953,349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: EXPRESSION DIAGNOSTICS, INC. APPLICANT: Wohlgemuth, Jay APPLICANT: Fry, Kirk APPLICANT: Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                               US-10-511-937-2413
Sequence 2413, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2992, Application US/10511937; Publication No. US20060088836A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5,
              CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE PAtentIn version 3.3 SEQ ID NO 34672 LENGTH: 382
                                                                                                                     ; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.2
SEQ ID NO 2413
LENGTH: 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.9%;
                                                                                                                                                                                                 57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morris, MacDonald
Rosenberg, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wohlgemuth, Jay
Fry, Kirk
Woodward, Robert
                                                                                                                                                                               Query Match
Best Local Similarity 54.5

Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ly, Ngoc
Prentice, James
                                                                                                                                                                                                                                                                                                      276 QGVLFNIQYVS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                2 OGVLONVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: ::||::|
508 FENIIQNLKF 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FQGVLQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-511-937-2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-511-937-2413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                 Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERENCE: 2750-15799082
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 34674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34673, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILLE OF INVENTION: ENCONDED THERBY
FILLE REPERENCE: 2750-15799F025
CURRENT FILLING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34672, Application US/10953349
Publication WO. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 6; Length 358;
Pred. No. 14;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 6; Length 331;
Pred. No. 13;
                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
ed. No. 12;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
  Pred. No.
                    . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Zea mays subsp. mays US-10-953-349-34674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Zea mays subsp. mays US-10-953-349-34673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.6%;
Best Local Similarity 36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54...
6; Conservative
                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.6
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 OGVLFNIOYVS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||| |:::|:
252 QGVLFNIQYVS 262
                                                         QGVLQNVRFVA 12
                                                                                :|::| |:|::
87 EGIIOGVKFIS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 QGVLQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 QGVLQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-953-349-34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-953-349-34673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 34673
LENGTH: 358
                                                           ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
                                                           ઠ
                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
Sequence 16527, Application US/10953349

Publication No. US20060107345A1

SEQUENCE INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF THE REPRENCE: 2706-16799US2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

SOFTWARE: Patentin version 3.3

SEQ ID NO 16527

LENGTH: 843

"WORL NOTE: NO
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2755. Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799W22
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PALENTIN Version 3.3
SEQ ID NO 27516
LENGTH: 213
                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                       Score 32; DB 6; Length 188;
Pred. No. 17;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 6; Length 213;
Pred. No. 20;
0; Mismatches 5; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.2%; Score 32; DB 6; Length 843; 54.5%; Pred. No. 91; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CS-10-953-349-16526
Sequence 16526, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.2%;
                                                                          54.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-27516
                                                                   Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 FSAALAEVRFVA 101
                                                                                                                                                                                                  1 FOGVLQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|:| | ||
780 FKGILDNYVFV 790
                                                                                                                                                                                                                                                         65 FSAALAEVRFVA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGULONVREVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRCANISM: Glycine max
US-10-953-349-16527
                US-10-953-349-27517
                                                                                                                                                                                                                                                                                                                                                                                       US-10-953-349-27516
                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27577, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL THORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
SUPPRESS OF SEQ ID NOS: 40252
SOFTWARE: Patentin Version 3.3
SEQ ID NO 27517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27518, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-15799PUS2
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTICATION version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REPERBENCE: 506612001104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
FRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR PELLING DATE: 2003-04-24
PRIOR PILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/135,899
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR PILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117-2
SOFTWARE: PALENTIN VERSION 3.2
LENGTH: 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 6; Length 1333;
Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 6; Length 186;
Pred. No. 17;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Triticum aestivum US-10-953-349-27518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|||: :|: |
327 FRGVLEQLRWFA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGULONVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FQGVLQNVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 FSAALAEVRFVA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-953-349-27517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-511-937-2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 27518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
1 FQGVLQNVRFVA 12
                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1625, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2700-1579PUS2
CURRENT PELING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 16525
LENGTH: 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19576, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PALENTIN version 3.3
SEQ ID NO 19576
LENGTH: 301
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILE REPERENCE: 2750-1579P082 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT PILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: Patentin version 3.3 SEQ ID NO 16526 LENGTH: 962
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 6; Length 301; Pred. No. 46; 2; Indels
                                                                                                                                                                                                                                                                Length 962;
                                                                                                                                                                                                                                                                Score 32; DB 6; Length 962
Pred. No. 1.1e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 6; Length 101
Pred. No. 1.1e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative 4
                                                                                                                                                                                                                                                                  54.2%;
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                       |:|| | ||
899 FKGILDNYVFV 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              951 FKGILDNYVFV 961
                                                                                                                                                                                                                                                                                                                                            1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Glycine max
US-10-953-349-19576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Glycine max US-10-953-349-16525
                                                                                                                                                                                                    , ORGANISM: Glycine max US-10-953-349-16526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-953-349-16525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-10-953-349-19576
                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

```
RESULT 15
US-10-953-349-19575
US-10-953-349-19575
US-10-953-349-19575
Sequence 19575, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT APPLICATION UNDER: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 19575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 6; Length 320;
Pred. No. 49;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: June 6, 2006, 00:12:56
Job time : 3.82414 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.5%;
50.0%;
211 FQGLLRTLKQVA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.5
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||:|: :: ||
230 FQGLLRTLKQVA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLONVRFVA 12
                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-19575
```

```
5, 2006, 22:08:53 ; Search time 91.1379 Seconds (without alignments) 60.201 Million cell updates/sec
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                               2589679
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      2589679 seqs, 457216429 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                        US-10-030-735-29
60
1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                          BLOSUM62
                                                                                                                          June
                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                          Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20018:* geneseqp20028:* geneseqp2003a8:* geneseqp2003b8:*

geneseqp1990s:* geneseqp1990s:* geneseqp2000s:*

A Geneseq 8:* 1: geneseqp19

Database

geneseqp2004s:* geneseqp2005s:* geneseqp2006s:*

... 10:

	Description	Aab35362 Alpha3bet	Aab35352 Alpha3bet	Aab35378 Alpha3bet	Abg72834 Thrombosp	Adl70641 Human thr	Adq39359 Human myo		Aau02916 Angiotens	Aab43602 Human can	Aau02915 Angiotens	Adn02474 TSF polyp		Aau02913 Angiotens	Aab00042 Human thr	Aau74771 Human thr	Abb82285 Human thr	Aab74450 Human var	Aab90800 Human she	Aae25030 Human thr	Aau75315 Human thr	Abp96780 Human COP	Abu03474 Angiogene	Abg74673 Human THB
SUMMARIES	αI	AAB35362	AAB35352	AAB35378	ABG72834	ADL70641	ADQ39359	ADQ39357	AAU02916	AAB43602	AAU02915	ADN02474	AAU02914	AAU02913	AAB00042	AAU74771	ABB82285	AAB74450	AAB90800	AAE25030	AAU75315	ABP96780	ABU03474	ABG74673
	DB	4	4	4	9	œ	œ	œ	4	m	4	7	4	4	m	ហ	S	4	4	S	ഹ	φ	ø	9
	% Query Match Length DB	12	12	12	12	240	432	432	459	466	546	548	555	731	1152	1152	1152	1170	1170	1170	1170	1170	1170	1170
	% Query Match	100.0	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7
	Score	09	55	55	22	55	52	52	52	52	55	25	52	55	55	25	55	55	55	22	52	55	22	22
	Result No.	п	7	٣	4	2	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

:

Aae36228 Human THB Abr62059 Human thr Adn39852 Cancer/an Adj76124 Marker ge Adj75296 Marker ge Adj7629 Human thr Add26070 Thrombosp Add39358 Human myo Add39358 Human hyo Add39358 Human chr Add39358 Human chr Add39358 Human chr Add39358 Human chr Add39358 Adpha3bet Add35374 Alpha3bet Add35374 Alpha3bet Add35374 Alpha3bet Add35376 Alpha3bet Add35376 Alpha3bet Add35376 Alpha3bet	ALIGNMENTS			e #27.	, cell proliferation, cancer; atherosclerosis, rheumatoid arthritis; ell adhesion; cell motility.					ICES.			cognized by alpha3-beta1 integrins, ito extracellular matrix, cell treating rheumatoid arthritis and		number of peptides which bind to seful in the modulation of cell adhesion t of cancer, diabetic retinopathy, eneration, atherosclerosis, psoriasis nce is an example of one of the peptides	
AAE36228 ADN39852 ADN36124 ADJ76124 ADJ76239 ADL36670 ADQ39358 ADQ3958 ADQ39 ADQ3958 ADQ3958 ADQ3958 ADQ3958 ADQ3958 ADQ3958 ADQ39 ADQ3958 ADQ3958 ADQ3958 A	ALIG	; 12 AA.		pepti	genesis nosis; a				ъ.	HUMAN SERVICE			or are re adhesion and for	English.	្នុកពីស្គ	
φ Γ Γ Φ Φ Φ Φ Φ Φ Φ Φ Φ Φ Φ Φ Φ Φ Φ Φ Φ			₹	din	angio reste psori			8986	549				d to o cell ation	Eng	ovi tr tr cul ent	
11170 1100 1100		; peptide	st entry)	rin binding	il integrin; an retinopathy; re egeneration; ps			000WO-US018	9US-0144	рт неастн &	sech HC	18.	bind t ting ce iferati	84pp;	9 H H 9 H	
rrrrrrrrrrrrrrrrrrrr			fir	egri	pa pa at:			000	99	Ξ	Krutzs	/9	that nhibit prol:	4	nventi ntegri and i thriti s. The	
3335566911111111111111111111111111111111		andard	Ξ	int	int	9	į	2		EPI	2	265	첉첉	e G	inven integ y, and arthri sis. T	Ä
0 0 0 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2		1 62 AB35362 Bt	AY-	pha3beta1	pha3beta abetic cular de	Synthetic.		2-JUL-2000;	5-JUL-1999;	(USSH) US DE	Roberts DD,	WPI; 2001-18	ew peptides seful for i stility and	aim 4; Pag	present a motility a motility seumatoid a restence the inverse	Sequence 12
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		5 E	₹ 0	Al	Al) dii	io S	. 0	7	7	_	œ.	3	ZäĔü	ប	The all h	Ø
		AAB XXX	#XE	X B	\$ \$ \$ \$ \$	\$8\$	E X E	X & 3	1 E 3	18	# Z X	8	\$&&&&	\$ 23 \$	\$8888888 \$ \$	Š

RESULT 2 AAB35352

g ò

```
The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                              diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                            New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; thrombospondin-1; cytostatic; immunostimulant; cancer; epithelial cancer; lung cancer; papillary renal cell carcinoma; colon cancer; small-cell lung cancer; SCLC; melanoma.
                                cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.7%; Score 55; DB 4; Length 12; 91.7%; Pred. No. 0.00063; 1; Indels
                                cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombospondin-1 sequence containing synthetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG72834 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2001; 2001US-0281994P.
                                                                                                                                                                                                          12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                            99US-0144549P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-APR-2002; 2002WO-US010535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                               Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOGVLONVRFVF
                                Alpha3betal integrin;
                                                                                                                                                                                                                                                                                                                                               WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200281630-A2.
                                                                                                                                       WO200105812-A2
                                                                                                                                                                                                                                            15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-2003
                                                                                                                                                                         25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG72834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of peptides which bind to alphalbetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid archritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                               Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                    Gaps
                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%; Score 55; DB 4; Length 12; 91.7%; Pred. No. 0.00063; ive 0; Mismatches 1; Indels
                                                  Indels
Score 60; DB 4; Ler
Pred. No. 6.4e-05;
                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                 Alpha3betal integrin binding peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha3betal integrin binding peptide #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                             AAB35352 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; peptide; 12
                Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 91.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krutzsch HC;
                                                                                      1 FQGVLANVRFVF 12
                                                                                                            FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||| |||||
FQGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200105812-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roberts DD,
                                                                                                                                                                                                                                                                                08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB35378;
                                                                                                                                                                                                                                                AAB35352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB35378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer
```

Best Loc Matches

AAB35378 RESULT

exaxexe

g

ð

ö

Gaps

```
The invention relates to diagnosing cancer other than prostate cancer in a male mammal, comprising assaying a test sample for increased level of semenogelin, or cancer in a female by assaying for the presence of semenogelin. Administering a semenogelin protein or polypeptide fragment or a semenogelin-specific antibody or active fragment, or a recombinant vector expressing the protein or antibody, is useful for inducing an immune response to a cancer in a mammal, where the cancer is not prostate cancer, particularly of epithelial origin such as lung cancer, particularly emalocall lung cancer, especially small-cell lung cancer, sequence containing synthetic peptide
                                             A new diagnosis for cancer other than prostate cancer in a mammal useful to detect cancer including lung cancer, particularly small cell lung cancer and melanoma comprises detecting semenogelin in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  purified thrombospondin fragment extracted from a body fluid, useful diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 6; Length 12;
Pred. No. 0.00063;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151. .164 /
/note= "Fibrinogen binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77. .82
/note= "Heparin binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .32
ce= "Heparin binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human thrombospondin-1 N-terminal domain.
                                                                                                                                                                                                                                                                                                                                                    which binds to alpha-3-beta-1 integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL70641 standard; protein; 240 AA.
                                                                                                               Example 1; Page 14; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2002; 2002US-0405494P.
21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2003; 2003WO-US026023
                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVLQNVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQGVLANVRFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WILL/) WILLIAMS K J.
             WPI; 2003-103329/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPI; 2004-226901/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004018995-A2
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL70641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
The present sequence is that of the N-returnal andmain of numan thrombospondin-1 (TSP) ALJV659. The invention relates to TSP fragments (G-100, 40-55 or 20-35 kDa mol.w.) found in plasma, and their use in clinical assays for cancer and for generation of antibodies and other clinical assays for cancer and for generation of antibodies and other clinical assays for cancer and for generation of the TSP fragment or chicical assays for cancer and for generation of the TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion of the plant and the TSP poly; and (3) using the difference between (1) and contain a quantitation of TSP plus TSP fragment or portion. Suitable epitopes are provided ADJV651 between or portion of other or portion of the TSP fragment or portion of a quantitation of the amount of TSP fragment or portion of the TSP fragment or portion of a quantitation of the amount of TSP fragment or portion of the TSP fragment or portion is performed in order to detect the presence or monitor the course, of a disease or condition or glace from cancer, renal failure, renal allogate, abthms, diabetes mallitus, mycoardial concerns, or monitor, liver disease, appending for the TSP fragment or portion is performed, in the TSP fragment or portion associated with histmanacous, Rawsaki condosa, systemic lupus erythematosus, a condition associated with clotting, a condition associated with placelet activation, a condition associated with endothelial experience of the respiratory 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human myocardial infarction-associated gene derived protein, SEQ ID 1022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
or leukemia or as calibrators, indicators, immunogens and analytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                              sequence is that of the N-terminal domain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 8; Length 240;
Pred. No. 0.018;
0; Mismatches 1; Indels
                                       Disclosure; SEQ ID NO 40; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ39359 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOGVLONVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ39359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ39359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXXXXXXXX
```

Gaps

.; 0

prostate

Human myocardial infarction-associated gene derived protein, SEQ ID 1020.

Myocardial infarction; detection; single nucleotide polymorphism; SNP;

cardiant; gene therapy; human

WO2004058052-A2. Homo sapiens.

15-JUL-2004.

```
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least curther comprises where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino comprising an amino acid sequence given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in the specification and which is between about 16 and 1000 nucleotides in length, a kit for detecting an SNP in a nucleic acid molecule, a buffer and an enzyme; a method of detecting an SNP in a mucleic acid molecule; a method of detecting an SNP in a method for identifying an agent useful in treating or preventing and a method for identifying an agent useful in treating or preventing method in the properties and an enzyme; and a variant polypeptide; and a method for identifying an agent useful in treating or preventing method in the properties and an enzyme; and a variant polypeptide; and a method for identifying an agent useful in treating or preventing and a method in the properties and an enzyme; and an enzyme; and a cardiant activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence was not shown in the specification. The sequence has come from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.034;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; SEQ ID NO 1022; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55;
                                                                                                                                                                                                                                                                                                                                                         Cargill M, Devlin JJ, Iakoubova O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                20-DEC-2002; 2002US-0434778P.
                                                                                                                                                                                                                       2003US-0453135P.
2003US-0466412P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.7%;
91.7%;
                                                                                                                                                      22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                                                               2003US-0504955P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FOGVLONVREVE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 91.7
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                             (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-533949/51.
N-PSDB; ADQ38531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 432 AA;
                                                              WO2004058052-A2.
                       Homo sapiens
                                                                                                                                                                                                                                                                 23-SEP-2003;
                                                                                                                                                                                                                       10-MAR-2003;
30-APR-2003;
                                                                                                          15-JUL-2004
```

The invention relates to a novel method for identifying an individual who

Claim 10; SEQ ID NO 1020; 145pp; English.

the individual's nucleic acids

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in

Iakoubova O;

Cargill M, Devlin JJ, (APPL-) APPLERA CORP

WPI; 2004-533949/51.

N-PSDB; ADQ38529

10-MAR-2003; 2003US-0453135P. 30-APR-2003; 2003US-0466412P. 23-SEP-2003; 2003US-0504955P.

22-DEC-2003; 2003WO-US040978.

2002US-0434778P

```
The inventor relates to a movel method to inclusive an interaction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleotide sequences given in the specification in the individual. The invention altered risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention truther comprises: an isolated nucleic acid molecule comprising at least second for incleation or its complement and encoding any one of the amino acid sequences given in the specification or its complement and encoding any one of the amino acid sequences given in the specification, an antibody that specifically binds to the polympeptide or its antigen-binding that specification and which is between about 16 and 1000 nucleotides in comprising the polymucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in clength; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing method for identifying an agent useful in treating or preventing and eccapance is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction. The novel detection method has cardiant activity. The nucleic acide of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence was not shown in the specification. The sequence has come from sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 8; Length 432;
Pred. No. 0.034;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
AAU02916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

ADQ39357 standard; protein; 432 AA.

RESULT 7 ADQ39357

ò

18-NOV-2004 (first entry)

ADQ39357;

dermatological; neuroprotective; thrombolytic; coagulant; noctropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allogic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.

diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;

Human; cancer associated gene; cancer antigen; detection; cancer;

Human cancer associated protein sequence SEQ ID NO:1047.

(first entry)

08-FEB-2001

AAB43602;

AAB43602 standard; protein; 466 AA.

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disponders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, immune disorders such as immune complex nephritis immune circust.
                                                                                                                                                                                                 granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic enphropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                 Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                     Angiotensin converting enzyme (ACEV) splice variant protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Khosravi R, Bernstein J;
AAU02916 standard; protein; 459 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 16; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Levine Z, David A, Azar I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            991L-00132978.
991L-00133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000; 2000WO-IL000766.
                                                                                        12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS06016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200136632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2001.
                                            AAU02916;
```

08-MAR-2000; 2000WO-US005882.

WO200055350-A1. Homo sapiens.

21-SEP-2000.

99US-0124270P.

12-MAR-1999;

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM; WPI; 2000-587533/55.

N-PSDB; AAC77811

Novel isolated nucleic acids comprising sequences encoding peptides

useful for treating or diagnosing e.g. cancer. Claim 11; Page 1636-1638; 2352pp; English.

```
antinflammatory; autithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; coopulant; coopu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4229. The proteins can have activities based on the ALB843398 to AAB4229. The proteins can have activities based on the include: cytostatic; proliferative, vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 3; Length 466;
Pred. No. 0.037;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 FOGVLONVREVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

ö

Gaps

ö

91.7%; Score 55; DB 4; Length 459; 91.7%; Pred. No. 0.036; ive 0; Mismatches 1; Indels

Conservative 1 FOGVLANVRFVF 12

Local Similarity tes 11; Conserv

Query Match Best Loc Matches FOGVLONVRFVF 219

208

ò

RESULT 9

(first entry)

```
Tumor suppressing polypeptide TSF and gene therapy vector composition.
                                                                                                                                                                                                                                     adenovirus vector; anti-neoplastic; TSF polypeptide; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TAID-) TAIDA LIFE SCI TECH RES CENT HEMATOLOGY.
                                             ADN02474 standard; protein; 548 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-2002; 2002CN-00129408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-469302/45.
N-PSDB; ADN02475.
                                                                                                                                                                                          TSF polypeptide.
                                                                                                                                             17-JUN-2004
                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       CN1401387-A.
                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-2003.
                                                                                             ADN02474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Han Z,
RESULT 11
                      ADN02474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU02914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic caids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various of candidate sandoraceand diseases such as artriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                     Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nonatcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                             Angiotensin converting enzyme (ACEV) splice variant protein #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.7%; Score 55; DB 4; Length 546; 91.7%; Pred. No. 0.044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.044;
0; Mismatches
                                               AAU02915 standard; protein; 546 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Fig 15; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99IL-00132978.
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 91.7
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS06015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200136632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1999;
                                                                                                                                                  12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levine Z,
```

```
ö
                                         The present invention relates to a novel recombinant adenovirus vector mediated anti-neoplastic composition is prepared through cloning the cDNA sequence from the human peripheral blood cell by specific primer and reverse transcription-polymerase chain reaction (RT-PCR) method for coding TSF polypeptide, construction in human embryonic kidney cell 293 by AdEasy system, and packaging and expressing the recombinant adenovirus vector of TSF. It can suppress the growth and transfer of cancer. The present sequence represents the TSF polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiotensin converting enzyme splice variant; ACBV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P5; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction, coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angiotensin converting enzyme (ACEV) splice variant protein #14.
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                            Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                               Score 55; DB 7;
Pred. No. 0.044;
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
Claim 2; SEQ ID NO 1; 13pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02914 standard; protein; 555 AA.
                                                                                                                                                                                                                                                                                                                                            91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 91.7 es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                               Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU02914;
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $$ $$ $$ $$ $$ $$ $$ $$ $$ $$ $$
```

ö

Gaps

ö

1; Indels

208

FOGVLANVRFVF 12

ò

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen P53, and vasoactive interleukin 6, polypeptide receptor 2. The polypeptides and their associated nucleic cacids are useful for identification of variant sequences and detection of cacids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as simmune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidote pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection; glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                      David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361. .416
/label= Type 1 repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB00042 standard; protein; 1152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 13; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human thrombospondon-1 (TSP-1).
     vascular disorder; asbestosis.
                                                                                                                                                                                                                                                          99IL-00132978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%;
91.7%;
                                                                                                                                                                                                        17-NOV-2000; 2000WO-IL000766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FÓGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                    (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-336004/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS06013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 731 AA;
                                                                                                    WO200136632-A2
                                                       Homo sapiens
                                                                                                                                                                                                                                                        17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                      25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                      Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB00042
     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovacular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases on such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon, hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme (ACEV) splice variant protein #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Levine Z, David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 4;
Pred. No. 0.045;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02913 standard; protein; 731 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 14; 519pp; English.
vascular disorder; asbestosis.
                                                                                                                                                                                                   17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                     991L-00132978
991L-00133455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.7%,
Thes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                               (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-336004/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS06014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 555 AA;
                                                                                                 WO200136632-A2
                                                                                                                                                                                                                                                     17-NOV-1999;
                                                  Homo sapiens
                                                                                                                                                                                                                                                                               10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2001
                                                                                                                                                   25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU02913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU02913
```

ô

Gaps

; 0

Score 55; DB 4; Length 731; Pred. No. 0.061; 0; Mismatches 1; Indels

g

ò

```
ocation/Qualifiers
                                                                                                                                                          13. .415
label= RFK motif
note= "Necessary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 7; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2001; 2001WO-US017250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000; 2000US-0207994P
                                                                                                                                                                                                                                                               /label= Ce<sup>7</sup>
                                                                                                                                                                                                                                                                                      .483
/label= He-
81
                                                                                                                                                                                                                                                                                                                                      .491
/label= r
                      263. .360
/label= Pr
                                              309
                                                                                                                                                                                                                                                                                                                                                                                                                 570. .601
/label= C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-106273/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200191781-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lawler JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carrier.
             Key
Region
                                                Domain
                                                                                   Domain
                                                                                                                                   Domain
                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                           Region
                                                                                                                                                                                                          Domain
  New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TGF (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1 caused by PCR (polymerse chain reaction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. Anti-

Cor treating human immunodeficiency virus (HIV) infection. Anti-
agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombospondin-1; TSP-1; cytostatic; anglogenesis; vasotropic; vulnerary; neovascularisation; cell proliferation inhibitor; cancer; solid tumour; haemangionas; acustic neuromas; neurofibroma; trachoma; acustic neuromas; progenic granulomas; rheumatoid arthritis; ocular anglogenic disease; retinopathy; psoriasis; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rebeosis; angiofibroma; obler-Webber syndrome; myocardial anglogenesis; haemophiliac joints; plaque neovascularisation; telangiectasia; wound granulation; apoptosis.
                                                                                                                                                                                                                               Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.7%; Score 55; DB 3; Length 1152; 91.7%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
417. .473
/label= Type 1 repeat region
474. .530
/label= Type 1 repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                           (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU74771 standard; protein; 1152 AA.
                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           does not induce drug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human thrombospondin-1 (TSP-1).
                                                                                                            01-FEB-2000; 2000WO-US002482
                                                                                                                                    99US-0118053P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLANVRFVF 12
                                                                                                                                                                                                           WPI; 2000-514823/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1152 AA;
                                                             WO200044908-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                    01-FEB-1999;
                                                                                     03-AUG-2000
                                                                                                                                                                                    Lawler JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU74771;
     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
  硆
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
The invention describes a composition comprising cDNA encoding fragments of human thrombospondin-1 (TSP -1), a type 1 repeat polypeptide and potent inhibitor of tumour growth and angiogenesis. The composition is useful for killing cancerous cells (preferably tumour); for reducing volume or inhibiting growth of a tumour (inhibiting neovascularisation the tumour); for decreasing proliferation of tumour cells; in the treatment of diseases and conditions associated with angiogenic activity or misregulated growth and angiogenesis-mediated diseases such as cancer, solid tumour, tumour metastasis, benign tumour, (e.g. haemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Type 3 repeat domain
/note= "This region contains 7 type 3 repeats, from
/note= "This region contains 7 type 3 residues 757-792,
residues 793-815, residues 816-853, residues 854-889 and
residues 890-925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition useful for treatment of cancer comprises cDNA encoding amino acids of human thrombospondin-1 or its conservative variant and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531. .673 — "A point domain habe Type 2 repeats, from horsidues 531-571, residues 572-629 and residues 630-673"
                                                                                                                                              361. .530
/label= Type_1 repeat_domain
/note= "This region contains 3 type 1 repeats, from
residues 361-416, residues 417-473 and residues 474-530"
                                                                                                                                                                                                                                                                                                                                                                                                                                               ō
                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Necessary and sufficient for activation transforming growth factor beta (TGF beta)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118. .423
|Jabel= TGF-beta_and_fibronectin_binding_domain
'note= "Transforming growth factor"
                                                                         label= Procollagen homology_domain
note= "Required in_inhibition of angiogenesis"
Procollagen_homology_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81. .499 -
label= Anti-angiogenesis_domain
                                                                                                                                                                                                                                                                                                 64. .370
label= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20. .426
|abel= Heparin_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heparin binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calcium_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
```

```
rheumatoid arthritis, psoriasis, ocular angiogenic diseases (e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasias, rebeosis), Osler-Webber syndrome, myocardial angiogenesis, telangiectasia, plaque neovascularisation, haemophiliac joints, angiofibroma or wound granulation. The composition induces apoptosis and inhibits neovascularisation in the tumour cells. This amino acid sequence represents human thrombospondin-1 (TSP-1), on which the recombinant proteins of the invention are based
      8888888888888
```

Sequence 1152 AA;

ö 0; Gaps Query Match 91.7%; Score 55; DB 5; Length 1152; Best Local Similarity 91.7%; Pred. No. 0.1; Matches 11; Conservative 0; Mismatches 1; Indels

190 FQGVLQNVRFVF 201 1 FOGVLANVRFVF 12 ò g

Search completed: June 5, 2006, 22:24:59 Job time: 91.1379 secs

THIS PAGE BLANK (USPTO)

Tue Jun

```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

Run on:

5, 2006, 22:25:22 ; Search time 13.9655 Seconds (without alignments) 82.675 Million cell updates/sec

1 FQGVLANVRFVF 12

Sequence:

US-10-030-735-29 60 Title: Perfect score:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	thrombospondin 1 -	thrombospondin 1 p	thrombospondin 1 p	ot	reverse gyrase (to	hypothetical prote	H+-transporting tw	transporter homolo	transporter homolo	thrombospondin 2 p	N	ge	hypothetical prote	protein F53C3.11 (hypothetical prote	mannuronan C-5-epi	hypothetical prote	CO2C2.2 protein -	hydrogenase (EC 1.	hydrogenase, cytoc	_	,	-	branched-chain ami	probable dehydroge	GTP-binding protei		in	5-oxoprolinase (AT
SUMMARIES																														
SUMIN	QI .	79	TSHUP1	A40558	T34271	H69377	T24890	D84938	AF1108	AG1469	TSHUP2	A42587	T14171	F69113	D88115	T15657	S77626	B71115	S44740	A64599	D71915	C87403	S56224	AG2221	D64056	T36704	AG1259	AI1621	A39804	T42756
	DB	7	-	7	7	7	7	7	0	0	н	0	0	7	7	0	0	0	~	-	0	N	7	0	7	~	N	(4	Н	7
	Length	229	1170	1170	304	1054	400	467	628	628	1172	1172	1285	248	425	481	1839	111	152	224	224	298	385	399	436	563	608	609	1178	1288
de	Query	91.7	91.7	91.7	66.7	63.3	61.7	61.7	61.7	61.7	61.7	61.7	61.7	0.09	60.09	60.0	60.09	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3
	Score	55	55	55	40	38	37	37	37	37	37	37	37	36	36	36	36	35	35	35	35	35	35	35	35	35	35	35	35	35
	Result No.	-	7	e	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	probable membrane	probable amidotran	probable 3-oxoacyl	3-oxoacyl-[acyl-ca	hypothetical prote	vancomycin resista	probable transport	probable transport	ybdG protein - Esc	probable calmoduli	hypothetical prote	probable ptrBa pro	oligopeptidase B (oligopeptidase B (proteinase II [imp
AE1864	S52596	T45249	A64590	B71923	B87397	JN0249	G90705	B85556	G64790	A85363	T33595	A70709	AC0741	E64946	C90948
~	~	7	-	7	7	~	7	~	7	7	~	~	~	-	0
1829	111	206	247	247	268	343	415	415	415	467	469	552	683	989	989
58.3	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	26.7	56.7	56.7	26.7
35	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

```
Ciprocies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cipate: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
Ciscession: 557957
Rilafeuillade, B.; Pellerin, S.; Keramidas, M.; Chambaz, E.M.; Feige, J.J.
submitted to the EMBL Data Library, July 1995
A;Reference number: 557955
A;Reference number: 557955
A;Accession: 557957
A;Accession: 557957
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-229 cLAF>
A;Cross-references: UMIPROT:Q28194; UNIPARC:UPI000008740A; EMBL:X89511; NID:g899228; PIIC;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v
```

Length 229; Score 55; DB 2; Length 229 Pred. No. 0.0033; 0; Mismatches 1; Indels 91.7%; 91.7%; Query Match
Best Local Similarity 91.77
Matches 11; Conservative

ö

Gaps

ö

1 FOGVLANVRFVF 12 ઠે

190 FQGVLQNVRFVF 201 셤

- human thrombospondin 1 precursor

Cispeciaes: Homo sapiens (man)
Cispeciaes: Homo sapiens (man)
Cispeciaes: Homo sapiens (man)
Cipate: 23-Aug-1987 #sequence revision 03-Aug-1995 #text change 09-Jul-2004
Cipate: 23-Aug-1987 #sequence revision 03-Aug-1995 #text change 09-Jul-2004
Cipate: 23-Aug-1987 #sequence revision 03-Aug-1995 #text change 09-Jul-2004
Cipate: 23-Aug-1987 #sequence revision A26155; Aug-1997 #sequence of human thrombospondin, an adhesive glycoprotein with multiple Axecession: A26155; MUID:87057617; PMID:2430973

A Molecule type: mRNA

A Molecule type: mRNA

A Residues: 1-1170 cLAM*

A Cross-references: UNIPROT: P07996; UNIPARC: UPI0000046821; GB: X04665; NID: g37137; PIDN: A Cross-references: UNIPROT: P07996; UNIPARC: UPI0000046821; GB: X04665; NID: g37137; PIDN: A NOte: parts of this sequence, including the amino end of the mature protein, were det R; Laherty, C.D.; Gierman, T.M.; Dixit, V.M.

J. Biol. Chem. 264, 11222-11227; 1989

A,Title: Characterization of the promoter region of the human thrombospondin gene. DNA

A,Reference number: A34274; MUID: 89291870; PMID: 2544587

A; Molecule type: DNA A; Accession: A34274

A;Rebidues: 1-166 <LLH>
A;Rebidues: 1-166 <LLH>
A;Cross-references: UNIPARC:UP100001742BF; GB:J04835
A;Cross-references: UNIPARC:UP100001742BF; GB:J04835
B;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, J. Cell Biol. 108, 729-736, 1989
A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in t

~

```
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: 1170 <LAM>
A;Molecule type: DNA
A;Cross-references: UNIPROT: P35441; UNIPARC: UPI0000028012; GB:M62449; GB:M62450; GB:M6246
I; GB:M62462; GB:M62463; GB:M62464; GB:M62465; GB:M62467; GB:M62468; GB:M6246
I; GB:M62462; GB:M62463; GB:M62464; GB:M62465; GB:M62467; GB:M62468; GB:M6246
J: Biol. Chem. 265, 16691-16698, 1990
A;Title: Characterization of the mouse thrombospondin gene and evaluation of the role of A;Reference number: A37905; MUID:90375546; PMID:2398070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-490 cBDR>
A;Cross-references: UNIPARC:UPI000016D076; GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40
A;Cross-references: UNIPARC:UPI000016D076; GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
A;Laherty, C.D.; O'Rourke, K.; Wolf, P.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A;Reference number: A42587; MUID:92147683; PMID:1371115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RiChen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
EBSE Lett. 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1 a
A;Reference number: S68787; MUID:96234006; PMID:8654563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: protein
A, Residues: 19-26, X', 28-37 < CHE>
A, Residues: 19-26, X', 28-37 < CHE>
A, Croplex: Homotrimer, disulfide linked
C, Complex: homotrimer, disulfide linked
C, Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc
C, Superfamils: signal sequence #status predicted < SIG>
F, 1-18/Domain: signal sequence #status predicted < SIG>
F, 19-1170/Product: thrombospondin 1 #status predicted < MAT>
F, 19-1375/Domain: von Willebrand factor type C repeat homology < VWC>
F, 378-429/Domain: thrombospondin type 1 repeat homology < THR1>
F, 491-49/TDomain: thrombospondin type 1 repeat homology < THR2>
F, 491-54/TDomain: thrombospondin type 1 repeat homology < THR3>
F, 551-586/Domain: BGF homology < BGF>
F, 551-586/Domain: BGF homology < BGF>
F, 248, 360, 708, 1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-304 <WIL>
A; Cross-references: UNIPARC:UPI00001793F8; EMBL:U41624; PIDN:AAA83323.1; CESP:F46C8.8
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F46C8.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary, not compared with conceptual translation A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-1152, P',1154-1170 <LAH>
A;Residues: 1-1152, P',1154-1170 <LAH>
A;Cross-references: UNIPARC:UP10000177A96; GB:M87276
A;Note: gequence extracted from NCBI backbone (NCBIE:81501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                          A,Title: Characterization of the murine thrombospondin 9
A,Reference number: A40558; MUID:92128941; PMID:1774063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: The sequence of C. elegans cosmid F46C8. A; Reference number: Z21497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T34271
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 2;
Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Wilcox, L. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%;
Best Local Similarity 91.7%;
Watches 11; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 FOGVLONVREVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGVLANVRFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A37905
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                    A; Accession: A40558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S68787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: T34271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
A,Reference number: A30140; MUD: 89139590; PMID: 2918029
A,Recenter number: A30140; MUD: 89139590; PMID: 2918029
A,Recenter A, Accession: A0140; MUD: 89139590; PMID: 891844; FIDN: CA32889.1; PID
A,Recenter Cercence: WRIPARC: UDIOGOGNABL: REBLE. X44787; NID: 891444; FIDN: CA32889.1; PID
A,ROCE: parts of this sequence, including the amino end of the mature protein, were deter
R.Kobayashi, S.; Red-McCutchan, F.; Framson, P.; Bornstein, P.
A,ROCESSION: A5281
A,ROCESSIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Dacies 05-Jun-1992 #sequence revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42887; S68787
R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55; DB 1; Length 1170; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 91.7%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FÓGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

```
H-transporting two-sector ATPase (EC 3.6.3.14), flagellum-specific [imported] - Buchne C; Species: Buchnera sp.
C; Species: Buchnera sp.
C; Species: Buchnera sp.
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C; Accession: D84938
R; Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R; Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R; Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
A; Attle: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A; Reference number: A84930; MUID:20445173; PMID:10993077
A; Residues: D1407 estrostype: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Status: D1467 estrostype: DNA
A; Cross-references: UNIPARC: UPI00005E44F; GB:AP000398; GSPDB:GN00144
A; Experimental source: strain APS
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: H(+)-transporting ATP synthase alpha chain
C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AFI108
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshhi, H.D.; Jones, L.M.; Karst, U.Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M. A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 2-7.Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG1469
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
c; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q8YA90; UNIPARC:UPI000054FB6; GB:NC_003210; PIDN:CAD00796.
A;Experimental source: strain EGD-e
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transporter homolog 1mo0269 [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transporter homolog lin0294 (imported) - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.7%; Score 37; DB 2;
60.0%; Pred. No. 34;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.0
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |::|| :|||
580 GLIANAKFVF 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:| |:||
10 FRGILMNLRF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGVLANVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-628 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: AF1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: 1mo0269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                 reverse gyrase (top-RG) homolog - Archaeoglobus fulgidus
C;Species: Arceesion: H6937
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J; Flaischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaech A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Moleoule type: DNA
A;Residues: 1-1054 «KLB>
A;Cross-references: UNIPROT:029238; UNIPARC:UP10000056EB5; GB:AE001033; GB:AE000782; NIE
C;Keywords: ATP; nucleotide-binding motif A
F;78-85/Region: nucleotide-binding motif A
F;257-262/Region: nucleotide-binding motif A
F;251-263/Region: DEAD motif #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T13F3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: Doct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24890
R;Gardner, A.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19948
A;Accession: T24890
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-400 *MIL>
A;Residues: UNIPROT: O18086; UNIPARC: UP10000080DD5; EMBL: Z93389; PIDN: CAB07670.1;
A;Experimental source: clone T13F3
C;Genetics:
A;Gene: CESP: T13F3.2
A;Map position: 5
A;Introns: 50/2; 87/1; 141/3; 171/3; 242/3; 315/1; 360/3
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 2; Length 1054;
Pred. No. 36;
0; Mismatches 3; Indels
                                                                                       Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 400;
                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
A;Gene: CESP:F46C8.8
A;Introns: 24/1; 56/1; 101/1; 123/1; 149/3; 219/1; 275/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 2;
Pred. No. 21;
4; Mismatches 2
                                                                                       DB 2;
                                                                                                                      Pred. No. 4.1;
2; Mismatches
                                                                                       Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :0
                                                                                66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.3%;
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.7%;
ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 FKSLLAEVRYIF 140
                                                                                Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  565 FHGVLVNGRFV 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLANVRFV 11
                                                                                                                                                                                                             1 FOGVLANVRF 10
                                                                                                                                                                                                                                               FOGMLANAKF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
```

```
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1-1172 cLAH
A;Residues: 1-1172 cLAH
A;Cross-references: UNIPROT: Q03350; UNIPARC: UPI0000029847; GB:L07803; GB:M87275; NID:g3*
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
A;Note: sequence 266, 12821-12824, 1991
A;Title: A second, expressed thrombosondin gene (Thbs2) exists in the mouse genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI000016D077; GB:M64866; NID:g201994; PIDN:AAA40432.1; PID:
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 2;19-37/Domain: von Willebrand factor type C repeat homology <VWC>
F;319-37/Domain: thrombospondin type 1 repeat homology <THR1>
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
F;553-588/Domain: EGF homology <EGF>>
F;652-691/Domain: EGF homology <EGF>>
                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42587; A3983:
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: A42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:O70305; UNIPARC:UPI0000027D7E; EMBL:AF041472; NID:g3005019; C;Genetics:
A;Gene: SCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14171
R;Nechiporuk, T.T.; Figueroa, K.; Sahba, S.; Nechiporuk, A.V.; Pulst, S.M.
Ribechiporuk, T.T.; Figueroa, K.; Sahba, S.; Nechiporuk, A.V.; Pulst, S.M.
R;Description: Mouse homolog of the SCA2 gene.
A;Reference number: 217900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 2; Length 1172;
Pred. No. 64;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T14171
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1285 <NEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.6'
                                                                                                         202 FRGLLQNVHLVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 FDGIYANVRMV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGVLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|:| || ||
202 FRGLLQNVHLVF
               1 FQGVLANVRFVF
                                                                                                                                                                                                                                                                                                                                                           thrombospondin 2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-873 < BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A39851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ataxin-2 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઢ
                    ઠ
                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
B;Complex: DBB:128789; OMIM:188061
A;Map position: 6427-6427
C;Complex: homotrimer, disulfide linked
C;Complex: homotrimer, asgradant aggregation; calcium binding; cell adhesion; glycoprotein; trimer
C;Complex: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
C;Complex: homotogondin 2 #status predicted < MAT>
F;19-1172/Product: thrombospondin type I repeat homology < WCS>
F;319-377/Domain: thrombospondin type I repeat homology < THRI>
F;436-492/Domain: thrombospondin type I repeat homology < THRI>
F;52-691/Domain: EGF homology < EGF>
F;52-691/Domain
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Scatus: preliminary
A;Residue: preliminary
A;Residues: 1-628 cGLA>
A;Residues: 1-628 cGLA>
A;Residues: 1-628 cGLA>
A;Residues: Comparative type: DNA
A;Residues: Comparative type: DNA
A;Residues: Comparative type: DNA
A;Residues: Comparative type: DNA
A;Residues: Loss cGLA>
A;Coss-references: UNIPROT:Q92F14; UNIPARC:UPI00000CC1A0; GB:AL592022; PIDN:CAC95527.1;
A;Gene: lin0294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A47379; A42173
R;LaBell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A;Titles: Sequence and characterization of the complete human thrombospondin 2 cDNA: pote A;Reference number: A47379; MUID:94010892; PMID:8406456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Wolecule Cype: mENA
A, Residues: 1-172 < LABs
A, Residues: 1-172 < LABs
A, Residues: 1-172 < LABs
A, Trailer Cype: mINPARC; UNIPARC; UPI0000046680; GB:L12350; NID:g307505; PIDN: R, LaBell, T.L.; Milewicz, D.J.; Disteche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992
A, Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression cA, Recession: A42173
A, Accession: A42173
A, Accession: A42173
A, Residues: 560-1172 < LA2>
A, Residues: 560-1172 < LA2>
A, Cross-references: UNIPARC; UPI00001742C1; GB:M81339
A, Cross-references: UNIPARC; UPI00001742C1; GB:M81339
A, Cross-references: tibroblast
A, Respection: mental source: fibroblast
A, Respectives: mental source: fibroblast
A, Respecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.7%; Score 37; DB 1; Length 1172;
58.3%; Pred. No. 64;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 2; Length 628;
Pred. No. 34;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.7%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     580 GLIANAKFVF 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombospondin 2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

Gaps

ö

ö

Gaps

ö

Length 1285 Indels

```
Search completed: June
Job time: 14.9655 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A; Reference muber: A5000; MUID: 9906.9613; PMID: 9851916
A; Rocession: Boshites genome. Wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A; Accession: D88115
A; Astatus: preliminary
A; Molecule type: DNA
A; Residues: 1.425 <STO>
A; Cross-references: UNIPROT: Q9TXT7; UNIPARC: UPI0000078A71; GB: chr_II; PIDN: AC67451.1; PI
A; Map position: 2
Cispecies: Methanobacterium thermoautotrophicum (strain Delta H)
Cibate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
CiAccession: F69113
Rismith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 1797 7135-7155, 1997
Afitle: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MuID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-248 <MTH>
A;Residues: 1-248 <MTH>
A;Cross-references: UNIPROT:027872; UNIPARC:UPI000062C0F; GB:AE000937; GB:AE000666; NIC C;Genetics: A;Genetics: A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C27D9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T1567
R;Chissoe, S.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid C27D9.
A;Reference number: Z18384
A;Accession: T15657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein F53C3.11 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May_2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0%; Score 36; DB 2; Length 248;
54.5%; Pred. No. 20;
tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 2; Length 425;
Pred. No. 35;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anonymous, The C. elegans Sequencing Consortium.
Hence 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 FENIIANVKRVF 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FQGVLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || :||::||:
14 FONLLADIRFL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: D88115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; anonymous
Science 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: That the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.0%; Score 36; DB 2; Length 481; Best Local Similarity 58.3%; Pred. No. 40; Matches 7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 | | ||: :|
347 FQNVCANVKRIF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FQGVLANVRFVF 12
```

5, 2006, 22:45:03

THIS PAGE BLANK (USPTO)

ruw
and
and
ruw
lon
lon
ami

xenopus

xenobna xenopus xenopus xenobns xenobns xenopus xenobna xenopus

Seguence:

ö

Run

Searched:

Database

Š.

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peige J.J.;
"Opposite regulation of thrombospondin-1 and corticotropin-induced
secreted protein/thrombospondin-2 expression by adrenocorticotropic
bormone in adrenocortical cells.";
J. Cell. Physiol. 167:164-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96331130; PubMed=8698834;
DOI=10.1002/(SICI)1097-4652(199604)167:1<164::AID-JCP19>3.3.CO;2-0;
Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chambaz B.M.,
                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
 Q3qdq5
Q3p5p7
Q3c718
Q3c718
Q5c3at
Q5c3at
Q5c3at
Q5c3t1
Q5c3t2
Q5c3t4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25015 MW; 90D9EBCE4E6B669C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X89511; CAA61682.1; -; mRNA.
PIR, S57957; S57957.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:007155; P:cell adhesion; IEA.
InterPro; IPR0131320; ConA like subgrp.
InterPro; IPR03129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                  01-NOV-1996, integrated into UniProtKB/TrEMBL.
01-NOV-1996, sequence version 1.
07-FEB-2006, entry version 24.
Thrombospondin-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
Q7SY84 XENLA
1D Q7SY84; XENLA PRELIMINARY; PRT; 496 AA.
AC Q7SY84;
DT 01-0CT-2003, integrated into UniProtKB/TrEMBL.
DT 01-0CT-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 2;
Pred. No. 0.027;
0; Mismatches
030D05-9GAMM
0315718-7GLOT
0563V1_XENLA
0563S6_9DPD
0563S8_9PPD
0563S9_9PPD
0563S9_9PPD
0563T0_9PPD
0563T1_9PPD
0563T2_9PPD
0563T1_9PPD
0563T2_9PPD
0563T1_9PPD
                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 91.7%;
Local Similarity 91.7%;
les 11; Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 FÓGVLONVRFVF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOGULANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00210; TSPN; 1.
 2214
2214
2216
3320
3380
3380
3380
3380
3380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 AA;
 QZ8194_BOVIN
Q28194;
 NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tetraodon n
tetraodon n
methanosarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      burkholderi
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tetraodon n
sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bos taurus
xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methanosarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methanosarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              syntrophus
burkholderi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human herpe
thiomicrosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         burkholderi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nocardia fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gibberella
                                                                                             5, 2006, 22:09:41; Search time 108.931 Seconds (without alignments) 101.901 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              028194 P078784 O278784 O278784 O278784 O278784 O278784 O278784 O278784 O28797 O2879 O28797 O2879 
               GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                         2849598
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                           2849598 seqs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              028194_BOVIN
075Y84_XENLA
TSP1_BOVIN
TSP1_HUMAN
TSP1_MOUSE
071R40_MOUSE
071R40_MOUSE
071R3_RAT
080YQ1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSP1 XENTA
OS9E99 HUMAN
OSSPG5 BRARE
Q4S758 TETNG
OSU903 PIG
Q4RLR5 TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4DWH6_TRYCR
Q7Z2B9_TRYCR
Q4ILJ7_GIBZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P90504 HHV8
Q311L6 THICR
Q5FA21 NEIG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOCFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SBURK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q4RQ74 TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9DELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9BURK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9BURK
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0467V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q4LLM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q5Z2D3_
                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q2LTC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q3F1U8<sup>-</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            044XL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q612H2
                                                                                                                                                                                                                                                                                                                                                                                                                      UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                      1 FQGVLANVRFVF 12
                                                                                                                                                         US-10-030-735-29
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
11496
11170
11170
11170
11171
11171
11171
11171
11171
11171
11171
11171
11171
11171
11171
11171
11171
11171
11171
                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           991177
991177
9911777
9911777
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
991177
                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                          Perfect score:
```

ö

Gaps

ö

```
214 FQGVLQNVRFVF 225
                                                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                           Straubberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
Altschul S.P., Zeeberg B. Buetow K.H., Schaefer C.R., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.E., Carninci P., Frange C.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Brownstein M.J., Widnin T.B., Tochhyuki S., Carninci P., Prange C.,
Brownstein M.J., Woffernan K.J., Markanon R.D., Mullahy S.J.,
Broke S., McZham P.J., McKernan R.J., Markanon R.J., Hulyk S.W.,
Whilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butchiglez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                  Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Whole;

BEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC054970; AAH54970.1; -; mRNA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR013320; Cona like_subgrp.
InterPro; IPR03329; Laminin_G_TSP_N.
InterPro; IPR00884; TSP1.
InterPro; IPR008085; TSP 1.
InterPro; IPR001009; TSP 1.
Ffam; PF00009; TSP 1; 2.
Pfam; PF00099; TSP 1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50184; VWFC_2; 1.
496 AA; 54843 MW; E4FD2F07CB7EF51B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.7%; Score 55; DB 2;
91.7%; Pred. No. 0.061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50092; TSP1; 2.
PROSITE; PS01208; WWFC 1; UNKNOWN_1.
PROSITE; PS50184; WWFC 2; 1.
SEQUENCE 496 AA; 54843 MW; E4FD21
                                                                                                                                                        Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1705; TSPIREPEAT.
SWART; SM00209; TSP1; 2.
SWART; SM00210; TSP1; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
           MGC64438 protein.
                                                                                                                                                                                   NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissue=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
           SOR SERVICE SERVICE CONTRACT TO THE SERVICE SE
```

```
C-1- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, call-to-matrix interactions. Can bind to fibrinogen, fibronectin, coll-to-matrix interactions. Can bind to fibrinogen, fibronectin, v. peta-3 and alpha-1Ib/beta-3. May play a role in dentinogenesis and/or maintenance of dentin and dental pulp.

C-1- SUBDIATT: Homotrimer; disulfide-linked.

C-1- SUBDIATT: Contains 3 EGF-like domains.

C-1- SIMILARITY: Contains 1 TSP C-terminal (TSPN) domain.

C-1- SIMILARITY: Contains 3 TSP type-1 domains.

C-1- SIMILARITY: Contains 7 TSP type-1 domains.

C-1- SIMILARITY: Contains 7 TSP type-3 domains.

C-1- SIMILARITY: Contains 1 TSP C-terminal (TSPN) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.,
                                                                                                                                                                                                                                                    STRAIN=HOlstein; TISSUE=Tooth; MEDLINE=98173773; PubMed=9507054; DOI=10.1016/S0167-4838(97)00188-X; Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                            Inoue H.; "CDNA cloning of bovine thrombospondin 1 and its expression in odontoblasts and predentin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
TSP1_BOVIN STANDARD; PRT; 1170 AA. 028178; 020179; 01-NOV-1997, integrated into UniProtKB/Swiss-Prot. 01-NOV-2000, sequence version 2. 07-MAR-2006, entry version 56. 7hrombospondin-1 precursor. Name-THBS1; Synonyms-TSP-1, TSP1; Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                   [2]
NUCLEOTIDE SEQUENCE [MRNA] OF 1-18 AND 710-1170.
TISSUE=Aortic endothelium;
                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 1382:17-22(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; $55501; $55501.

HSSP; P07996; 1LSL.

SMR; Q28178; 549-1169.

GlycoSuiteDB; Q28178; ...

InterPro; IPR013320; ConA like subgrp.

InterPro; IPR006210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro: IPR000742; EGF 3.
Interpro: IPR00181; EGF Ca bd.
Interpro: IPR01801; EGF Clike.
Interpro: IPR01302; EGF like reg.
Interpro: IPR013129; Laminin G TSP N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB005287; BAA21115.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X87618; CAA60950.1; -; mRNA.
EMBL; X87619; CAA60951.1; -; mRNA.
                                                                                                                                                                             Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP 1.
InterPro; IPR003867; tsp 3.
InterPro; IPR001007; VWF C.
InterPro; IPR001007; VWF C.
Pfam; PF00090; TSP 13.
Pfam; PF02412; TSP 13.
                                                                                                                                                                                                                      [1]
NUCLEOTIDE SEQUENCE [MRNA].
```

Gaps

ö

1; Indels

Mismatches

.; 0

Local Similarity ...

Best Loc Matches

Gaps

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Endothelial cell;
MEDLINE=87057617; PubMed=2430973; DOI=10.1083/jcb.103.5.1635;
Lawler J., Hynnes R.O.,
"The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUCLEOTIDE SEQUENCE.
MEDLINE=89139590; PubMed=2918029; DOI=10.1083/jcb.108.2.729;
Hennessy S.W., Fraziter B.A., Kim D.D., Deckwerth T.L.,
Baungartel D.M., Rotwein P., Fraziter W.A.;
"Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region.";
J. Cell Biol. 108:729-736(1989).
J. Cell Biol. 108:729-736(1989).
NUCLECTIDE SEQUENCE OF 1-397.
NUCLECTIDE SEQUENCE OF 1-397.
Robaysshi S., Eden-Mccutchan F., Framson P., Bornstein P.;
"Partial amino acid sequence of human thrombospondin as determined by annalysis of CDNA clones: homology to malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 1-374.
MEDLINE=86287276; PubMed=3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
"Characterization of a CDNA encoding the heparin and collagen binding domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUCLECTIDE SEQUENCE OF 1-166.

NUCLECTIDE SEQUENCE OF 1-166.

MUCLECTIDE SEQUENCE OF 1-166.

Laherty C.D., Gierman T.M., Dixit V.M.;

"Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.";

J. Biol. Chem. 264:11222-11227(1989).

[6]

NUCLECTIDE SEQUENCE OF 1028-1170.

Ia Fleur M., Jobin C., Gauthier J., Kreis C.G.;

"Expression of thrombospondin in chronic inflammation: neutrophils from synovial fluids synthesize a novel 3.9 kb TSP mRNA.";

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441; THR-450; TRP-498 AND THR-507.
TISSUB-Platelet; MEDLINE=21125860; PubMed=11067851; DOI=10.1074/jbc.M008073200;
Length 1170;
                                               Indels
                                                                                                                                                                                                                                                          TSP1 HUMAN STANDARD; PRT; 1170 AA. P07956; 015667; 01-AUG-1988, integrated into UniProtKB/Swiss-Prot. 01-AUG-1988, sequence version 1. 07-MAR-2006, entry version 78. Thrombospondin-1 precursor. Name-THS1; Synonyms-TSP, TSP1; Homo sapiens (Human).
                                               0; Mismatches
  Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Biol. 103:1635-1648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 25:8418-8425(1986)
                                                                                                                                         208 FOGVLQNVRFVF 219
                                               11; Conservative
                                                                                               1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins.
                                                  Matches
                                                                                                                                            셤
                                                                                               ઠે
                                                                                                                                                                                                                                                                  TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
TSP type-1 3.
EGF-like 1.
EGF-like 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 4.
TSP type-3 4.
TSP type-3 7.
TSP type-3 6.
TSP type-3 7.
TSP type-3 6.
TSP type-3 6.
TSP type-1 6.
TSP ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-linked (GlCNAC...) (Potential).
N-linked (GlCNAC...) (Potential).
N-linked (GlCNAC...) (Potential).
N-linked (GlCNAC...) (Potential).
Interchain (Probable).
By similarity.
By similarit
                                                    R SWART; SW00181; BGF; 3.

R SWART; SW00181; BGF; 3.

R SWART; SW00210; TSP1; 3.

R SWART; SW00210; TSP1; 3.

R SWART; SW00210; TSP3; 1.

R PROSITE; PS0022; BGF 1; FALSE_NEG.

R PROSITE; PS0022; EGF 2; 1.

R PROSITE; PS00202; TSP1; 3.

R PROSITE; PS00202; TSP1; 3.

R PROSITE; PS01208; VWPC_1; 1.

R PROSITE; PS01208; VWPC_1; 1.

R PROSITE; PS01208; VWPC_2; 1.

R PROSITE; PS01208; VWPC_1; 1.

R PROSITE; PS01208; VWPC_1; 1.

R PROSITE; PS01308; VWPC_2; 1.

R PROSITE; PS01308; VWPC_1; 1.

R PROSITE; PS01308; VWPC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ODD6ADF3E5FA031A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Thrombospondin-1.
/FTId=PRO_0000035841.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΜW.;
                                          PRINTS; PRO1705; TSPIREPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
```

```
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
REGION
MOTIF
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                       CHAIN
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                  Characteristics and a particular solutions. The contains a state of the contai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                               MEDLINE=22338361; PubMed=12450399; DOI=10.1021/bi026463u;
Huwiler K.G., Vestling M.M., Annis D.S., Mosher D.F.;
"Stophysical characterization, including disulfide bond assignments,
of the anti-angiogenic type 1 domains of human thrombospondin-1.";
Biochemistry 41:14329-14339(2002).
Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J., Mosher D.F., Peter-Katalinic J.; "C-mannosylation and O-fucosylation of the thrombospondin type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGNC., HGNC.11785, THBS1.

MIM; 188060; gene.

Reactome; P0796; C:extracellular region; NAS.

GO; GO:0004866; F:endopeptidase inhibitor activity; TAS.

GO; GO:0004871; F:signal transducer activity; TAS.

GO; GO:0007275; P:development; TAS.

InterPro; IPR01320; Cona_like_subgrp.
                                                                                                                                                                                                                       CARBOHYDRATE-LINKAGE SITES ASN-248 AND ASN-1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M25631; AAA36741.1; -; mRNA.
EMBL; X04665; CAA28370.1; -; mRNA.
EMBL; X1487; CAA3289.1; -; mRNA.
EMBL; M14326; AAA61237.1; ALT SEQ; mRNA.
EMBL; J04835; AAA61178.1; -; Genomic_DNA.
EMBL; M94425; AAB59366.1; -; mRNA.
PIR; A26155; TSUPP1.
                                                                                                    THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000742; EGF 3.
InterPro; IPR001891; EGF Ca bd.
InterPro; IPR001891; EGF Ca bd.
InterPro; IPR001803; EGF like reg.
InterPro; IPR0018084; TSP1.
InterPro; IPR008084; TSP1.
InterPro; IPR0080859; TSP 1.
InterPro; IPR0080859; TSP C.
InterPro; IPR00180859; TSP C.
InterPro; IPR00180859; TSP C.
InterPro; IPR00180959; TSP C.
InterPro; IPR0018099; TSP C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENSG0000137801; Homo sapiens
                                                            uie:";
Biol. Chem. 276:6485-6498(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1LSL; X-ray; A=434-546.
PDB; 1LX6; X-ray; A=834-1170.
PDB; 1Z78; X-ray; A=19-233.
PDB; 1ZA4; X-ray; A=19-233.
PDB; 2ERF; X-ray; A=19-257.
SMR; P07996; 549-1169.
GlycoSultedB; P07996; -.
```

```
R PFAMTS; PRO0093; VWC; 1.

R PRINTS; PRO1093; VWC; 1.

R SMART; SM00181; EGF; 3.

SMART; SM00181; EGF; 3.

SMART; SM00210; TSPN; 1.

R SMART; SM00210; TSPN; 1.

R PROSITE; PS01186; EGF_2; 1.

R PROSITE; PS01208; VWFC_1; 1.

R PROSITE; PS01208; VWFC_1; 1.

R PROSITE; PS01208; VWFC_2; 1.

R PROSITE; PS01284; VWFC_2; 1.
                                                                                                                                                                                                                                                             TYPE TYPE-1 1.

TSP type-1 2.

TSP type-1 3.

EGF-like 1.

EGF-like 3.

TSP type-3 1.

TSP type-3 2.

TSP type-3 4.

TSP type-3 5.

TSP type-3 6.

TSP type-3 7.

TSP C-terminal.

Heparin-binding (Potential).

Cell attachment site (Potential).

N-linked (GLONAC. ..).

N-linked (GLONAC. ..).

N-linked (GLONAC. ..).

N-linked (GLONAC. ..).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-linked (Mail).
(FIId=CAR 000210.
0-linked (Fuc. .).
/FIId=CAR 000211.
N-linked (GlcNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 1; Length 1170;
Pred. No. 0.15;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-linked (GlcNAc. . . Interchain (Probable) Interchain (Probable)
                                                                                                                                                                                                                Thrombospondin-1.
/FTId=PRO_000035842.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=CAR 000205.
O-linked (Fuc. .)
/FTId=CAR 000206.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=CAR 000208.
O-linked (Fuc. .)
/FTId=CAR 000209.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=CAR 000207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-linked (Man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91...
Local 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 FOGVLONVRFVF 219
PF02412; TSP_3; 12.
PF05735; TSP_C; 1.
PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1067
270
274
423
428
413
484
                                                                                                                                                                                                                                            1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507
                                                                                                                                                                                                        13
                                                                                                                                                                                                                                            24
3316
3316
3379
3379
4435
549
646
723
723
723
818
                                                                                                                                                                                                                                                                                                                                                                                                            879
915
951
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248
360
385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391
395
444
447
451
462
504
508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507
```

```
MOTIF
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE OF 19-37.

PubMed=8654563; DOI=10.1016/0014-5793(96)00460-7;

Chen H., Aeachlimann D., Nowlen J., Mosher D.F.;

Chen H., Aeachlimann D., Nowlen J., Mosher D.F.;

Expression and initial characterization of recombinant mouse thrombospondin 1 and thrombospondin 3.";

FEBS Lett. 387:36-41(1996).

-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type V collagen and integrins alpha-V/beta-1, alpha-V/bet
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUCLEOTIDE SEQUENCE OF 1-490.
MEDLINE=90375546; PubMed=2398070;
Bornstein P., Alfi D., Devarayalu S., Framson P., Li P.;
"Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";
J. Biol. Chem. 265:16691-16698(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development."; J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
MEDLINE-29128941; Pubmed=1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
Jenkins N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
MEDLINE=92147683; PubMed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBUNIT: Homotrimer; disulfide-linked.
-1- SIMILARITY: Belongs to the thrombospondin family.
-1- SIMILARITY: Contains 3 EGF-like domains.
-1- SIMILARITY: Contains 1 TSP C-terminal (TSPC) domain.
-1- SIMILARITY: Contains 3 TSP type-1 domains.
-1- SIMILARITY: Contains 3 TSP type-1 domains.
-1- SIMILARITY: Contains 1 TSP type-3 domains.
-1- SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of the murine thrombospondin gene."; Genomics 11:587-600(1991).
                                                                                                       01-JUN-1994, integrated into UniProtKB/Swiss-Prot. 01-JUN-1994, sequence version 1. 07-MAR-2006, entry version 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M62470; AAA50611.1; -; Genomic_DNA.
M62451; AAA50611.1; JOINED; Genomic_DNA.
M62451; AAA50611.1; JOINED; Genomic_DNA.
M62453; AAA50611.1; JOINED; Genomic_DNA.
M62454; AAA50611.1; JOINED; Genomic_DNA.
M62454; AAA50611.1; JOINED; Genomic_DNA.
M62455; AAA50611.1; JOINED; Genomic_DNA.
M62456; AAA50611.1; JOINED; Genomic_DNA.
M62456; AAA50611.1; JOINED; Genomic_DNA.
M62459; AAA50611.1; JOINED; Genomic_DNA.
M62459; AAA50611.1; JOINED; Genomic_DNA.
M62459; AAA50611.1; JOINED; Genomic_DNA.
M62459; AAA50611.1; JOINED; Genomic_DNA.
M62450; AAA50611.1; JOINED; Genomic_DNA.
                                                                       PRT; 1170 AA
                                                                                                                                                           Thrombospondin-1 precursor.
Name=Thbs1; Synonyms=Tsp1;
Mus musculus (Mouse).
                                                                     STANDARD;
                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                     TSP1 MOUSE
P35441;
                              KESULT 5
TSP1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
```

```
| Britis | Marcial Advisoring | October | Octo
```

```
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEOUENCE
                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE-Aorta and vein;
PubMed=16141072; DOI=10.1126/science.1112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Balico S., Barchov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Ambesi-Implombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CSTBL/6J; TISSUE=Aorta and vein; MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carininci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adult male aorta and vein cDNA, RIXEN full-length enriched library, clone:A530055N06 product:thrombospondin 1, full insert sequence. Name=Thbs1;
   (Potential)
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                         0443E493615E7F06 CRC64;
N-linked (GlcNAC...)
Interchain (Probable).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 1
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                    946 1167 by 8
1025 1025 F - 1170 AA; 129647 MW;
                                                                                                                                                                                                                                                                                                                                                                91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTTR40 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                         208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.7
Marches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=10090;
 CARBOHYD
DISULFID
DISULFID
                                 DISULFID
                                                                                                            DISULFID
                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                      DISULFID
                                                                 DISULFID
                                                                           DISULFID
                                                                                       DISULFID
                                                                                                 DISULFID
                                                                                                                                 DISULFID
                                                                                                                                                       DISULFID
                                                                                                                                                                  DISULFID
                                                                                                                                                                            DISULFID
                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                  SULFID
                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                  DISULPID
                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

Bensell W. Bensel W. Secretary V. Christoffels A. Culterbuck D. Bancel W. Groen M. Chail E. Dolly Christoffels A. Culterbuck D. Ballone G. Croes M. Chail E. Dolly Christoffels A. Culterbuck D. Ballone G. Croes M. Chail E. Dolly Christoffels A. Culterbuck D. Ballone G. G. Garbaldi M., Fallone G. G. Garbaldi M., Rallone G. G. Garbaldi M., Rallone G. C. Groen R. E. M. Georgi-Hemming P. Gingers H. R. Golocot T. Green R. E. M. Georgi-Hemming P. Gingers H. R. Golocot T. Green R. E. M. Georgi-Hemming P. Gingers H. M. Golocot T. Green R. E. M. Mitchell J. W. Landen B. M. Kitzen G. M. Gilla G. W. Kitzen G. W. Gilla G. W. Witzen G. W. Watcher G.

```
DDT T DD B B DD B DD B B D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                              RC STRAIN-GSTBL/647. TISSUB-Aorta and vein;

RC STRAIN-GSTBL/67. TISSUB-Aorta and vein;

RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

RAWai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

RA Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalow S., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalow S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Baldarelli R., Barsh G.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Bult C., Fletcher C., Fullia M., Mansho G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shipata Y., Storch K.-F.,

Mynshaw-Boris A., Yoshida K., Haeegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

"Functional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Aorta and vein; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazati Y., Muramatsu M., Hayashizaki Y., Inch M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATRAIN-CSTBL/6J; TISSUE-Aorta and vein;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CSTBL/6J; TISSUE-Aorta and vein;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoro R., Matsunuoto H., Sakaguchi S., Ikegami T., Kashiiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AK163092; BAE37190.1; -; mRNA.
MGI; MGI:98737; Thbs1.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0005615; P:negative regulation of angiogenesis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPRO00742; EGF 3.
Interpro; IPRO01881; EGF Ca bd.
Interpro; IPRO05209; EGF like.
Interpro; IPR013032; EGF_like_reg.
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006210; EGF.
InterPro; IPR000742; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley;
Iwabu A., Hirohata S., Kusachi S., Nakamura K., Murakami
Ninomiya Y., Tsuji T.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1170 AA; 129619 MW; 55BF04A20D91B194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMR; Q71SA3; 834-1169.
GO; GO: 0005576; C: extracellular region; IEA.
GO; GO: 0005599; F: calcium ion binding; IEA.
GO; GO: 0005199; F: calcium ion binding; IEA.
GO; GO: 0007155; P: cell adhesion; IEA.
InterPro; IRR0053109; ConA_like_subgrp.
InterPro; IRR006510; EGF_3.
InterPro; IRR006510; EGF_3.
InterPro; IRR001881; EGF_3.
InterPro; IRR013039; EGF_like.
InterPro; IRR013039; EGF_like.
InterPro; IRR013039; EGF_like reg.
InterPro; IRR013039; EGF_like reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.7%; Score 55; DB 2;
91.7%; Pred. No. 0.15;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY; PRT; 1170 AA.
Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF309630; AAQ14549.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO1186; EGF 2; UNKNOWN 1. PROSITE; PS50026; EGF 3; 2. PROSITE; PS50092; TSPI; 3. PROSITE; PS601208; VWPC 1; 1. PROSITE; PS50184; VWPC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004, sequence version 1.
07-FBB-2006, entry version 9.
Thrombospondin 1.
                   InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP1.
InterPro; IPR003867; tsp_3.
InterPro; IPR001007; VWF_C.
Pfam; PP00009; TSP_1; 3.
Pfam; PP00090; TSP_1; 3.
Pfam; PP00735; TSP_2; 7.
Pfam; PP00735; TSP_2; 7.
Pfam; PP00735; TSP_2; 7.
Pfam; PP0093; VWC; 1.
                                                                                                                                                                                                                                                                                           PRINTS; PR01705; TSPIREPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FOCVLONVREVE 219
                                                                                                                                                                                                                                                                                                                  SMART; SM00181; EGF; 3.
SMART; SM00209; TSP1; 3.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q71SA3_RAT
Q71SA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Tsp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q71SA3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

ω

```
OSCGB2

OSCGB2
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESIDENCE SUCENCE SUCENCE SERVENCE SUCENCE SUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 91.7%; Score 55; DB 2; Length 1170; Local Similarity 91.7%; Pred. No. 0.15; les 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS-BL/6; TISSUB=Brain;
Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                               1170 AA; 129671 MW; 6F3BD3DCE733060F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003, integrated into UniProtKB/TrEMBL. 01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBOXQI MOUSE PRELIMINARY; PRT; 1171 AA QBOXQI;
                                                                                                                                                                                                                                                                                             PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50092; TSP1; 3.
PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PSCSITE; PS50184; VWFC 2; 1.
SEQUENCE 1170 AA; 129671 MW; 6F36
                    Pfam; PF00008; BGF; 2. Pfam; PF00009; TSP 1; 3. Pfam; PF0012; TSP 2; 1.2. Pfam; PF05735; TSP C; 1. Pfam; PF005735; TSP C; 1. PRINTS; PR01705; TSPIREPEAT. SMART; SM00209; TSP1; 3. SMART; SM00210; TSP1; 3. SMART; SM00210; TSP1; 3. SMART; SM00210; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVLANVRFVF 12
InterPro; IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 22.
Thrombospondin 1 (Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library, clone:G930018021 product:thrombospondin 1, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANGELIATE CECH INTEGRAL TRISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously,
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemeen C.M., Schuler G.D.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 2; Length 1171;
Pred. No. 0.15;
EMBL; BC050917; AAH50917.1; -; mRNA.

HSSP; P07996; ILSL.

SNR; Q80701; 835-1170.

Ensembl; ENSMUSG0000040152; Mus musculus.

MG1; MG1:98737; Thbs1.

GO; GO:0005615; C:extracellular space; RCA.

GO; GO:0015525; P:negative regulation of angiogenesis; IDA.

InterPro; IPR013320; ConA. like.subgrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1171 AA; 129690 MW; 12E077B50C64E2D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                             Interpro; IPR000742; EGF 3.
Interpro; IPR001881; EGF Ca bd.
Interpro; IPR001881; EGF Ca bd.
Interpro; IPR0013032; EGF like reg.
Interpro; IPR0013031; EGF like reg.
Interpro; IPR001884; TSP1.
Interpro; IPR001884; TSP1.
Interpro; IPR001307; tsp 3.
Interpro; IPR0018859; TSP 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS50092; TSPI; 3.
PROSITE; PS01208; VWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_2; 1.
SEQUENCE 1171 AA; 129690 MW; 12EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBCGB2_MOUSE PRELIMINARY;
Q8CGB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERINTS; PRO1705; TSPIREPEAT.
SWART; SW00181; EGF; 3.
SWART; SW00210; TSP1; 3.
SWART; SW00210; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001007; VWF_C
Pfam; PF00008; EGF; 2.
Pfam; PF00090; TSP 1; 3.
Pfam; PF02412; TSP 3; 12.
Pfam; PF05735; TSP 2; 1.
Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FOGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 91.7 es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
```

```
RC TISSUE-Mammary gland;
RN PUNCECTILE SEQUENCE.
RN PUNCECTILE SEQUENCE.
RN PARAMEMARY Gland;
RN PARAMEMARY G. Addinis V., Allen J.E.,
RN Bajic V.B., Berener S.E., Batalov S., Forrest A.R., Zavolan M.,
RN Bajic V.B., Berener S.E., Addinis V., Allen J.E.,
RN Ambiombato A., Apweiler R., Attraliya R.M., Bailey T.L.,
RN Bansal M., Baxter L., Beisel K.M., Bersano T., Bono H., Chalk A.M.,
RN Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RN Glin Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RN Glin Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RN Glin Bernardo D., Down T., Brostrom P., Fagiolini M., Faulkner G.,
RN Glin Corpiller, I., Iacono M., Ikeo K., Iwana A., Ishikawa T.,
Antil D., Huminiecki L., Iacono M., Ikeo K., Iwana A., Ishikawa T.,
RN Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Anteuda H., Matulawa S., Mikh H., Mignone F., Miyake S., Morris K.,
Muteuda H., Matulawa S., Mikh H., Mignone F., Miyake S., Morris K.,
Muteuda H., Matulawa S., Mikh H., Mignone F., Miyake S., Morris K.,
Muteuda H., Matulawa S., Mishikawa S., Nori F., Ohara O.,
Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pescole G.,
Rosaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pescole G.,
Rosaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pavesi G.,
Schonbach C., Sekiguchi K., Sambon D., Sinclair B.,
Schonbach C., Sekiguchi K., Sambon W., Mater W., Midan S., Kanamoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Bannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Bannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Bannoja K., Tan S.L., Tang S., Taylor M.S., Zenger S., Morkawa M., Wannishi H., Kananishi H., Wanishi W., Naki K., Mananishi H., Wanishi W., Ravashima T., Soliama M., Kondo S., Konnon H., Nakano W., Shiraki J., Kanamori-K., Ilda J., Imamura K., Itoh M., Ravashima 
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahet J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schort R.M., Schain J.E., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.
```

Science 309:1559-1563 (2005)

NUCLEOTIDE SEQUENCE

```
RC TISSUE=Mammary gland;

RX ONCLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RX OKAZAKI Y., Puruno M., Kaaukawa T., Adachi J., Bonon H., Kondo S.,

RA OKAZAKI Y., Puruno M., Kaaukawa T., Adachi J., Bonon H., Kondo S.,

RA OKAZAKI Y., Puruno M., Kaato R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Madarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Konagaya A., Kurchkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Konagaya A., Kurchkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wapner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Wilming L.G., Whoshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

Wilming L.G., Wanshaw-Boris A., Yanagisawa M., Saka K.,

RA Hirozane-Kishkawa T., Konno H., Nakamura M., Saka X.,

RA Hara A., Hashizume W., Imotani K., Shibata K., Shihata R.,

Shiraki T., Waki K., Sakai J., Shibata R.,

Shiraki T., Pulvick M., Shibata R.,

Shiraki T., Pulvick M., Shibata R.,

Shiraki R., Shibata R.,

Shibata R.,

Shibata R., Shibata R.,

Shibata R.,

Shibata R.,

Shibata R.,

Shibata R.,

Shibata R.,

Shibata R.,

Shibata R.,

Shibata R.,

Shibata R.,

Shibata R.,

Shibata R.,

Shibata R.,

Shiba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McULEDIDE SAUGNACE.

A REDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

A REDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

A REDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

A Arakawa T., Hara A., Fukunishi Y., Konno H., Kadchi J., Fukuda S., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Schriml L.M., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Austhin D.A., Kamiya M., Lee N. H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Sasaki H., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hassegawa Y., Kawaji H., Kohtsuki S., Hasseshishishi V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yasunishi A., Yoshino M., Waterston R., Lander B.S., Rogers J., Birney E., Haysshizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Mammary gland;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Garnino P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
TISSUE=Mammary gland;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
```

```
By similarity.
                                          EMBL; L04278; -; NOT_ANNOTATED_CDS; mRNA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-linked
N-linked
N-linked
N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-linked
N-linked
                                                                                         InterPro; IPR013220; ConA_like_subgrp.
InterPro; IPR006210; EGF.
InterPro; IPR00042; EGF.3.
InterPro; IPR001881; EGF.Ca_bd.
InterPro; IPR006209; EGF_like.
InterPro; IPR013032; EGF_like reg.
InterPro; IPR003129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heparin-binding, Repeat, Signal.
SIGNAL 1 22 Pote
CHAIN 23 1173 Thro
                                                                                                                                                                                                      InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP1.
InterPro; IPR003657; tsp2.
InterPro; IPR001007; VRFC.
InterPro; IPR001007; VRFC.
Pfam; PF00008; EGF; 1.
Pfam; PF002412; TSP2.; 1.
Pfam; PF05735; TSP2; 1.
Pfam; PF05735; TSP2; 1.
                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01705; TSPIREPEAT.
                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00181; EGF; 2.
SMART; SM00209; TSP1; 3.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               917
953
1173
235
235
331
158
158
158
363
705
711
1070
426
481
487
477
                                                                             SMR; P35448; 552-1172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               882
918
954
23
929
155
1158
158
250
705
705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398
4409
454
454
454
507
511
522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGION
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis embryos.";

Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.

I. Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.

C. I. FUNCTION: Adhesive glycoprotein that mediates cell-co-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminn, type V collagen and integrins alpha-V/beta-1, alpha-V/beta-3 and alpha-ID/beta-3 (By similarity).

C. I. SUBUNIT: Homotriner; disulfide-linked.

C. I. SIMILARITY: Contains 3 EGF-like domains.

C. I. SIMILARITY: Contains 1 TSP C-terminal (TSPC) domain.

C. I. SIMILARITY: Contains 3 TSP Cype-1 domains.

C. I. SIMILARITY: Contains 3 TSP type-1 domains.

C. I. SIMILARITY: Contains 7 TSP type-3 domains.

C. I. SIMILARITY: Contains 7 TSP type-3 domains.
                                                                                                                                                                                                                                        TISSUE=Mammary gland;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y., Shimited (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
           TISSUE-Ammary gland;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Mateminoto H., Sakaguchi S., Ikegami T., Kashiiwagi K.,
Fujiwak S., Inoue K., Togawa Y., Izawa M., Ohara B., Matahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipelin with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name-thbs1; Synonyms-tsp1;
Senopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Urry L.A., Ramos J., Duquette M., Desimone D.W., Lawler J., "Cloning, characterization and expression of thrombospondin-1 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.7%; Score 55; DB 2; Best Local Similarity 91.7%; Pred. No. 0.15; Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC042422; AAH42422.1; -; mRNA.
EMBL; AK145202; BAE26293.1; -; mRNA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994, sequence version 1.
07-MAR-2006, entry version 54.
Thrombospondin-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FOGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGULANVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSP1 XENLA P35448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
TSP1_XENLA
```

g

ò

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSP type-1 1.
TSP type-1 1.
TSP type-1 2.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 3.
TSP type-3 1.
TSP type-3 4.
TSP type-3 4.
TSP type-3 6.
TSP type-3 7.
TSP type-3 7.
TSP type-3 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heparin-binding (Potential)
Cell attachment site (Poten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022; EGF_1; PALSE_NEG.
PROSITE; PS0186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS50092; TSPI; 3.
PROSITE; PS50108; WWFC_1; 1.
Calcium; Cell adhesion; EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombospondin-1.
/FTId=PRO_0000035844.
TSP N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GlcNAc.
(GlcNAc.
(GlcNAc.
(GlcNAc.
```

us-10-030-735-29.rup

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barker D.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collagen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OSSPGS:
21-DEC-2004, integrated into UniProtKB/TrEMBL.
21-DEC-2004, sequence version 1.
21-DEC-2004, sequence version 1.
21-EEB-2006, entry version 12.
Novel protein similar to vertebrate thrombospondin 1.\n\ (Fragment).
ORFNames=DKFY-11E23-1001;
Brachydanio rerio (Zebrafish) (Danio rerio).
Britaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Vill_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 2; Length 1225;
Pred. No. 0.16;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                     1225 AA; 134849 MW; 9888B16E57157B12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL928866; CAI20599.1; -; Genomic_DNA.

SMR; QSSPG5; 751-804, 754-1089.

Ensembl; ENSDARG000000101085; Danio rerio.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:000515; F:protein binding; IEA.

GO; GO:0007155; P:cell adhesion; IEA.

InterPro; IRR002109; EF hand_Ca_bd.

InterPro; IRR006210; EGF.

InterPro; IRR006210; EGF.

InterPro; IRR006209; EGF like.

InterPro; IRR006209; EGF like.
              Pfam; PP00008; EGF; 2.

Pfam; PP00009; TSP 1; 3.

Pfam; PP00090; TSP 1; 3.

Pfam; PP00093; VWC; 1.

Pfam; PF00093; VWC; 1.

Pfam; PF00093; VWC; 1.

PRINTS; PR01705; TSPIREPEAT.

SMART; SM00210; TSPN; 3.

SMART; SM00210; TSPN; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01026; EGF 2; 1.

PROSITE; PS01026; EGF 2; 1.

PROSITE; PS01024; VWFC; 1; 1.

PROSITE; PS01024; VWFC; 2; 1.

CG11 adhesion; EGF-1; de dmain.

NON TER.

SEQÜENCE 1225 AA; 134849 MW;
                                                                                                                                                                                                                                                                                                                                                                                           91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008085; TSP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 FÓGVLONVRFVF 274
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 91.7 les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQGVLANVRFVF 12
    InterPro; IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
Q5SPG5 BRA
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Aorta endothelial cell;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
Obara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1173;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                   By similarity.
MW; A9F036D6516C0F24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB209912; BAD93149.1; -; mRNA.
SMR; Q59E99; 886-939, 889-1225.
R Ensembl; ENSG0000137801; Home sapiens.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005510; F:heparin binding; IEA.
GO; GO:0005510; F:heparin binding; IEA.
GO; GO:0005115; F:protein binding; IEA.
GO; GO:0005115; P:cell adhesion; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR006210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                       91.7%; Score 55; DB 1; 91.7%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 HUMAN
Q59E99 HUMAN PRELIMINARY; PRT; 1225 AA.
Q59E99<sup>;</sup>
                                                                                                                                                                                             similarity.
similarity.
                                                                                                                 similarity.
                                                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                            similarity
                                                                              similarity
                                                                                                similarity
                                                                                                                                                         similarity
                                                                                                                                                                         similarity
                                                                                                                                                                                                                                                      similarity
Similarity
                                                                                                                                                                                                                                                                                                                   similarity
                                                                                                                                                                                                                                                                                            similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF 3.
EGF Ca bd.
EGF like.
EGF like reg.
Laminin G TSP N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2005, sequence version 1.
21-FEB-2006, entry version 10.
Thrombospondin 1 variant (Fragment)
    .;
0
                                                                                                                                                                                                                                                                                                                                                     130020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR008085; TSP 1.
InterPro; IPR003367; tsp 3.
InterPro; IPR008859; TSP C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 FOGVLONVŘEVĚ 222
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006209;
InterPro; IPR013032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000884;
                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR008859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                   1173
  554
559
559
602
623
660
681
721
721
780
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                              DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                             DISULFID
                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
Q59E99_HUM
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DER NEUEN DE NE
```

ઠ

SO THE PROPERTY OF THE PROPERT

à

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
Zhang K., Mauco G., Hauet T.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1193 AA; 133256 MW; 6E8781648FCEC7F2 CRC64;
                                                                                                                                                             GO; 0005576; C:extracellular region; IEA.
GO; 00005576; C:extracellular region; IEA.
GO; 00000509; F:calcium ion binding; IEA.
GO; 00000810; F:heparin binding; IEA.
GO; 00000515; F:protein binding; IEA.
GO; 000007155; P:cell adhesion; IEA.
GO; 00007155; P:cell adhesion; IEA.
InterPro; IPR006710; EGF.
InterPro; IPR00191; EGF.
InterPro; IPR013021; EGF.
InterPro; IPR013022; EGF. Takereg.
InterPro; IPR013022; EGF. Takereg.
                                                                                                    EMBL; CAAE01014723; CAG03524.1; -; Genomic_DNA.
SMR; Q4S758; 811-1148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 2;
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
07-FEB-2006, entry version 7.
Thrombospondin 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO1705; TSPIREPEAT.
SWART; SM00181; EGF; 2.
SWART; SM00209; TSP1, 3.
SWART; SM00210; TSP1, 3.
SWART; SM00214; VWC, 1.
PROSITE; PS01186; EGF 2; UNKNOWN_1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50026; TSP1; 3.
PROSITE; PS50092; TSP1; 3.
PROSITE; PS50184; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AY773342; AAV38110.1; -; mKNA.
InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP_1.
InterPro; IPR01007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000884; TSP1.
InterPro; IPR000085; TSP 1.
InterPro; IPR001007; WWF_C.
Pfam; PF00008; EGF; 2.
Pfam; PF00009; TSP 1; 3.
Pfam; PF005715; TSP 2; 12.
Pfam; PF005715; TSP C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 FMGVLONVRFVF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 83.3
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PIG
Q5U903 PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q5U903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATA DE DATA DE LA PARTE DA LA
       Whedels496914; DOI=10.1038/nature03025;

Aurolis Doi: Bouneau L.; Fischer C., Ozouf-Costaz C., Bernot A.,

Muccali E., Bouneau L.; Fischer C., Ozouf-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

Anthouard V., Jubin C., Castelli V., Katinha M., Vacherie B.,

Biemont C., Salanoubat M., Levy M., Boudet N., Castellano S.,

A part of, Lardier E., Cattolico L., Poulain J., De Berardinis V.,

Relis M., Volff J.-N., Guigo R., Zody M.C., Meeirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Rahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Rahn D., Roset Crollius H.,

Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2005, sequence version 1.
21-FBB-2006, entry version 8.
Chromosome 14 SACF14123, whole genome shotgun sequence. (Fragment)
ORFNames=GSTENG00022976001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis (Green puffer).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryotaj, Neoplerygii, Teleostei; Euteleostei; Neoteleostei;

Acathomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
Genoscope, Whitehead Institute Centre for Genome Research,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.3%; Score 50; DB 2; Length 1090;
83.3%; Pred. No. 1.4;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1090 AA; 120978 MW; 5A9320504A22D836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00018; EF HAND 1; UNKNOWN_1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50092; TSPI; 2.
PROSITE; PS501208; WPPC 1; 1.
PROSITE; PS50184; VWPC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell adhesion; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                       Pfam; PF00090; TSP_1; 2.
Pfam; PF02412; TSP_3; 12.
Pfam; PF0735; TSP_C; 1.
Pfam; PF00093; VWC; 1.
PRINTS; PR01105; TSPIREPEAT.
          InterPro; IPR003367; tsp_3.
InterPro; IPR008859; TSP_C.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 FMGVLQNVRFVF 196
                                                                                                                                                                                                                                                                                                                                                   SM00210; TSP1; 2.
SM00210; TSPN; 1.
SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 83.3
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGULANVRFVF 12
                                                                                                                                                                                                                                                                                                                       SMART; SM00181; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58_TETNG
Q4S758_TETNG
Q4S758;
                                                                                                           Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
                                                                                                                                                                                                                                                                                                                                                       SMART;
SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
CAS758 TEET
CO45758 TEET
DD CAS758
D
```

```
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A PubMed-15496914; DOI=10.1038/nature03025;
A Jaillon O. Aury J.-M., Brunet F., Peeit J.-L., Stange-Thomann N.,
A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fischer C., Lutfalla G., Dossat C., Segurens B.,
A nathouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                RESULT 15

QARLRS_TETNG

QARLRS_TETNG

QARLRS_TETNG

AC

QARLRS_TETNG

AC

QARLRS_TETNG

AC

QARLRS_TETNG

DT

19-JUL-2005, integrated into UniProtKB/TrEMBL.

DT

19-JUL-2005, sequence version 1.

DT

21-FEB-2006, entry version 8.

DE

Chromosome 10 SCAF15019, whole genome shotgun sequence. (Fragment).

GN

ORNNameseSTETNG00123374001;

GN

Tetraodon nigroviridis (Green puffer).

CC

Rukaryotta; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC

Actinopterygii; Neopterygii; Teleostei; Mereleostei;

CC

Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;

CC

Tetradontoidea; Tetraodontidae; Tetraodontiformes;

CC

NEDI_TAXID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope: Whitehead Institute Centre for Genome Research,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                81.7%; Score 49; DB 2; Length 249; 90.9%; Pred. No. 0.47; tive 0; Mismatches 1; Indels
                                                                                                                                                249 AA; 27560 MW; 465D664BE0329C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QARLR5; 834-897, 837-1111.
GO:0005576; C:extracellular region; IEA.
GO:0005209; F:calcium ion binding; IEA.
GO:0005515; F:protein binding; IEA.
GO:005515; F:protein binding; IEA.
GO:005198; F:structural molecule activity; IEA.
GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; CAAE01015019; CAG10667.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                            PROSITE; PS50092; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
                             PRINTS; PRO1705; TSPIREPEAT.
SMART; SM00209; TSP1; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                  Local Similarity 90.9
nes 10; Conservative
Pfam; PF00090; TSP 1; 2.
Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                    2 OGVLANVREVF 12
                                                                                                                                                                                                                                                                                         1 QGVLQNVRFVF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                  NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88888
8888888FF8
                                                                                                                                                                                                                                                                      ઠે
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.7%; Score 49; DB 2; Length 1171; 83.3%; Pred. No. 2.4; 2:ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1171 1171
1171 AA; 129304 MW; 865F3749693F7FCE CRC64;
EGF Ca bd.
EGF like reg.
Laminin G TSP N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June 5, 2006, 22:42:43
                                                                                                                                                                                                                                                                                                                             PROSITE; PSO1186; EGF_2; UNKNOWN_1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS50092; TSPI; 3.
PROSITE; PS01208; WWFC_1; 1.
  InterPro; IPR001881; EGF_Ca_b
InterPro; IPR01303; EGF_like
InterPro; IPR003129; Laminin_
InterPro; IPR000884; TSP1.
InterPro; IPR0008085; TSP1.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                               TSP1REPEAT
                                                                                                                                                                                                                           PRINTS; PRO1705; TSPIREPEAT
SMART; SM00101; EGF; 2.
SMART; SM00209; TSP1; 3.
SMART; SM00214; TSP1, 1.
SMART; SM00214; VWC; 1.
                                                                                                                       Pfam; PF00008; EGF; 1. Pfam; PF00000; EGF; 1. 3. Pfam; PF001412; TSP 3; 12. Pfam; PF05735; TSP C; 1. Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 FTGVLONVREVE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 83.3
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGULANVREVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Job time : 108.931 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```



```
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                               RESULT 1
US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 482
LENGTH: 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6441, Ap
11112, A
5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6333, Ap
61396, A
45864, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17, Appl
17, Appl
12, Appl
5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20866, A
6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 482, App
Sequence 97, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19, App]
                                                        5, 2006, 22:43:07; Search time 23.8966 Seconds (without alignments) 43.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                             Issued Patents AA:*

1. / EMC Celerra SIDS3/prodata/2/laa/5_COMB.pep:*

2. / EMC_Celerra SIDS3/prodata/2/laa/6_COMB.pep:*

3. / EMC_Celerra SIDS3/prodata/2/laa/7_COMB.pep:*

4. / EMC_Celerra SIDS3/prodata/2/laa/H_COMB.pep:*

5. / EMC_Celerra SIDS3/prodata/2/laa/H_COMB.pep:*

5. / EMC_Celerra SIDS3/prodata/2/laa/R_COMB.pep:*

5. / EMC_Celerra SIDS3/prodata/2/laa/RE_COMB.pep:*

7. / EMC_Celerra SIDS3/prodata/2/laa/RE_COMB.pep:*

7. / EMC_Celerra SIDS3/prodata/2/laa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1
Sequence 1
Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-939-853A-98
US-09-131-288B-20
US-09-657-47-2-2
US-09-949-002-350
US-09-230-637-24
US-10-003-637-24
US-09-083-268-17
US-09-081-998A-17
US-09-981-12
US-09-949-016-11112
US-09-949-016-11112
US-09-949-016-11112
US-09-949-016-1333
US-09-949-016-6333
US-09-949-016-6333
US-09-270-767-45864
US-09-270-767-45864
US-09-270-767-45864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-252-991A-20866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-252-991A-20770
                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-286-819A-8
-08-980-357-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -08-762-428A-6
                                                                                                                                                                   650591 segs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                            Listing first 45 summaries
                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                        Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                  FQGVLANVRFVF 12
                                                                                             US-10-030-735-29
60
1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   831
1170
1170
1170
1170
175
175
175
418
418
418
418
1172
1172
1173
1173
1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                June
                                                                                              Title:
Perfect score:
                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                Database
                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š.
```

```
Sequence 482, Application US/09949002
| Sequence 482, Application US/09949002
| Patent No. 6900016
| GENERAL INFORMATION:
| APPLICANT: VORTER, J. Craig et al. |
| APPLICANT: VORTER, J. Craig et al. |
| TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION |
| TITLE OF INVENTION: AND USES THEREOF |
| FILE REFERENCE: CLOO790 |
| CURRENT APPLICATION NUMBER: US/09/949,002 |
| CURRENT PILING DATE: 2000-01-28 |
| PRIOR PILING DATE: 2000-09-08 |
| PRIOR FILING DATE: 2000-09-08 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                             8288, Ap
47, Appl
5, Appli
6, Appli
5, Appli
14121, A
22, Appl
22, Appl
      Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                        Sequence 7, Sequence 16 Sequence 16 Sequence 16 Sequence 7, Sequence 6, Sequence 6, Sequence 6, Sequence 5, Sequen
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
US-09-064-033-7
US-09-357-37-8
US-09-357-37-8
US-09-083-268-16
US-08-891-998A-16
US-08-922-635-6
US-08-922-635-6
US-09-389-487-7
US-09-343-681A-8288
US-09-543-681A-8288
US-09-543-681A-8288
US-09-344-643-6
US-08-922-635-5
US-09-489-039A-14121
US-09-489-039A-14121
US-09-414-643-5
US-09-411-886-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 2;
Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 FQGVLQNVRFVF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOGVLANVRFVF 12
  444444444444444444444444
```

```
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-09-657-472-2
                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: siz
                                                                                                                                                                                                                                                                                                                                                                                                              US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                              general 80, Application US/09939853A

| Sequence 80, Application US/09939853A
| Patent No. 6989232
| GENERAL INFORMATION:
| APPLICATION:
| APPLICATION: No. 6989232el Proteins and Nucleic Acids Encoding Same TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099
| CURRENT PILING DATE: 2001-08-27
| PRIOR APPLICATION NUMBER: 60/267,300
| PRIOR PAPLICATION NUMBER: 60/267,300
| PRIOR PRILING DATE: 2001-02-08
| PRIOR PLIING DATE: 2001-02-08
| PRIOR PLIING DATE: 2001-02-06
| PRIOR PLIING DATE: 2001-03-20
| PRIOR FILING DATE: 2001-03-20
| SOFTWARE: PatentIN Ver. 2.1
| SEQ ID NO 98
| LENGTH: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                     ·
0
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/08313288B
; Sequence 20, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
    APPLICANT: Jessell, Thomas M. and Avihu Klar
    TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
    TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
    NUMBER OF SEQUENCES: 20
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Cooper & Dunham LLP
    STREET: 1185 Avenue of the Americas
    CITY: New York
    STATE: New York
    STATE: New York
    COUNTRY: USA
                                                                                                                                                                         Score 55; DB 2; Length 831;
Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 2; Length 831;
Pred. No. 0.026;
                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%;
91.7%;
                                                                                                                                                                           Query Match 91.7%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                          ||||| |||||
208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FOGVLONVRFVF 219
NUMBER OF SEQ ID NOS: 159
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 97
LENGTH: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLANVREVF 12
                                                                                                                                                                                                                                                               1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-939-853A-98
                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-313-288B-20
                                                                                                                                     US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                              US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTEIL NO. 6'72'064

GENERAL INFORMATION ETIC S.

APPLICANT: Lander, Exic S.

APPLICANT: Cargill, Michele

APPLICANT: Treland, James S.

APPLICANT: Treland, James S.

APPLICANT: Baley, George Q.

APPLICANT: MCCATCHY, Jeanette J.

TILLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES FILE REFERENCE: 2825.11027-001

CURRENT PILING DATE: 200.096/657,472

CURRENT FILING DATE: 200.096.01

PRIOR FILING DATE: 200.006.07.26

PRIOR FILING DATE: 1999-09-10

PRIOR FILING DATE: 1999-09-10

PRIOR FILING DATE: 2000-07-26

PRIOR FILING DATE: 2000-07-26

PRIOR FILING DATE: 2000-07-26

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2551

SOFTWARRE PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 1; Length 1170;
pred. No. 0.038;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 2;
Pred. No. 0.038;
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-949-002-350
US-09-949-002-350
; Sequence 350, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09657472 Patent No. 6727063
                                                                                                                                                                                                                                     20:
                                                                                                                                                          LELEFAX: (212) 278-0400
TELEFAX: (212) 391-0526
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                      91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.78;
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11||| ||||||
208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 91.7
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-083-268-17
Sequence 17, Application US/09083268
Fatent No. 6673535
GENERAL INFORMATION:
APPLICANT: Pulst, Stefan M
TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
TITLE OF INVENTION: ATAXIA-2 AND PRODUCTS RELATED THERETO
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 326
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/083,268 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Mueting, Raaach & Gebhardt, P.A. STREET: 119 No. 6673535th Fourth Street CITY: Minneapolis STATE: Minneapolis COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.7%; Score 37; DB 2;
63.6%; Pred. No. 31;
live 1; Mismatches
                                                                                                                                                                 Score 38; DB
Pred. No. 10;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/727,084
FILING DATE: 08-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCOrmack, Myra H
REGISTRATION NUMBER: 232.00010101
TELECOMMUNICATION INFORMATION:
TELEFPHONE: 612/305-1220
TELEFPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 17, Application US/08981998A ; Patent No. 6844431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
                                                                                                                                                               Query Match 63.3%;
Best Local Similarity 70.0%;
Matches 7; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 326 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 63.0.
           SOFTWARE: Patentin Ver 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 FDGIYANVRMV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLANVRFV 11
                                                                                                                                                                                                                                                                                    |: :||||||
51 FEAMLANVRF 60
                                                                                                                                                                                                                                                        1 FQGVLANVRF 10
                                              ; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-632C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-981-998A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10003632C

Patent No. 6964199
GRNERAL INFORMATION:

APPLICANT: Lee, Chichang; Ly, Celia; Moore, Gordon; Chi, Xiamei
TITLE OF INVENTION: Methods and Compositions for Enhanced Protein Expression and/or G
TITLE OF INVENTION: Cultured Cells Using Co-Transcription of a Bcl2 Encoding Nucleic
FILE REFERENCE: CENO269
CURRENT APPLICATION NUMBER: US/10/003,632C
CURRENT PLING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 14
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INPLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hayward, Gary
APPLICANT: Hayward, Gary
APPLICANT: Nicholas, John
APPLICANT: Nicholas, John
APPLICANT: Advin
APPLICANT: Hayward, Gary
APPLICANT: Hayward, Gary
APPLICANT: Amrvin
TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
TITLE OF INVENTION: ABSOCIATED Herpesvirus
FILE REFERENCE: 1107.78372
CURRENT APPLICATION NUMBER: US/09/230,637
CURRENT APPLICATION NUMBER: 60/022,591
PRIOR FILING DATE: 1996-07-25
PRIOR FILING DATE: 1996-07-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                           Score 55; DB 2; Length 1170;
Pred. No. 0.038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.3%; Score 38; DB 2; Length 175; 70.0%; Pred. No. 10; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Kaposi's sarcoma-associated herpes-like virus US-09-230-637-24
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/09230637
Patent No. 6264958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.3
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGVLANVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: :||||||
51 FEAMLANVRF 60
                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                 US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-10-003-632C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-230-637-24
                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

ò g

ò

```
ö
                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-083-268-5
; Sequence 5, Application US/09083268
; Sequence 5, Application US/09083268
; Patent No. 6673535
; GENERAL INFORMATION:
; APPLICANT: PULBE, Stefan M
TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
TITLE OF INVENTION: ATAXIA-2 AND PRODUCTS RELATED THERETO
NUMBER OF SEQUENCES:
; ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6673535th Fourth Street
; STATE: Minnesota
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 2; Length 418;
Pred. No. 40;
1; Mismatches 3; Indels
                                                       Score 37; DB 2; Length 418;
Pred. No. 40;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232.00010101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/727,084
FILING DATE: 08-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCOTMACK, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 232.001010(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                             61.7%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.0
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-083-268-5
                                                                                                                                                                                      1 FQGVLANVRFV 11
                                                                                                                                                                                                                                                85 FDGIYANVRMV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | |: |||| |
85 FDGIYANVRMV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                          Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-134-000C-6441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
US-09-648-281-12
                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MS-09-648-281-12
Sequence 12, Application US/09648281
Sequence 12, Application US/09648281
Sequence 12, Application US/09648281
Sequence 12, Application US/09648281
Sequence 12, Application of States Information
GENERAL INFORMATION:
TITLE OF INVENTION: Transgenic Animal Model of
TITLE OF INVENTION: Neurodegenerative Disease and Methods of Use
FILE REFERENCE: P-CE 4336
CURRENT APPLICATION NUMBER: US/09/648,281
CURRENT FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                          APPLICANT: PULST, STEFAN M.
TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
ATAXIA-2 AND PRODUCTS RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION NUMBER: US/08/981,998A
FILING DATE: 11-May-1998
CLASSIFICATION NUMBER: W0 97/42314
FILING DATE: 08-May-1997
APPLICATION NUMBER: US 08/727,084
FILING DATE: 08-0CT-1996
APPLICATION NUMBER: US 60/022,207
FILING DATE: 19-UUL-1996
APPLICATION NUMBER: US 60/017,388
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
WAND. WINDER: 08-MAY-1996
ATTORNEY/AGENT INFORMATION:
WAND. W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 2; Length 326;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: WUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٠.
۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232,00010120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 326 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.7%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                 STATE: MINNESOTA COUNTRY: 55401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 FDGIYANVRMV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: mus musculus
   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-981-998A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 12
LENGTH: 418
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
```

ö ô Sequence 6411, Application US/09134000C
Betent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BATEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C Gaps Gaps

```
Search completed: June 5, 2006, 22:48:55
Job time: 23.8966 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-981-998A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLTMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                    ; NAME/KEY: MISC_FEATURE
; LOCATION: (11)
; OTHER INFORMATION: Amino acid 11 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-6441
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR ATAXIA-2 AND PRODUCTS RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.7%; Score 37; DB 2; Length 1045; 58.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                         Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 2;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-949-016-11112
; Sequence 11112, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08981998A Patent No. 684431 GENERAL INFORMATION: APPLICANT: PULST, STEFAN M.
                                                                                                                                                                          TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                      Query Match 61.7%;
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       728 FCGILGNINFIY 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|:| || ||
281 FRGLLQNVHLVF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.7
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLANVREVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: 55401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 11112
LENGTH: 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-981-998A-5
                                                                                                                          SEQ ID NO 6441
LENGTH: 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                 COMPUTER: IS FILDLY COMPUTER: FILDLY COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/981,998A FILING DATE: "Unkay-1998 CLASSIFCATION: "Unknown>
PRIOR APPLICATION DATA: #00 P7/42314
APPLICATION DATA: #00 P7/42314
APPLICATION NUMBER: WS 08/727,084
FILING DATE: 08-MAY-1996
APPLICATION NUMBER: US 60/022,207
FILING DATE: 09-JUL-1996
APPLICATION NUMBER: US 60/017,388
FILING DATE: 08-MAY-1996
APPLICATION NUMBER: US 60/017,388
FILING DATE: US 60/017,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.7%; Score 37; DB 2; Length 113
63.6%; Pred. No. 1.2e+02;
:ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 232.00010120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 612-305-1217
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.7
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 FDGIYANVRMV 89
```

THIS PAGE BLANK (USPTO)

```
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simil
Matches 11; (
 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1020, Ap
Sequence 1022, Ap
Sequence 1042, App
Sequence 454, App
Sequence 456, App
Sequence 456, App
Sequence 455, App
Sequence 457, App
Sequence 97, App
Sequence 97, App
Sequence 98, Appl
Sequence 98, Appl
Sequence 98, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1, Appli
7, Appli
12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2, Appli
1170, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Appl
                                                                                                                                                                                                                                                                                                          Published Applications AA Main:*

: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                                                                  5, 2006, 23:46:43 ; Search time 78.6207 Seconds (without alignments) 70.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1170,
Sequence 38, Ag
Sequence 482, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40,
Sequence 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
        GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                             2097797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-110-782-988-40
US-110-741-600-1020
US-110-741-600-1020
US-111-043-806-462
US-111-043-806-454
US-111-043-806-455
US-111-043-806-455
US-111-043-806-455
US-111-043-806-455
US-111-043-806-455
US-111-043-806-455
US-111-043-806-451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-008-093-2
US-10-295-027-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-211-462-38
US-10-231-956A-482
                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-021-660-114
                                                                                                                                                                                        2097797 seqs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
                                                                                                                                    1 FOGVLANVRFVF 12
                                                                                                           US-10-030-735-29
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        June
                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                  OM protein
                                                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                             Database
                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
```

```
28 55 91.7 1170 4 US-10-419-462-38 Sequence 38, Appl 29 55 91.7 1170 5 US-10-741-600-1018 Sequence 1018, Ap 31 55 91.7 1170 5 US-10-741-600-1019 Sequence 1019, Ap 32 55 91.7 1170 5 US-10-741-600-1021 Sequence 1021, Ap 32 55 91.7 1170 5 US-10-741-600-1021 Sequence 1021, Ap 34 55 91.7 1170 5 US-10-81-968-38 Sequence 38, Appl 35 55 91.7 1170 5 US-10-631-467-1376 Sequence 2, Appl 36 55 91.7 1170 5 US-10-631-67-594 Sequence 594, Appl 37 55 91.7 1170 5 US-10-995-561-594 Sequence 594, Appl 38 55 91.7 1170 5 US-10-995-561-594 Sequence 594, Appl 41 55 91.7 1170 6 US-11-037-713-51 Sequence 596, Appl 41 55 91.7 1170 6 US-11-046-644-28 Sequence 28, Appl 41 55 91.7 1170 6 US-11-046-644-28 Sequence 28, Appl 41 55 91.7 1170 6 US-11-046-644-28 Sequence 28, Appl 44 38 63.3 86 4 US-10-285-394-153 Sequence 153, Appl 44 38 63.3 175 4 US-10-093-632-5 Sequence 153, Appl 45 38 63.3 175 4 US-10-003-632-5 Sequence 5, Appli
```

ALIGNMENTS

```
US-10-74-21-28
PAPLICANT ROBERTS
PAPLICANT ROBER
```

~

```
US-11-043-806-462

Sequence 462, Application US/11043806

Sequence 462, Application US/11043806

Sequence 462, Application O. US20060051774A1

Sequence 462, Application O. US20060051774A1

Fublication No. US20060051774A1

TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer

FILE REFERENCE: 1847-1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

LENGTH: 459
                                                                                                                                                                                                        Sequence 1022, Application US/10741600
Sequence 1022, Application US/10741600
Sequence 1022, Application US/2005026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 91.7%; Score 55; DB 6; Best Local Similarity 91.7%; Pred. No. 0.045; Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 5;
pred. No. 0.042;
Pred. No. 0.042;
                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(432)
; OTHER INFORMATION: Xaa = Any Amino Acid US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1047, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.7%;
91.7%;
                                                                                              208 FOGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7
Marches 11, Conservative
                      11; Conservative
                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FOGVLANVREVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-043-806-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                           US-10-182-968-40

US-10-182-968-40

Sequence 40, Application US/10782968

Publication No. US20050065324A1

GENERAL INFORMATION:
APPLICANT: Williams, Kevin J.
APPLICANT: Williams, Kevin J.
TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
TITLE OF INVENTION: UNMER: US/10/782,968

CURRENT APPLICATION NUMBER: US/10/419,462

PRIOR FILING DATE: 2003-04-21

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.2

SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1020, Application US/10741600
Sequence 1020, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT CARGILL, Michele et al.
APPLICANT CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INPARCTION, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 1020
LENGTH: 432
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                  FEATURE:
; OTHER INFORMATION: Thrombospondin Region plus N-terminal domain
US-10-419-462-40
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-782-968-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.7%; Score 55; DB 5; Length 432;
                                                                                                                                                          Score 55; DB 4; Length 240;
Pred. No. 0.022;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.7%; Score 55; DB 5; Length 240; 91.7%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
LOCATION: (1)...(432)
OTHER INFORMATION: Xaa = Any Amino Acid
                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                          Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 FQGVLQNVRFVF 201
                                                                                                                                                                                                                                                                                          190 FOGVLONVRFVF 201
                                                                                                                                                                                                                                                   1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGULANVREVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-10-741-600-1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-741-600-1020
         LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                             g
```

```
Sequence 452, Application US/11043806

Publication No. US20060051774A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Method

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

FILE REPERENCE: 1847.1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 453, Application US/11043806

Publication No. US20060051774A1

GENERAL INFORMATION:

APPLICATY: Compugen Ltd

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

FILE REFERENCE: 1847.1003

CURRENT APPLICATION UNDER: US/11/043,806

UNDERED FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Squence 455, Application US/11043806

Publication No. US20060051774A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

FILE REFERENCE: 1847.1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 6; Length 685;
Pred. No. 0.07;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.7%; Score 55; DB 6;
91.7%; Pred. No. 0.084;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%;
91.7%;
                                                    1|||| |||||
208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 FOGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FOGVLONVRFVF 219
                            1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGULANVREVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
COGANISM: Homo sapiens
US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                               RESULT 10
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 453
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 454, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: UNMBER: US/11/043,806
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9

US-11-043-806-456

US-11-043-806-456

SQUENCE 456, Application US/11043806

Publication No. US20060051774A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: Last 1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT PILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 91.7%; Score 55; DB 6; Length 578; Best Local Similarity 91.7%; Pred. No. 0.058; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                        Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 6; Length 555;
Pred. No. 0.055;
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                        Score 55; DB 3;
Pred. No. 0.046;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 FOGULQNVRFVF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-456
                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-043-806-454
                                                                                                                                                                                                              SEQ ID NO 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 454
LENGTH: 555
                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
```

Gaps

.; 0

```
Publication No. US20060051774A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: UNMBER: US/11/043,806

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 461

LENGTH: 855
                                    91.7%; Score 55; DB 3; Length 831; 91.7%; Pred. No. 0.087; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%; Score 55; DB 6; Length 855; 91.7%; Pred. No. 0.09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6, 2006, 00:00:11
                                                                                                                                                                      208 FQGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FQGVLQNVRFVF 219
                                         Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FQGVLANVRFVF 12
                                                                                                                                1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-11-043-806-461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June
Job time: 79.6207 secs
                                                                                                                                                                                                                                             RESULT 15
US-11-043-806-461
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                  8
                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                      RESULT 13

US-09-939-853A-97

US-09-939-853A-97

Sequence 97, Application US/09939853A

Publication No. US20040039163A1

GENERAL INFORMATION:

APPLICATION:

APPLICATION NOBER: US/09/939,853A

CURRENT APPLICATION NUMBER: US/09/939,853A

CURRENT APPLICATION NUMBER: 60/228,191

PRIOR PILING DATE: 2001-08-27

PRIOR PILING DATE: 2001-08-27

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOFTWARE: PARCENTIN VET: 2.1

SEMENTED NOS: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NESCULE 14
Sequence 98, Application US/09939853A
Sequence 98, Application US/09939853A
Sequence 98, Application US/09939853A
Sequence 98, Application No. US20040039163Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-099
CURRENT APPLICATION NUMBER: US/09/939,853A
CURRENT FILING DATE: 2001-08-25
PRIOR APPLICATION NUMBER: 60/28,191
PRIOR PLING DATE: 2001-08-25
PRIOR APPLICATION NUMBER: 60/267,300
PRIOR APPLICATION NUMBER: 60/267,300
PRIOR PLING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/269,961
PRIOR APPLICATION NUMBER: 60/269,961
PRIOR PLING DATE: 2001-02-20
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 159
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 3; Length 831; Pred. No. 0.087;
                                                                                                           Score 55; DB 6; Length 828;
Pred. No. 0.087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                         0; Mismatches
                                                                                                         Query Match 91.7%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.7%;
                                                                                                                                                                                                                                           208 FOGVLONVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 FOGVLQNVRFVF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLANVRFVF 12
                                                                                                                                                                                                  1 FOGVLANVRFVF 12
; LENGTH: 828
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                             В
                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    원
```

ö

Gaps

ö

1; Indels

0; Mismatches

Tue Jun

```
JS-10-953-349-34674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-953-349-34673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 662, App
Sequence 15318, A
Sequence 27518, A
Sequence 27516, A
Sequence 27516, A
Sequence 36109, A
Sequence 36109, A
Sequence 11050, A
Sequence 11048, A
Sequence 21828, A
Sequence 21828, A
Sequence 21828, A
Sequence 21826, A
Sequence 22826, A
Sequence 22826, A
Sequence 22826, A
Sequence 22826, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1159, Ap
1158, Ap
1157, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282, App
36, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34674, A
Sequence 34673, A
Sequence 34672, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                       June 6, 2006, 00:00:38; Search time 3.72414 Seconds (without alignments) 37.266 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                     Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US09 NEW PUB.pep:*

2: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-34674
US-10-953-349-34673
US-10-503-349-34673
US-10-953-349-15318
US-10-953-349-15318
US-10-953-349-27517
US-10-953-349-27517
US-10-953-349-27517
US-10-953-349-27517
US-10-953-349-36109
US-10-953-349-36108
US-10-953-349-11048
US-10-953-349-11048
US-10-953-349-21827
US-10-953-349-21827
US-10-953-349-21828
US-10-953-349-21828
US-10-953-349-21828
US-10-953-349-21828
US-10-953-349-21828
US-10-953-349-21828
US-10-953-349-21828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-953-349-1159
US-10-953-349-1158
US-10-953-349-1157
                                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-242-505A-36
                                                                                                                                                                                                              58871 seqs, 11565156 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                   US-10-030-735-29
60
1 FQGVLANVRFVF 12
                                                                                                                                                                                                                                                                seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331
358
388
1504
1182
1182
1186
1198
2213
224
225
223
223
223
392
407
407
407
407
407
250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556.77
566.77
566.77
566.77
566.77
566.77
566.77
566.77
566.77
566.77
566.77
566.77
566.77
566.77
                                                                                                                                                                                                                                         oŧ
                                                                                                                                     Perfect score:
                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number
                                                                                                                                                                                                                                                                Minimum DB
Maximum DB
                                                                                                                                                    Sequence:
                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                         Database
                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
```

```
Sequence 34674, Application US/10953349

Publication No. US20060107345A1

Publication No. US20060107345A1

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: US/10/953,349

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT PILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SEQ ID NO 34674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34673, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROW, Nickolai et al.

TITLE OF INVENTION: ENCONDED THERBY

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT PILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PatentIn version 3.3

SEQ ID NO 34673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                        9203, Ap
9202, Ap
9202, Ap
13, Ap
2333, Ap
2333, Ap
16521, Ap
16526, A
6895, Ap
6895, Ap
6895, Ap
29183, Ap
29183, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                         Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
US-10-953-349-9204
US-10-953-349-9208
US-10-953-349-9203
US-10-953-349-9203
US-10-953-349-9203
US-10-953-349-9203
US-10-953-349-2333
US-10-953-349-16526
US-10-953-349-16526
US-10-953-349-16526
US-10-953-349-16526
US-10-953-349-1693
US-10-953-349-1693
US-10-953-349-1693
US-10-953-349-1693
US-10-953-349-1693
US-10-953-349-1693
US-10-953-349-1693
US-10-953-349-1693
US-10-953-349-1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 6
Pred. No. 12;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.7%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315
362
4000
4000
4000
4453
863
1014
1114
1143
1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 QGVLFNIQYV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QGVLANVRFV 11
```

Length 358;

DB 6;

Score 34;

56.78;

Gaps

ö

Length 182; 2; Indels

```
Sequence 27518, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
11TLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
11TLE OF INVENTION: ENCONDED THERBY
11TLE OF INVENTION: US/10/953,349
CURRENT APPLICATION UNDER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE PATENTIN VETSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 6; Length 186;
Pred. No. 10;
                                                                                                                                                                                                     Score 33; DB 6;
Pred. No. 10;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 10;
0; Mismatches
             CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
EEQ ID NO 15318
LENGTH: 182
                                                                                                                                                                                                         55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.6%;
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Triticum aestivum US-10-953-349-27518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6.
Tr Conservative
                                                                                                                                                                                       Query Match
Best Local Similarity 60.v
Local Similarity 60.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLANVRFV 11
                                                                                                                                                                                                                                                                                                                    104 GLLMNMNFVF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 FSAALAEVRFV 73
                                                                                                                                                                                                                                                                                  3 GVLANVRFVF 12
                                                                                                                              ; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-15318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-10-953-349-27517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-27517
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-10-953-349-27518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 27518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15318, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORWATION:
; APPLICANT: ALEXANDROW, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                               Sequence 34672, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 6; Length 1504;
Pred. No. 63;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 6; Length 382;
Pred. No. 14;
3; Mismatches 1; Indels
                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 662, Application US/10505928
| Publication No. U320060088532A1
| GENERAL INFORMATION:
| APPLICATION NO. U320060088532A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
| FILE REFERENCE: 28967/39178
| CURRENT APPLICATION NUMBER: US/10/505,928
| CURRENT FILING DATE: 2004-08-27
| PRIOR FILING DATE: 2002-03-07
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: Patentin 3.2
| LENGTH: 1504
 Pred. No. 13;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Zea mays subsp. mays US-10-953-349-34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.5%;
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.3
SEQ ID NO 34672
LENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.5
Matches 6; Conservative
 Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :|:::||||
751 QHILSSLRFVF 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 OGVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 QGVLFNIQYV 285
                                                                               252 QGVLFNIQYV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 QGVLANVRFV 11
                                                         2 QGVLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-10-953-349-15318
                                                                                                                                                                         US-10-953-349-34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-10-505-928-662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-505-928-662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                           δ
                                                                                            셤
```

ö

Gaps

```
Sequence 27517, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROW, Nickolai et al.

APPLICANT: ALEXANDROW, Nickolai et al.

TITLE OF INVENTION: ENCONDED THERBY

CURRENT PELICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NO 27517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.0%; Score 33; DB 6; Length 188; 63.6%; Pred. No. 10; ive 0; Mismatches 4; Indels
```

셤

```
Sequence 36109, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROW, Nickolai et al.

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SEQ ID NO 36109
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (45)...(45)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                              OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                               LOCATION: (43)..(43)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa can be any naturally occurring amino acid FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (16)...(16)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (50)...(50)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (52)...(52)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.3%; Score 32; DB 6; Length 173; 85.7%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                               Length 166
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 6;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                      TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                          53.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                               FEATURE:
NAME/KEY: misc feature
LOCATION: (9)..(9)
                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (43)...(43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (16)...(16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||:||
159 FQGVVAN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||:||
166 FQGVVAN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLAN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVLAN 7
                                                                                                                                                                                                                                                                                                                                   US-10-953-349-36110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-10-953-349-36109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-36109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-10-953-349-36108
  SEQ ID NO 36110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                    APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
PILE REPERBURCE: 2750-1579PUS
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 27516
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36110, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVERTION: ENCONDED THERBY
FILE REPERENCE: 2750-15799US2
CURRENT PELING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 6; Length 213;
Pred. No. 12;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.0%; Score 33; DB 7; Length 297; 70.0%; Pred. No. 17; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4132, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
    APPLICANT: HELIX RESEARCH INSTITUTE
    TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT FILING DATE: 2005-12-05
; PRIOR PILING DATE: 2005-12-05
; RIOR FILING DATE: 2005-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4132
                                                                                                   Sequence 27516, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Triticum aestivum US-10-953-349-27516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 55.0
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 FSAALAEVRFV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLANVRFV 11
65 FSAALAEVRFV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 GVVFNVRVVF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GVLANVRFVF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4132
                                                                             10-953-349-27516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-10-953-349-36110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-293-697-4132
```

ઠે 셤 ઠે g

```
Sequence 11049, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: 2004-09-30
CURRENT FILING DAIR: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 11049
IERNOTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June 6, 2006, 00:12:56 Job time: 3.82414 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT , ORGANISM: Arabidopsis thaliana US-10-953-349-11048
                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Arabidopsis thaliana US-10-953-349-11049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.3
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.3
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||||:|:
243 ILANVKFI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||||:|:
275 ILANVKFI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 VLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                       TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILL REFERRENCE: 2750-1579PUS2 CURRENT PAPLICATION NUMBER: US/10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SEQ ID NOS: 40252 SEQ ID NO 3:0108 LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11050, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONNED THERBY
FILE REFERENCE: 2750-1579FUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (88)
COTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-36108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (38)...(38)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (52) .. (52)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (30)...(30)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (86)...(86)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.3%; Score 32; DB 6; Length 249; Best Local Similarity 62.5%; Pred. No. 22; Matches 5; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.3%; Score 32; DB 6; Length 209; 85.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 11050
LENGTH: 249
Sequence 36108, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Arabidopsis thaliana
US-10-953-349-11050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||||:|:
238 ILANVKFI 245
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VLANVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 FOGUVAN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLAN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-10-953-349-11050
                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Sequence 11048 Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROW, Nickolai et al.

APPLICANT: ALEXANDROW, Nickolai et al.

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-157991082

CURRENT APPLICATION VUMBER: US/10/953,349

CURRENT APPLICATION VUMBER: US/10/953,349

CURRENT APPLICATION VUMBER: US/10/953,349

CURRENT APPLICATION VUMBER: US/10/953,349

SOFTWARKE: PatentIN version 3.3

SEQ ID NO 11048
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 286
                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 6;
Pred. No. 26;
3; Mismatches (
Score 32; DB 6;
Pred. No. 23;
                                           3; Mismatches
```

Length 254;

```
5, 2006, 22:08:53 ; Search time 83.5431 Seconds (without alignments) 60.201 Million cell updates/sec
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                   June
                                                                                                                                                     Run on:
```

US-10-030-735-30 55 1 FQGVLQNVRFV 11 **BLOSUM62** score: Scoring table: Sequence:

2589679 segs, 457216429 residues Gapop 10.0 , Gapext 0.5 Searched:

2589679 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* geneseqp2006s:* geneseqp1980s:* A_Geneseq_8:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 [1000		ئ ئ ۇ				
No.	Score	Match	Watch Length	8	ΩI	Description
	55	100.0		4	AAB35360	Aab35360 Alpha3bet
7	55	100.0	12	4	AAB35352	Aab35352 Alpha3bet
3	55	100.0	12	4	AAB35366	9
4		100.0	12	4	AAB35378	_
Ŋ		100.0	12	9	ABG72834	Abg72834 Thrombosp
9	55	100.0	240	ω	ADL70641	Adl70641 Human thr
7	25	100.0	432	œ	ADQ39359	Adq39359 Human myo
80	55	100.0	432	œ	ADQ39357	_
σ	55	100.0	459	4	AAU02916	Aau02916 Angiotens
10		100.0	466	٣	AAB43602	Aab43602 Human can
11	55	100.0	546	4	AAU02915	Aau02915 Angiotens
12	55	100.0	548	7	ADN02474	Adn02474 TSF polyp
13		100.0	555	4	AAU02914	Aau02914 Angiotens
14	55	100.0	731	4	AAU02913	Aau02913 Angiotens
15		100.0	1152	М	AAB00042	Aab00042 Human thr
16	55	100.0	1152	S	AAU74771	Aau74771 Human thr
17	55	100.0	1152	ß	ABB82285	Abb82285 Human thr
18		100.0	1170	4	AAB74450	Aab74450 Human var
19	55	100.0	1170	4	AAB90800	Aab90800 Human she
20	55	100.0	1170	Ŋ	AAE25030	Aae25030 Human thr
21	55	100.0	1170	ß	AAU75315	Aau75315 Human thr
22	55	100.0	1170	9	ABP96780	Abp96780 Human COP
23	55	100.0	1170	9	ABU03474	Abu03474 Angiogene

Abg74673 Human THB Aae36228 Human THB Abr62059 Human thr Adn39852 Cancer/an	Adj76124 Marker ge Adj75296 Marker ge Adl70639 Human thr	Adl35874 Human thr Adq26070 Thrombosp Adp54179 Human PRO	Adq39358 Human myo Adq39356 Human myo Adq39355 Human myo	Thromb Human Human		
ABG74673 AAE36228 ABR62059 ADN39852		ADL35874 ADQ26070 ADPS4179		9 ADZ21688 9 AEB87781 9 AEB46751		
1170				0711		
1000.0	100.0	100.0	100.0	100.0	2 4 6 0 2 4 4 0 2 5 7 5 1	92.7 92.7 92.7
	5 5 5 5 5 5 5 5	0 0 0 0 0	20 CC	, n n n	222	2122
24 25 27	3 5 8 3 6 8	31 32 33	8 8 4 4 8 4		9 4 4 ¢	4 4 4 4 8 4 8

Alpha3betal integrin binding peptide #25. AAB35360 standard; peptide; 11 AA (first entry) 08-MAY-2001 AAB35360;

Alphalbetal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility. Synthetic.

WO200105812-A2.

25-JAN-2001.

12-JUL-2000; 2000WO-US018986. 99US-0144549P 15-JUL-1999; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Roberts DD, Krutzsch HC;

WPI; 2001-182656/18.

New peptides that bind to or are recognized by alpha3-betal integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and

Claim 4; Page 34; 84pp; English.

The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, disbetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides of the invention

Sequence 11 AA;

RESULT 2 AAB35352

ઠે 셤

```
The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
              Alpha3beta1 integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenosis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                      New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55; DB 4; I
100.0%; Pred. No. 0.00084;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha3betal integrin binding peptide #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB35378 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                               12-JUL-2000; 2000WO-US018986.
                                                                                                                                                                                                                                  99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                       Roberts DD, Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                          WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200105812-A2.
                                                                                                                          WO200105812-A2
                                                                                                                                                                                                                                    15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2001.
                                                                                                                                                             25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB35378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB35378
ID AAB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of peptides which bind to alpha3betal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                      Alpha3betal integrin; angiogenesis; cell proliferation; cancer; diabetic retinopathy; restenssis; atherosclerosis; rheumatoid arthritis; macular degeneration; psoriasis; cell adhesion; cell motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 11; Conservative 0; Mismatches 0; Indels
 Length 11;
                                     Indels
                                     .
 Score 55; DB 4; L Pred. No. 0.00076; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha3betal integrin binding peptide #31.
                                                                                                                                                                                                                                                                                                          Alpha3betal integrin binding peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                  AAB35352 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 34; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB35366 standard; peptide; 12
Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2000; 2000WO-US018986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0144549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Krutzsch HC;
                                                                                                         1 FQGVLÓNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLQNVRFV 11
                                                                          1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOCVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200105812-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2001
                                                                                                                                                                                                                                                                       08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB35366;
                                                                                                                                                                                                                                    AAB35352;
```

cancer.

AAB35366
ID AAB3
XX
AC AAB3
XX
DT 08-M
XX

RESULT 3

셤

ઠે

ö

Gaps

```
888888
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                              alphalbetal integrins. They are useful in the modulation of cell adhesion and motility, and in the treatment of cancer, disbetic retinopathy, rheumatoid arthritis, macular degeneration, atherosclerosis, psoriasis and restenosis. The present sequence is an example of one of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to diagnosing cancer other than prostate cancer in a male mammal, comprising assaying a test sample for increased level of semenogelin, or cancer in a female by assaying for the presence of semenogelin. Administering a semenogelin protein or polypeptide fragment or a semenogelin-specific antibody or active fragment, or a recombinant ovector expressing the protein or antibody, is useful for inducing an immune response to a cancer in a mammal, where the cancer is not prostate cancer and semenogelin is a marker. The invention is used to diagnose cancer, particularly of epithelial origin such as lung cancer, papillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A new diagnosis for cancer other than prostate cancer in a mammal useful to detect cancer including lung cancer, particularly small cell lung cancer and melanoma comprises detecting semenogelin in a sample.
                                                                                          New peptides that bind to or are recognized by alpha3-beta1 integrins, useful for inhibiting cell adhesion to extracellular matrix, cell motility and proliferation and for treating rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                  present invention provides a number of peptides which bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; thrombospondin-1; cytostatic; immunostimulant; cancer; epithelial cancer; lung cancer; papillary renal cell carcinoma; colon cancer; small-cell lung cancer; SCLC; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombospondin-1 sequence containing synthetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 4; I 100.0%; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                Example 2; Page 34; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG72834 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 14; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2001; 2001US-0281994P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-2002; 2002WO-US010535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krutzsch HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOGVLONVRFV 11
                           WPI; 2001-182656/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-103329/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200281630-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roberts DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG72834;
                                                                                                                                                                                                                                                                                                                                  The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
```

셤

ò

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of the N-terminal domain of human thrombospondin-1 (TSP) ADL70639. The invention relates to TSP fragments (80-100, 40-55 or 20-35 kDa mol.wt.) found in plasma, and their use in clinical assays for cancer and for generation of antibodies and other binding agents. A method that distinguishes TSP from a TSP fragment or portion involves: (1) using an epitope shared by TSP and the TSP fragment or portion as a target for a binding molecule, e.g. an antibody, to obtain a quantitation of TSP plus TSP fragment or portion; (2) using an epitope present in TSP but not in the fragment or portion to obtain a quantitation of TSP only; and (3) using the difference between (1) and (2) as a quantitation of the amount of TSP fragment or portion. Suitable epitopes are provided ADL70602-ADL70638. Detection or quantification of the TSP fragment or portion of the presence, or monitor the course, of a disease or condition selected from cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes.
               (SCLC), or a melanoma. The present sequence represents the amino acid sequence of the thrombospondin-1 sequence containing synthetic peptide which binds to alpha-3-beta-1 integrin
                                                                                                                                                                Gaps
renal cell carcinoma, colon cancer, especially small-cell lung
                                                                                                                                                                ö
                                                                                                                            Length 12;
                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; thrombospondin-1; epitope; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151. 164 /
/note= "Fibrinogen binding region"
                                                                                                                           100.0%; Score 55; DB 6; I
100.0%; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23. .32
/note= "Heparin binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Heparin binding region"
                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human thrombospondin-1 N-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 40; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              ADL70641 standard; protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2003; 2003WO-US026023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-2002; 2002US-0405494P.
21-APR-2003; 2003US-00419462.
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77. .82
                                                                                                                                                                                                                                     11
                                                                                                                                                                                                   1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                     FOGVLONVRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WILL/) WILLIAMS K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-226901/21.
                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004018995-A2
                                                                                         Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                    ADL70641;
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                            RESULT
```

WPI; 2004-533949/51

```
hypersensitivity, scleroderma, conditions associated with plugging of vessels, a condition associated with a cryotibrinogen, a condition associated with a cryotibrinogen, a condition associated with a cryotibrinogen, a condition carcer in a selected from adenoma, adenoma, adenoma, carcinoma, lymphoma, leukaemia, solid cancer, liquid cancer, metastatic cancer, no-metastatic cancer, cancer, metastatic cancer, internal cancer, skin cancer, part, tendon or ligament, digestive system, liver or biliary system, pancreas, head, neck, endocrine system, reproductive system (male or female), genitourinary system, kidney, urinary tract, sensory system, nervous system, lymphoid organ, blood, a gland, mammary glasue, prostate gland, endometrial tissue, mesodermal tissue, ectodermal tissue, a teratoma, a poorly differentiated cancer, a well-differentiated cancer or a moderately differentiated cancer,
                   vasculitis, renal allograft, atthma, diabetes mellitus, myocardial infarction, liver disease, splenectomy, dermatomyositis, polyarteritis nodosa, systemic lugus erythematosus, lugus erythematosus, Kawasaki syndrome, non-specific vasculitis, juvenile rheumatoid arthritis, rheumatoid arthritis, vasculitis, juvenile rheumatoid arthritis, thrombocytopenic purpura, purpura, an inflammatory condition, a condition associated with platelet activation, a condition associated with consumption of platelet activation, a condition associated with consumption of platelets, heparin-induced thrombocytopenia, disseminated intravascular coagulation, intravascular coagulation, extravascular coagulation, a condition associated with endothelial activation, a condition associated with pproduction associated with pproduction associated with production associated with the middle activation, a condition associated with production associated with production associated with production associated with the middle activation, a condition associated with production associated with the middle activation, a condition associated with the middle activation, a condition associated with production associated with the middle activation associated with the middle acti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human myocardial infarction-associated gene derived protein, SEQ ID 1022.
                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment, urticaria, hives, angioedemā, a drug reaction, an antibiotic
reaction, an aspartame reaction, atopic dermatitis, eczema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
renal disease, atopic dermatitis, vasculitis, acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 8; Length 240; 100.0%; Pred. No. 0.023; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Devlin JJ, Iakoubova O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ39359 standard; protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-2002; 2002US-0434778P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity luv...
Best Local 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 FOGVLONVRFV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004058052-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ39359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ39359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                             composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarctionsespecial associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human myocardial infarction-associated gene derived protein, SEQ ID 1020.
                           Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 8; Length 432; 100.0%; Pred. No. 0.044; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Prec. ...
                                                                    Claim 10; SEQ ID NO 1022; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ39357 standard; protein; 432 AA.
                                                 the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiant; gene therapy; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          Sequence 432 AA;
          N-PSDB; ADQ38531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004058052-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ39357;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ39357
g
                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
WO200136632-A2
                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB43602
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                               The invertion fractace to a movel method tot indeficion. The method comprises detecting a single nucleotide approachism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an antered risk for myocardial infarction in the individual's nucleic acids, where the presence of the SNP is correlated with an attered risk for myocardial infarction in the individual. The invention of altered risk for myocardial infarction in the individual. The invention of curtee comprising at least a contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino of acid sequence given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification, an antibody that specification and which is between about 16 and 1000 nucleotides in the specification and which is between about 16 and 1000 nucleotides in comprising the specification and which is between about 16 and 1000 nucleotides in a nucleic acid molecule; a method of detecting an SNP in a nucleic acid molecule; a method of detecting an agent useful in treating or preventing contraction. The novel detection method has cardiant activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-sasociated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                        The invention relates to a novel method for identifying an individual who
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nultiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a
                                                                                                                                   Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiotensin converting enzyme (ACEV) splice variant protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 55; DB 8; Length 432; 100.0%; Pred. No. 0.044; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                      Claim 10; SEQ ID NO 1020; 145pp; English.
                                                 Iakoubova 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU02916 standard; protein; 459 AA.
                                                                                                                                                                      the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FQGVLQNVRFV 11
                                                 Cargill M, Devlin JJ,
                 (APPL-) APPLERA CORP.
                                                                               WPI; 2004-533949/51.
N-PSDB; ADQ38529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptides are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various also disorders including cardiovascular diseases such as attributing cardiovascular diseases such as thericosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases concer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antishematic; antishematic; antishemit; antishemit; antishemit; antishemit; antishemit; antishemit; antishemit; antishemit; cardiant; dermatological; neuroprotective; thrombolytic; captibacterial; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; attoimmune disorder; haematopoietic cell disorder; autoimmune disorder; haemostatic; cardiovascular disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 55; DB 4; Length 459; 100.0%; Pred. No. 0.047; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cancer associated protein sequence SEQ ID NO:1047.
                                                                                                                                                                                                                                                                                                                                    Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB43602 standard; protein; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 16; 519pp; English.
                                                                                                                                                                                                                                                                                                                                Azar I,
                                                                      17-NOV-2000; 2000WO-IL000766
                                                                                                                                                99IL-00132978
                                                                                                                                                                                   99IL-00133455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                          (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                    David A,
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS06016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 459 AA;
                                                                                                                                            17-NOV-1999;
                                                                                                                                                                                   10-DEC-1999;
25-MAY-2001
                                                                                                                                                                                                                                                                                                                                    Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB43602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
```

```
ADN02474 standard; protein; 548 AA.
                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 15; 519pp; English.
                                                                                                                                              17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                          99IL-00132978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FQGVLQNVRFV 11
                                                                                                                                                                                                                    (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                              WPI; 2001-336004/35
                                                                                                                                                                                                                                                                                             N-PSDB; AAS06015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSF polypeptide
                                                                                      WO200136632-A2
                                                                                                                                                                           17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                           Homo sapiens
                                                                                                                                                                                          10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CN1401387-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-2003.
                                                                                                                 25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN02474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN02474
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antitathermatic; antitathermatic; antiathermitic; antidabetic; antitathermatic; antiathermatic; antibacterial; antitathermatic; antipacterial; antitathermatic; antipacterial; antitathermatic; antipacterial; antitathermatic; antipacterial; antitation; noorropic; vasotropic; antipacitic and antianglogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, mucleotides, antibodies, agonists and antegonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                       AAC77607 to AAC78448 encode the human cancer associated proteins given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumnour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiotensin converting enzyme (ACEV) splice variant protein #15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 3; Length 466; Pred. No. 0.048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                           Claim 11; Page 1636-1638; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU02915 standard; protein; 546 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                     08-MAR-2000; 2000WO-US005882
                                                                                                                                  99US-0124270P
                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 FÓGVLÓNVRFV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention
                                                                                                                                                                                                                      2000-587533/55.
                                                                                                                                                                                            Ruben SM
                                                                                                                                                                                                                                   N-PSDB; AAC77811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 466 AA;
                                            WO200055350-A1
                                                                                                                                  12-MAR-1999;
                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2001
                                                                          21-SEP-2000
                                                                                                                                                                                            Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU02915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU02915
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glueapon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and vasoactive intestinal colypeptides receptor 2. The polypeptides and their associated mucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adenovirus vector; anti-neoplastic; TSF polypeptide; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 4; Length 546; 100.0%; Pred. No. 0.057; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Levine Z, David A, Azar I, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             abnormality such as deep vein thrombosis
```

```
WPI; 2001-336004/35
N-PSDB; AAS06014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU02913;
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
AAU02913
                                                                                                                                                                                                                                                                                                                                                                         윱
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                          The present invention relates to a novel recombinant adenovirus vector mediated anti-meoplastic composition is prepared through cloning the cDNA sequence from the human peripheral blood cell by specific primer and reverse transcription-polymerase chain reaction (RT-PCR) method for coding TSF polypeptide, construction in human embryonic kidney cell 293 by Addasy system, and packaging and expressing the recombinant adenovirus vector of TSF. It can suppress the growth and transfer of cancer. The present sequence represents the TSF polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin converting enzyme splice variant; ACEV; interleukin 6; grannlocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; mycoardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nonarcoidotic pulmonary granulômatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                Tumor suppressing polypeptide TSF and gene therapy vector composition.
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiotensin converting enzyme (ACEV) splice variant protein #14.
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 7; Length 548; 100.0%; Pred. No. 0.057; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bernstein J;
                                                    (TAID-) TAIDA LIFE SCI TECH RES CENT HEMATOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  David A, Azar I, Khosravi R,
                                                                                                                                                       Claim 2; SEQ ID NO 1; 13pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02914 standard; protein; 555 AA.
          21-AUG-2002; 2002CN-00129408.
                               21-AUG-2002; 2002CN-00129408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000; 2000WO-IL000766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99IL-00132978
99IL-00133455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
ses 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                     1 FOGULONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMP-) COMPUGEN LTD
                                                                                                 WPI; 2003-469302/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-336004/35
                                                                                                            N-PSDB; ADN02475
                                                                                                                                                                                                                                                                                  Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200136632-A2.
                                                                           Liu P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Levine Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU02914;
                                                                                                                                                                                                                                                                                                        Query Match
                                                                           Han Z,
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
셤
                                                                                                                                                                                                                                                                                                                                                     ઠે
```

```
The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, ancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis, cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiotensin converting enzyme (ACEV) splice variant protein #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 4; Length 555; 100.0%; Pred. No. 0.058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Azar I, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU02913 standard; protein; 731 AA.
                                                                                                                                                                Claim 4; Fig 14; 519pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99IL-00132978
99IL-00133455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FOGVLONVRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200136632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2001
```

```
Search completed: June
Job time: 83.5431 secs
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                          The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen P53, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and cononary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as abbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection; glaucoma.
                            Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 4; Length 731; 100.0%; Pred. No. 0.079; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361. .416
/label= Type 1 repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417. .473
/label= Type 1 repeat region
474. .530
/label= Type 1 repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                    abnormality such as deep vein thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB00042 standard; protein; 1152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                     Claim 4; Fig 13; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human thrombospondon-1 (TSP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0118053P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-2000; 2000WO-US002482
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.vv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-514823/46
 N-PSDB; AAS06013
                                                                                                                                                                                                                                                                                                                                                                  Sequence 731 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200044908-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawler JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB00042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
   δ
```

5, 2006, 22:24:59

```
New nucleic acids are described which encode a protein comprising the second and third type I repeats of human TSP (thrombospondin)-1, but not second and third type I repeats of human TSP (thrombospondin)-1 containing the second and third type-I repeats and the COMP (cartilage oligomeric matrix protein) the type-I repeats and the COMP (cartilage oligomeric matrix protein) sembly sequence (COMPYTSP-I) was produced by PCR (polymerse chain caction). Expression of COMPYTSP-I caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. Anti-
cretinopathy corneal graft rejection, does not require the therapeutic gent to enter tumour calls or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 3; Length 1152; 100.0%; Pred. No. 0.13; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                           Disclosure; Fig 1; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    does not induce drug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1152 AA;
```

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

5, 2006, 22:25:22 ; Search time 12.8017 Seconds (without alignments) 82.675 Million cell updates/sec June

US-10-030-735-30 55 1 FQGVLQNVRFV 11 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mbospondin 1	thrombospondin 1 p	thrombospondin 1 p	b	N		pilin, t	probable 3-oxoacyl	3-oxoacyl-[acyl-ca	reverse gyrase (to	hypothetical prote	hypothetical prote	neuraminidase, pro	two component resp	auto	probable transcrip	Q.	hypothetical prote		lipo	NADH oxidase SP146	NADH oxidase (EC 1	zona pellucida gly	hypothetical prote	hypothetical prote	surfactin syntheta	hetical	_	hypothetical prote
SUMMARIES	ID	95	TSHUP1	A40558	D84938	TSHUP2	A42587	B75421	A64590	B71923	H69377	T34271	B89832	G95153	AE2929	AC0368	A98353	A39804	F96625	D81929	E72462	B95171	B98037	S70397	T05178	AE1864	I40486	T31048	C87403	нв3708
	08	7	П	N	N		•					N	~	N	N	~	~	ч	~	~	7	7	7	7	~	~	N	7	~	7
	å Query Match Length	229	1170	1170	467	1172	1172	186	247	247	1054	304	498	740	747	759	783	1178	82	212	295	459	459	715	1308	1829	3587	93	298	417
	Query Match	. 0	100.0	100.0	69.1	67.3	67.3	•	65.5	S.	65.5	'n.	63.6	ω.	63.6	63.6	ω.	63.6	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	•	60.0	0.09
	Score		55	55	38	37	37	36	36	36	36	35	35	35	35	35	35	35	34	34	34	34	34	34		34	34	33	33	33
	esult No.	-	7	m	4	ស	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	probable DNA topoi	neprilysin (EC 3.4	neprilysin (EC 3.4	_	probable receptor	Ca2+-transporting	protein envelope C	Ca2+-transporting	Ca2+-transporting	rep protein homolo	Ca2+-transporting	Ca2+-transporting	sulfonylurea recep	sulfonylurea recep	laminin alpha-1 ch
T23531	T03504	HYHUN	HYRTN	HYRBN	B96693	S71168	D86402	T51925	T51926	T02634	C85349	T08551	T42751	T46645	\$18253
0	~	H	-	-	~	7	N	N	~	~	N	N	~	~	7
555	652	750	750	751	876	946	1020	1020	1020	1038	1069	1093	1545	1545	3712
0.09	0.09	0.09	0.09	0.09	60.0	60.0	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09
33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 RESULT 1 S57957 thrombospondin 1 - bovine (fragment) C;Species: Bos primigentius faurus (cattle) C;Apecies: José #somnang ravision 10_hrv=1006 #ravi change 00_Tul_2004
C. Accession: S57957 R. Lafeuillade, B.; Pellerin, S.; Keramidas, M.; Chambaz, E.M.; Feige, J.J. submitted to the EMBL Data Library, July 1995
A; Description: Opposite regulation of thrombospondin-1 and CISP/thrombospondin-2 expres A; Reference number: S57955 A; Racfession: S57957 A; Status: preliminary A; Molecule type: mRNA
A;Residues: 1-229 <laf> A;Residues: 1-229 <laf> A;Cross_references: UNIPROT:028194; UNIPARC:UPI00008740A; EMBL:X89511; NID:g899228; PI C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v</laf></laf>
Query Match 100.0%; Score 55; DB 2; Length 229; Best Local Similarity 100.0%; Pred. No. 0.0015; Marches 11: Conservative n. Mismarte 0. Tridals n. Gans n.

11; Conservative

1 FOGVLONVRFV 11 ò

190 FQGVLQNVRFV 200 셤

thrombospondin 1 precursor - human C; Species: Homo sapiens (man) C; Stacession: A26155; A34244; A30140; A25812; A05172; A42927 A42927 A3244; A34244; A30140; A25812; A05172; A42927 A42927 A32927 A3292

A;Molecule type: DNA A;Residues: 1-166 <LAH: A;Cross-ternecs: UNIPARC:UP100001742BF; GB:J04835 A;Cross-ternecs: UNIPARC:UF1000001742BF; GB:J04835 B;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, J. Cell Biol. 108, 729-736, 1989 A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in t

```
A Molecule Type: DNA

**Residues: 1-1170 cLAM**

A; Residues: 1-1170 cLAM*

A; Residues: 1-1170 cLAM*

A; Cross-references: UNIPROT: P35441; UNIPARC: UP1000028012; GB: M62469; GB: M62468; GB: M6246

1; GB: M62462; GB: M62463; GB: M62464; GB: M62465; GB: M62466; GB: M62467; GB: M62468; GB: M6246

R; Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P.

J; Biol. Chem. 265, 16691-16698, 1990

A; Title: Characterization of the mouse thrombospondin gene and evaluation of the role of A; Reference number: A37905; MUID: 90375546; PMID: 2398070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1490 *20R.

A; Residues: 1490 *20R.

A; Cross-references: UNIPARC:UP1000016D076; GB:U05605; GB:U05606; NID:G201991; PIDN:AAA4C

B; Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.

G. Biol. Chem. 267, 3274-3281, 1992

A; Title: Characterization of mouse thrombospondin 2 sequence and expression during cell

A; Reference number: A42587; MUID:92147683; PMID:1371115

A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-1152, "P.,1154-1170 <LAH>
A;Cross-references: UNIPARC:UPI0000177A96; GB:M87276
A;Cross-references: UNIPARC:UPI0000177A96; GB:M87276
A;Note: sequence extracted from NCB1 backbone (NCBIP:81501)
B;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FBBS Lett. 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1 a
A;Reference number: S68787; MUID:96234006; PMID:8654563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: protein
A;Residues: 19-26, X. 28-37 < CHE>
A;Residues: 19-26, X. 28-37 < CHE>
A;Residues: 19-26, X. 28-37 < CHE>
A;Crosm-references: UNIPARC:UP10000177A97
C;Complex: homorrimer, disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vC
C;Keywords: calcium binding; glycoprotein; homorrimer
F;1-18/Domain: signal sequence #status predicted < SIG>
F;19-1170/Product: thrombospondin 1 #status predicted < MAT>
F;317-375/Domain: thrombospondin type 1 repeat homology < THR1>
F;317-375/Domain: thrombospondin type 1 repeat homology < THR2>
F;317-375/Domain: BGF homology < BGF>
F;5151-586/Domain: BGF homology < BGF>
F;5151-586/Domain: BGF homology < BGF>
F;5151-586/Domain: BGF homology < BGF>
F;511-586/Domain: BGF homology < BGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Buchnera sp. C;Dact: 02-Mar-2001 #text_change 31-Dec-2004 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 B4938 R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H. Nature 407, 81-86, 2000 A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Reference number: A84930; MUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H+-transporting two-sector ATPase (EC 3.6.3.14), flagellum-specific [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-467 <STO>
A;Coss-references: UMIPARC:UPI000005E44F; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55; DB 2; Length 1170; 100.0%; Pred. No. 0.009;
                                                  A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
A;Accession: A40558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
D84938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
A;Reference number: A30140; MUID:89139590; PMID:2918029
A;Accession: A30140
A;Molecule type: mRNA
A;Residues: 1-83, A, 85-522, 'A',524-1170 < HEN>
A;Cross-references: UNIPARC:UPIO00033AB1; EMBL.X14787; NID:937464; PIDN:CAA32889.1; PIL
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
R;Kobayashi, S; Eden-McCutchan, F; Framson, P; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A;Title: Partial amino acid sequence of human thrombospondin as determined by analysis c
A;Reference number: A25812; MUID:87157592; PMID:303036
A;Accession: A25812
A;Molecule type: mRNA
A;Residues: 1-83, A, 85-397 < KOB>
A;Cross-references: UNIPARC:UPI00016B0CA; ROIMS: NID:9538353; PIDN:AAA36741.1; PID:
R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Brocc. Natl. Acad. Sci. U.S. A. 83, 5449-5453, 1986
A;Reference number: A05172; MUID:86287276; PMID:3461443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'penalcroin' participates in cell migration and adhesion, and in platelet aggregation 'penalcroin' barticipates in cell migration and adhesion, and in platelet aggregation 'Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; voly. Kewvords: beta-hydroxyspazagine; calcolum binding; cell adhesion; glycoprotein; trimer '1.14D'Domain: signal sequence #status predicted <202.
'19-1170/Product: thrombospondin 1 #status predicted <MAT>
'137-375/Domain: won Willebrand factor type C repeat homology <TWR2>
'134-490/Domain: thrombospondin type 1 repeat homology <TRR2>
'491-547/Domain: thrombospondin type 1 repeat homology <TRR2>
'551-586/Domain: thrombospondin type 1 repeat homology <TRR3>
'551-586/Domain: EGF homology <EGF1>
'550-689/Domain: EGF homology <EGF2>
'171-232/Disulfide bonds: #status predicted /springlide bonds: #status predicted /springlide bonds: #status predicted /springlide bonds: interchain #status predicted /springlide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A05172
A;Molecule type: mRNA
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
B;Sun, X.; Skorstengaard, X.; Mobher, D.F.
J. Cell Biol. 118, 693-701, 1992
A;Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A;Reference number: A42927; MUID:92348511; PMID:1379247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42887; S68787
R;Lawler, J; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted;1051/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 1; Length 1170; 100.0%; Pred. No. 0.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Molecule type: protein
A;Residues: 987-1003 <SUN>
A;Cross-references: UNIPARC:UPI00001742C0
A;Note: Cys-992 is shown to have a free sulfhydryl
A;Genetics:
A;Gene: GDB:THBS1; TSP
A;Cross-references: GDB:120438; OMIM:188060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A/ROSSILLELEINCES: US1515.

A/ROSSILLELEINCES: US1515.

A/ROTOSSILLELEINCES: US1615.

A/ROCE: the list of introns may be incomplete
C/COMPLEX: homotrimer, disulfide linked
C/Function:
A/ROSSILLELEINCES
C/Function:
A/ROSSILLELEINCES
C/Function:
A/ROSSILLELEINCES
C/Function:
A/ROSSILLELEINCES
C/Function:
A/ROSSILLELEINCES
C/ROSSILLELEINCES
C/ROSSILLE
C/ROSSILL

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombospondin 1 precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A42927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
```

- Buchner

ö

Gaps

ö

0; Indels

```
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Datesion: 442587; A3281; A3281, A3
                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: nucleic acid
A; Residues: 1-1172 < LAM+)
A; Cross-references: UNIPROT.003350; UNIPARC:UPI0000029847; GB:L07803; GB:M87275; NID:g3
A; Cross-references: UNIPROT.003350; UNIPARC:UPI0000029847; GB:L07803; GB:M87275; NID:g3
A; Note: sequence extracted from NCBI backbone (NCBIP:81502)
B; Biol. Chem. 266, 12821-12824, 1991
A; Title: A second, expressed thrombogondin gene (Thbs2) exists in the mouse genome.
A; Reference number: A39851; MUID:91302287; PMID:1712771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-873 <BOR>
A;Cross-references: UNIPARC:UPI00016D077; GB:M64866; NID:g201994; PIDN:AAA40432.1; PID
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 2; Length 1172;
Pred. No. 44;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Keywords: calcium binding; glycoprotein
F;319-377/Domain: von Willebrand factor type C repeat homology
F;380-431/Domain: thrombospondin type 1 repeat homology «THRL»
F;436-492/Domain: thrombospondin type 1 repeat homology «THR2»
F;493-494/Domain: thrombospondin type 1 repeat homology «THR3»
F;555-589/Domain: EGF homology «EGF1»
F;655-691/Domain: EGF homology «EGF»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.0
Tr Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.5
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 FRGLLONVHLV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QGVLQNVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: A39851
A,Status: preliminary
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: B75421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: DR1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
A64590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc 5: Keywords is beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer 7: 1-18/Domain: signal sequence #status predicted <SIG>+ 10-1172/Product: thrombospondin 2 #status predicted <AMI>+ 19-1172/Product: thrombospondin 2 #status predicted <AMI>+ 19-1172/Product: thrombospondin 2 #status predicted <AMI>+ 19-1172/Product: thrombospondin type I repeat homology <THRI>+ 19-1172/Pomain: thrombospondin type I repeat homology <THRI>+ 19-1172/Pomain: thrombospondin type I repeat homology <THRI>+ 19-1172/Pomain: EGF homology <EGFI>+ 19-1172/Pomain: GGF homology <EGFI>+ 19-1172/Pomain: CGF homology <EGFI>+ 19-1172/Pomain: CGF homology <EGFI>+ 19-1172/Pomain: CGFI homology <EGFI>+ 19-1172/Pomain: CGFI attachment (R-G-D) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;928-930/Region: cell attachent (R-G-D) motif
;151.316.330,457,584,710,1069/Binding site: carbohydrate (Asn) (covalent) #status predi
;157-226/Disulfide bonds: #status predicted
;266,270/Disulfide bonds: interchain #status predicted
;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
             C;Genetics:
A;Gene: [llIr] BU076
C;Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A47379; A42173
K;Labell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A;Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: pote
A;Reference number: A47379; MUID:94010892; PMID:8406456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-112 <LABA
A;Kesidues: 1-112 <LABA
A;Cross-references: UNIPROT:P35442; UNIPARC:UPI0000046680; GB:L12350; NID:G307505; PIDN:
R;LaBell, T.L.; Milewicz, D.J.; Disteche, C.M.; Byers, P.H.
R;LaBell, T.L.; Milewicz, D.J.; Disteche, C.M.; Byers, P.H.
A;Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression capterence number: A42173; MUID:92217961; PMID:1559694
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Homo sapiens (man)
Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
Accession: A47379; A42173
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Accession: A42173
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 560-1172 cLA2>
A.Cross-references: UNIPARC:UPI00001742C1; GB:M81339
A.Experimental source: fibroblast
A.Mote: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
C.Genetics:
A.Gene: GDB:THBS2; TSP2
A.Gross-references: GBB:128789; OMIM:188061
A.Map position: 6q27-6q27
C.Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Length 1172;
Pred. No. 44;
                                                                                                                                                                                                                         Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                    Score 38; DB 2;
Pred. No. 10;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombospondin 2 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombospondin 2 precursor - mouse
                                                                                                                                                                                                                         69.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|:|||| |
FRGLLQNVHLV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLONVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|:| |:||
10 FRGILMNLRF 19
                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A47379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
```

```
J.D.; Dodson, R.J.;
T.; Zalewski, C.; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9RUZ7; UNIPARC:UPI00000D3E03; GB:AE001971; GB:AE000513; NI
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A,Reference number: A75250; MUID:20036896; PMID:10567266
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                  probable pilin, type IV - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Baces 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B75421
R;White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Do, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S; Smith, H.O.; Venter, J.D.; DC.; Fraser, C.M.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.5%; Score 36; DB 2; Length 186; 87.5%; Pred. No. 9.3; ive 1; Mismatches 0; Indels
```

us-10-030-735-30.rpr

4

Page

ö

Gaps

ö

3; Indels

Length 1054;

2;

```
Smith, H.O.; Woese, C.R.; Venter, J.C.

A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaes
A; Reference number: A69250; MUID: 98049343; PMID: 9389475
A; Reference number: A69250; MUID: 98049343; PMID: 9389475
A; Accession: H69377
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-1054 «KLE»
A; Cross-references: UNIPROT: C29238; UNIPARC: UPI0000056EB5; GB: AE001033; GB: AE000782; NI|
C; Keywords: ATP; nucleotide binding; P-loop
F; 78-85, Region: nucleotide-binding motif A (P-loop)
F; 257-262, Region: nucleotide-binding motif B
F; 261-263/Region: DEAD motif #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-304 <WIL>
A;Residues: 1-304 <WIL>
A;Cross-references: UNIPARC:UP100001793F8; EMBL:U41624; PIDN:AAA83323.1; CESP:F46C8.8
C;Genetics:
A;Gene: CESP:F46C8.8
A;Introns: 24/1; 56/1; 101/1; 123/1; 149/3; 219/1; 275/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F46C8.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T34271
R;Wilcox, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F46C8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7
62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2
Pred. No. 62;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.6%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565 FHGVLVNGRFV 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGULONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGVLQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 FOGMLANAKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: T34271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: SA0581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
T34271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                               C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A464500
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 389, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: A6450
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: UNIPROT:025286; UNIPARC:UPI000003178; GB:AE000570; GB:AE000511; NID
C;Superfamily: short-chain dehydrogenase; honclogy <SADH>
C;Keywords: fatty acid biosynthesis; NAD; oxidoreductase
F;6-186/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cidate: 12-Eeb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004
Cidate: 12-Eeb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004
Cidate: 12-Eeb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004
Cidate: 12-Eeb-1999
Ridius R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
I laves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A,Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A,Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: B71923
A;Accession: B71923
A;Molecule type: DNA
A;Residues: 1-247 cARN>
A;Residues: 1-247 cARN>
A;Coss-references: UNIPROT:092LS0; UNIPARC:UPI0000003648; GB:AE001484; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
A;Gene: fabG
C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase
F;6-186/Domain: short-chain alcohol dehydrogenase homology <SAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reverse gyrase (top-RG) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69377
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.Reischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
probable 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - Helicobacter pylori
C;Species: Helicobacter vylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - Helicobacter pylori (strain C;Species: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Variety: strain J99
C,Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 2; Length 247;
Pred. No. 13;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 1; Length 247;
Pred. No. 13;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.v.
Set Local Similarity
Source
Local Similarity
Source
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 YEGALRNIRF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 YEGALRNIRF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FQGVLQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGVLONVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
```

```
hypothetical protein SA0581 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: BB9832
R;Kuroda, M; Ohta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L; Ogu ma, A.; Mizutani-Ui, Y; Kobayashi, N; Sawano, T; Inoue, R; Kaito, C; Sekimizu, K; C, Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Accession: B89832
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 14-98 «KUR»
A;Cross-references: UNIPROT:Q99VY9; UNIPARC:UPI00000CADE1; GB:BA000018; PID:g13700516;
A;Experimental source: strain N315
                                                                    ö
                                                                       Gaps
                                                                       ..
0
63.6%; Score 35; DB 2; Length 304; 60.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 498;
                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 44;
                                                                       2; Mismatches
```

us-10-030-735-30.rpr

```
Search completed: June
Job time: 12.8017 secs
                                                                                                                                                                                                                                                             A; Accession: AC0368
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: YPO3028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                          Describes probable [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C;Accession: G95153

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; Milte, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt. I.E.

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: G95153

A;Accession: G95153

A;Accession: Diam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: AE2929
A, Status: preliminary
A, Status: preliminary
A, Holecule type: DNA
A, Residues: 1-747 < KUR>
A, Experimental source: strain C58 (Dupont)
C, Genetics: Atu3035
A, Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Residues: 1-740 <KUR>
A,Residues: 1-740 <KUR>
A,Cross-references: UNIPROT:097099; UNIPARC:UPI00000517D9; GB:AE005672; PIDN:AAK75424.1;
B,Experimental source: strain TIGR4
C,Genetics:
A,Gene: SP1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AE2994
C;Accession: AE2994
C;Accession: AE2994
C;Accession: AE2994
C;Accession: A; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two component response regulator Atu3035 [imported] - Agrobacterium tumefaciens (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 2; Length 740; Pred. No. 68; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%; Score 35; DB 2; Length 747; 66.7%; Pred. No. 68;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
3;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0°
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.73
Matches 6; Conservative
6; Conservative
                                                                                  396 FQGALQNGNYI 406
                                                 1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 FNGTLENIKF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|::||||
42 GILESVRFV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
AC0368
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

```
probable autotransporter YPO3028 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0368
R;Parkhill, J; Ware, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Croin, A.; Davies, R.M.; Davies, P.D.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Teference number: AB0001; MUID:21470413; PMID:11586360
A;Reference number: AB0001; MUID:21470413; PMID:115863
```

THIS PAGE BLANK (USPTO)

Scoring table:

Searched:

Perfect score:

Run on:

Sequence:

Minimum DB seq Maximum DB seq

Database

Result ٠ و

```
0722b9 trypanosoma
06fxf candida gla
02tyf aspergilus
06c422 yarrowia li
p57178 buchnera ap
08595 bacreriopha
03c718 alkaliphilu
041vb6 desulfitoba
08bvv4 mus musculu
035142 homo sapien
055152 homo sapien
057152 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Opposite regulation of thrombospondin-1 and corticotropin-induced secreted protein/thrombospondin-2 expression by adrenocorticotropic hormone in adrenocortical cells.", J. Cell. Physiol. 167:164-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96331130; PubMed=8698834;
DOI=10.1002/(SICI)1097-4652(199604)167:1<164::AID-JCP19>3.3.CO;2-0;
Lafeuillade B., Pellerin S., Keramidas M., Danik M., Chambaz E.M.,
                                                                                                                                                                                                                                                                                                                                             QZ8194 BOVIN PRELIMINARY; PRT; 229 AA.
QZ8194;
QZ8194;
QZ8194;
QZ8194;
QZ8194;
QZ8195, integrated into UniProtKB/TrEMBL.
QZ8196, sequence version 1.
QZ7-FEB-2006, entry version 24.
Thrombospondin-1 (Fragment).
Thrombospondin-1 (Fragment).
Bos taurus (Bovinne).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Peccra; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25015 MW; 90D9EBCE4E6B669C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, X89511, CAA61682.1, -; mRNA.
PIR, S57957, S57957.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:005155; P:cell adhesion; IEA.
InterPro; IPR013320; ConA like subgrp.
InterPro; IPR013129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 2;
100.0%; Pred. No. 0.02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7,7AEM. XENLA PRELIMINARY; PRT; 496 AA. 078Y84.
078Y84.
01-0CT-2003, integrated into UniProtKB/TrEMBL. 01-CT-2003, sequence version 1.
07-FEB-2006, entry version 12.
Q4DWH6_TRYCR
Q722B9_TRYCR
QFEXF4_CRNGA
Q2TY18_ASPOR
Q6C422_YARLI
BELII BUCAI
Q6SPP9_BRN4
Q3C7L8_9CLOT
Q41VB6_DESHA
Q41VB6_DESHA
Q41VB6_DESHA
G5FY2_MOUSE
TSP2_MOUSE
TSP2_MOUSE
                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 FQGVLQNVRFV 200
 1034
1034
1172
1367
1367
261
261
438
750
1172
11172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00210; TSPN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 AA;
 70.9
70.9
70.9
70.9
70.9
69.1
69.1
67.3
67.3
67.3
67.3
67.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feige J.J.;
   NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12444
1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aspergillus
drosophila
drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tetraodon n
sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tetraodon n
tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bos taurus
xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homo sapien
brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methanosarc
methanosarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                burkholderi
burkholderi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ustilago ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methanosarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thermoanaer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thiomicrosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  burkholderi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drosophila
                                                                                                             5, 2006, 22:09:41 ; Search time 99.8534 Seconds (without alignments) 101.901 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             028194
028184
028184
0201841
0101841
011841
011841
011841
011841
011841
011841
011841
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
01184
0118
                 GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                2849598 seqs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q28194_BOVIN
Q75Y84_XENLA
TSP1_BOVIN
TSP1_HUMAN
TSP1_MOUSE
Q3TR40_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q48758 TETNG
Q5U903 PIG
Q4RLR5 TETNG
Q4RQ74 TETNG
Q4P665 USTMA
Q8PRY3 METWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSP1 XENLA
Q59E99 HUMAN
Q5SPG5 BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAT
MOUSE
MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEET
9BURK
9BURK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSAVO8 EMENI
O86NR6 DROME
Q9VTHO DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9BURK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIOIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q31IL6_THICR
Q5FA21_NEIG1
                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04P665 08PRY3 0467V1 08TLX6 08TLX6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSVH52<sup>7</sup>
O2LZ43<sup>7</sup>
                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q44XL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4LLM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                            US-10-030-735-30
55
                                                                                                                                                                                                                1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1170
1170
1171
1171
1173
1225
1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249
1171
1034
704
```

ö

Gaps

ö

```
214 FQGVLQNVRFV 224
                                                                                                                                                                                                       Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A physins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsheh F.,
Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Bloychenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Ceneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
  MGC64438 protein.
Sanopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Whole;
BEDLINES-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 55; DB 2; Length 496; 100.0%; Pred. No. 0.047; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, BC054970; AAH54970.1; -; mRNA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0007155; P:cell adhesion; IEA.

InterPro; IPR0131320; ConA like subgrp.

InterPro; IPR003129; Laminin_G_TSP_N.

InterPro; IPR008084; TSP1.

InterPro; IPR008084; TSP1.

InterPro; IPR008085; TSP1.

Pfam; PP00090; TSP2.1; 2.

Pfam; PP00090; TSP2.1; 2.

Pfam; PR01705; TSP1REPEAT.

SMART; SM00210; TSP1; 1.

SMART; SM00210; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFC_2, 1.
54843 MW; E4FD2F07CB7EF51B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50092; TSP1; 2.
PROSITE; PS01208; VWFC 1; UNKNOWN 1.
PROSITE; PS50184; VWFC 2; 1.
                                                                                    Kenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissum=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

Gaps

.. 0

0; Mismatches

Local Similarity 100.

Best Loc Matches

1 FOGVLONVRFV 11

ઠે

```
C. --- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type v collagen and integrine alpha-v/beta-1, alpha-v/beta-3 and alpha-IIb/beta-3. May play a role in dentinogenesis and/or maintenance of dentin and dental pulp.

C. --- SUBUNIT: Homotrimer, disulfide-linked.

---- SIMILARITY: Belongs to the thrombospondin family.

C. --- SIMILARITY: Contains 1 EGF c-terminal (TSPN) domain.

C. --- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

C. --- SIMILARITY: Contains 1 TSP V-terminal (TSPN) domain.

C. --- SIMILARITY: Contains 1 TSP V-terminal (TSPN) domain.

C. --- SIMILARITY: Contains 1 TSP V-terminal (TSPN) domain.

C. --- SIMILARITY: Contains 1 TSP V-terminal (TSPN) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Aortic endothelium;
Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin stimulatory effect of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=HOlstein; TISSUE=Tooth;
MEDLINE=98173773; PubMed=9507054; DOI=10.1016/S0167-4838(97)00188-X;
Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
TSPI BOVIN STANDARD; PRT; 1170 AA.

Q28178; Q28179; Q28179;
01-NOV-1997; integrated into UniProtKB/Swiss-Prot.
01-NOV-2000, sequence version 2.
07-MAR-2006, entry version 56.
17-MAR-2006, entry version 56.
Name-THBS1; Synonyms-TSP-1, TSP1;
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovinae; Bos.
NCBI_TAXID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inoue H.; "cDNA cloning of bovine thrombospondin 1 and its expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGF-beta.";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA] OF 1-18 AND 710-1170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   odontoblasts and predentin.";
Biochim. Biophys. Acta 1382:17-22(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S55501; S55501.
HSSP; P07996; LISL.
SMR, Q28178; -1.5SL.
GlycocuiteDB, Q28178; -.
InterPro; IPR013320; ConA_like_subgrp.
InterPro; IPR0013120; EGF.
InterPro; IPR001881; EGF.
InterPro; IPR001881; EGF_Ca_bd.
InterPro; IPR001891; EGF_Ca_bd.
InterPro; IPR001302; EGF_like_reg.
InterPro; IPR013029; EGF_like_reg.
InterPro; IPR013129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB005287; BAA21115.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X87618; CAA60950.1; -; mRNA.
EMBL; X87619; CAA60951.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008085; TSP 1.
InterPro; IPR003367; tsp 3.
InterPro; IPR008859; TSP C.
InterPro; IPR001007; VWF C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00008; EGF; 1.
Pfam; PF00090; TSP 1; 3.
Pfam; PF02412; TSP 3; 13.
          HE TO THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TRANSPORT OF THE TOTAL THE
```

```
J. Cell Biol. 103:1635-1648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 25:8418-8425(1986)
                100.0%;
Query Match
Best Local Similarity luv.
Local 11, Conservative
                                                                                                                                                                                                                 STANDARD;
                                                                                                                         FOGVLONVRFV 218
                                                                                       1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                   TSP1 HUMAN
                                                                                                                           208
                                                                                                                         g
                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                       calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .) (Potential).
.) (Potential).
.) (Potential).
.) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heparin-binding (Potential).

Cell attachment site (Potential).

N-linked (GlCNAC. .) (Potential)

N-linked (GlCNAC. .) (Potential)

N-linked (GlCNAC. .) (Potential)

N-linked (GlCNAC. .) (Potential)
                                     | Pram, | Pram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G (in Ref. 2).
ODDGADF3E5FA031A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-linked (GlCNAC...) ((N-linked (GlCNAC...) (
                                                                                                                                                                                                                                                                                  By similarity.
Thrombospondin-1.
/FTId=PRO_0000035841.
TSP_N-terminal.
                                                                                                                                                                                                                                                                                                                                                                            TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 3.
TSP type-3 4.
TSP type-3 5.
TSP type-3 5.
TSP type-3 5.
TSP type-3 5.
TSP type-3 7.
TSP type-3 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1067
1085
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         910 93
946 116
805 80
1170 AA;
                  PF05735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULFID
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                  Pfam;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Endochelial cell, MEDINE-8705717; PubMed=2430973; DOI=10.1083/jcb.103.5.1635; MEDINE-87057677; PubMed=2430973; DOI=10.1083/jcb.103.5.1635; Lawler J., Hynes R.O., The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=8919590; PubMed=2918029; DOI=10.1083/jcb.108.2.729; Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L., Baungartel D.M., Rotwein P., Frazier W.A.; Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region."; J. Cell Biol. 108:729-736 (1989).

[3] NUCLEOTIDE SEQUENCE OF 1-397.

MEDLINE=87157592; PubMed=3030396; Medline=87157592; PubMed=3030396; Pramson P., Bornstein P.; Robayashi S., Eden-Mccutchan F., Framson P., Bornstein P.; Partial amino acid sequence of human thrombospondin as determined by analysis of CDNA clones: homology to malarial circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 1-374.
MEDLINE=86287276; PubMed=3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
UCharacterization of a cDNA encoding the heparin and collagen binding domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [5]
NUCLEOTIDE SEQUENCE OF 1-166.
NUCLEOTIDE SEQUENCE OF 1-166.
Laberty C.D., Gierman T.M., Dixit V.M.;
Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.";
[6]
[6]
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 1028-1170.

La Fleur M., Jobin C., Gauthler J., Kreis C.G.;

La Fleur M. Hrombospondin in chronic inflammation: neutrophils from synovial fluids synthesize a novel 3.9 kb TSP mRNA.";

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYDRATE-LINKAGE SITES TRP-385; SER-394; TRP-438; TRP-441; THR-450; TRR-488 AND THR-507.
TISSUE-Placelet; MEDLINE=21125860; Pubmed=11067851; DOI=10.1074/jbc.M008073200;
Score 55; DB 1; Length 1170; Pred. No. 0.12;
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     907956; 015667; 01-AUG-1988, integrated into UniProtKB/Swiss-Prot. 01-AUG-1988, sequence version 1. 07-MAR-2006, entry version 78. Thrombospondin-1 precursor. Name=THBS1; Synonyms=TSP, TSP1; Homo sapiens (Human).
                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1170 AA.
                                                                                      0; Mismatches
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                          CARBOHYDRATE-LINKAGE SITES ASN-248 AND ASN-1067.

Pubmed=16335952; DOI=10.1021/pr0502065;

Liu T., Qian W.-J., Griteenko M.A., Camp D.G. II, Monroe M.E.,

Liu T., Gian W.-J., Griteenko M.A., Camp D.G. II, Monroe M.E.,

Moore R.J., Smith R.D.;

"Human plasma N-glycoproteome analysis by immunoaffinity subtraction,

"Human plasma N-glycoproteome analysis by immunoaffinity subtraction,

"Human plasma N-glycoproteome analysis by immunoaffinity subtraction,

"Thydrazide chemistry, and mass spectrometry.";

"J. Protecome Res. 4:2070-2080(2065).

"J. Protecome Res. 4:2070-2080 and integrins alpha-V/beta-1, alpha-

"Vbeta-3 and alpha-III/beta-3.

"Vbeta-3 and alpha-III/beta-3.

"Vbeta-1 and alpha-III/beta-3.

"Vbeta-3 and alpha-III/beta-3.

"Vbeta-1 and alpha-III/beta-3.

"SIMILARITY: Contains 1 TSP C-terminal (TSPN) domain.

"SIMILARITY: Contains 7 TSP type-3 domains.

"SIMILARITY: Contains 7 TSP type-3 domains.

"SIMILARITY: Contains 7 TSP type-3 domains.

"SIMILARITY: Contains 7 TSP type-3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                MEDLINE-22338361; PubMed=12450399; DOI=10.1021/bi026463u;
Huwiler K.G., Vestling M.M., Annis D.S., Mosher D.F.;
"Biophysical characterization, including disulfide bond assignments,
of the anti-anglogenic type 1 domains of human thrombospondin-1.";
Biochemistry 41:14329-14339(2002).
Hofsteenge J., Huwiler K.G., Macek B., Hess D., Lawler J., Mosher D.F., Peter-Katalinic J.; "C-mannosylation and O-fucosylation of the thrombospondin type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   # MIM, 180060; gene.

R MIM, 180060; gene.

R Reactome; P07996; -.

R GO; GO:0008576; C:extracellular region; NAS.

GO; GO:000486; F:endopeptidase inhibitor activity; TAS.

GO; GO:0004871; F:eignal transducer activity; TAS.

GO; GO:007275; P:edevelopment; TAS.

R GO; GO:007275; P:development; TAS.

R InterPro; IPR001320; EGF 3.

R InterPro; IPR00181; EGF 2.

R InterPro; IPR00181; EGF 2.

R InterPro; IPR00181; EGF 1.

R InterPro; IPR00181; EGF 1.

R InterPro; IPR00181; TSP 1.

R InterPro; IPR00881; TSP 1.

R InterPro; IPR00885; TSP 1.

R InterPro; IPR00885; TSP 2.

R InterPro; IPR00885; TSP 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M25631, AAA36741.11; -; mRNA.
EMBL; X04665; CAA28370.1; -; mRNA.
EMBL; X14787; CAA32899.1; -; mRNA.
EMBL; M14326; AAA61237.1; ALT SEO; mRNA.
EMBL; J04835; AAA61237.1; ALT SEO; mRNA.
EMBL; J04835; AAA61178.1; -; Genomic_DNA.
PNB; J265; TSHUP1.
PDB; L265; TSHUP1.
PDB; L265; TSHUP1.
PDB; L276; X-ray; A=19-237.
PDB; L278; X-ray; A=19-257.
PDB; L274; X-ray; A=19-257.
PDB; ERF; X-ray; A=19-257.
PDB; ERF; X-ray; A=169.
GNF; P07996; 549-1169.
GNF; P07996; 549-1169.
GNF; P07996; --
ENSGONOOUSJ37801; HOMO SADIENS.
                                                                                          THROMBOSPONDIN DOMAIN DISULFIDE BRIDGES.
                                                           Biol. Chem. 276:6485-6498(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGNC; HGNC:11785; THBS1.
```

```
| PRINTS; PROUSS; VECTORS |
| R PRINTS; PROUSS; VECTORS |
| R SMART; SM00181; EGF; 3.
| R SMART; SM00210; TSP1; 3.
| R SMART; SM00210; TSP1; 3.
| R SMART; SM00210; TSP1; 3.
| R PROSITE; PS00226; EGF 3; 2.
| R PROSITE; PS0026; EGF 3; 2.
| R PROSITE; PS01086; WFC 1; 1.
| R PROSITE; PS01086; WFC 2; 1.
| R PROSITE; PS010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSP type-1 1.
TSP type-1 2.
TSP type-1 3.
EGF-like 1.
EGF-like 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 3.
TSP type-3 4.
TSP type-3 5.
TSP type-3 5.
TSP type-3 6.
TSP type-3 6.
TSP type-3 7.
TSP type-3 6.
TSP type-3 7.
TSP C-terminal.
Heparin-binding (Potential).
Cell attachment site (Potential).
N-linked (GLOMAC. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-linked [Man].
/Frid=CAR 000208.
O-linked [Fuc. . .).
/Frid=CAR 000209.
C-linked [Man].
/Frid=CAR 000210.
O-linked [Fuc. . .).
/Frid=CAR 000211.
N-linked [GlonAc. .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 55; DB 1; Length 1170; 100.0%; Pred. No. 0.12; Live 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interchain (Probable)
Interchain (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombospondin-1.
/FTId=PRO 0000035842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTIG-CAR 000205.
O-linked (Fuc. .)
/FTIG-CAR 000206.
C-linked (Man).
/FTIG-CAR 000207.
C-linked (Man).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSP N-terminal
Pfam; PF02412; TSP 3; 12.
Pfam; PF05735; TSP C; 1.
Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222

3333

4490

5644

6646

6646

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7666

7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391
395
406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447
451
462
504
508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              951
19
926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
```

```
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
REGION
MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
PROTEIN SEQUENCE OF 19-37.

PROTEIN SEQUENCE OF 19-37.

PROMEd=8654563; DOI=10.1016/0014-5793(96)00460-7;

Chen H., Aeschlimann D., Nowlen J., Mosher D.F.;

Thrombospondin 1 and thrombospondin 3.";

Thrombospondin 1 and thrombospondin 3.";

FRES Lett. 387:36-41(1996).

Chen H., Adhesive glycoptein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, Valuatin, type V collagen and integrins alpha-V/beta-1, alpha-Colladin, type V collagen and integrins alpha-V/beta-1, alpha-Colladins, type Cherminal (TSPC) domain.

Chen H., Abdera J. Manial J. Contains 1 TSP N-terminal (TSPC) domain.

Chen H., Asimilarity: Contains 3 TSP type-1 domains.

Chen H., Asimilarity: Contains 7 TSP type-1 domains.

Chen H., Manial J. WEC domains.

Chen H., Asimilarity: Contains 7 TSP type-3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 1-490.
MEDLINE=90375546; PubMed=2398070;
Bornstein P., Alfi D., Devarayalu S., Framson P., Li P.;
"Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";
J. Biol. Chem. 265:16691-16698(1990).
                                                                                                                                                                                                                                                                                                                                                                "Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development."; J. Biol. Chem. 267:3274-3281 (1992).
                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE.
MEDIJNE=92128941; PubMed=1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J., Jenkins N.A.;
"Characterization of the murine thrombospondin gene.";
                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=92147683; PubMed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
Dixit V.M.;
                                                                        01-JUN-1994, integrated into UniProtKB/Swiss-Prot. 01-JUN-1994, sequence version 1. 01-JUN-1994, sequence version 1. Thrombognomin-1 precursor. Thrombognin-1 precursor. Name-Thbs1; Synonyms=Tep1; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L; M62470; AAA50611.1; -; Genomic_DNA.
L; M62451; AAA50611.1; JOINED; GENOMIC_DNA.
L; M62452; AAA50611.1; JOINED; GENOMIC_DNA.
L; M62453; AAA50611.1; JOINED; GENOMIC_DNA.
L; M62453; AAA50611.1; JOINED; GENOMIC_DNA.
L; M62454; AAA50611.1; JOINED; GENOMIC_DNA.
L; M62455; AAA50611.1; JOINED; GENOMIC_DNA.
L; M62456; AAA50611.1; JOINED; GENOMIC_DNA.
L; M62459; AAA50611.1; JOINED; GENOMIC_DNA.
L; M62450; AAA50611.1; JOINED; GENOMIC_DNA.
L; M62460; AAA50611.1; JOINED; GENOMIC_DNA.
L; M62460; AAA50611.1; JOINED; GENOMIC_DNA.
                                                PRT; 1170 AA.
                                                                                                                                                                                                                                                                                     Genomics 11:587-600(1991)
                                                STANDARD;
                                                                                                                                                                                            NCBI_TaxID=10090;
                                                ISP1 MOUSE
                                                              P35441;
                                    ISP1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
```

```
| PRESENTE | MASSAGES | MASSAGES
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUB=Aorta and vein;
PubMed=16141072; DOI=10.1126/science.112014;
PubMed=16141072; DOI=10.1126/science.112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUE=Aorta and vein; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-lengh cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530055N06 product:thrombospondin 1, full insert sequence. Name=Thbs1;
(Potential).
                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                   Score 55; DB 1; Length 1170;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                               0443E493615E7F06 CRC64;
      Interchain (Probable).

Interchain (Probable).

By similarity.
                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1170 AA
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                        ٨
                                                                                                                                                                                                                                                                                                                  1170 AA; 129647 MW;
                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                     100.08;
                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q3TR40_MOUSE PRELIMINARY;
Q3TR40;
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                             1 FOGVLONVRFV 11
                                                                                                                                                             617
644
663
676
689
                                                                                                                                                                                                                                                                                   930
1167
1025
                                                                                                                                                                                                               7113
738
774
797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                       DISULFID
DISULFID
                                                                     DISULFID
                                                                                                                      DISULFID
                                                                                                                                          DISULFID
                                                                                                                                                     DISULFID
                                                                                                                                                              DISULFID
                                                                                                                                                                         DISULFID
                                                                                                                                                                                 DISULFID
                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                          SULFID
                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                               SULFID
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                         DISULFID
                                                                                                   DISULFID
                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
  원
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

```
Chiur K. P. Ghoudhary V. Christoffels A., Cillterbuck D. R.,

R. Gassal M., Barter L., Beisels K.W., Berson T., Bolls Gate G.,

R. Growe M.L., Dilla E., Dalympile B. P., Glide Bone D., Dells Gate G.,

R. Gergi-Herming P., Gingeres T.R., Golobort T., Green R.E.,

R. Hill V., Barthers W. H., Haysain Y., Renson T., Hitchews M.,

R. Hill W., Barthers W. H., Raysain Y., Renson T., Richams H.,

R. Hill M., Barthieck L., Lacono M., Rake Y., Rabad A., Athenara H.,

R. Hill M., Barthieck L., Lacono M., Rake Y., Ramerfeld S. K.,

R. Mitchen H., Mathers W. M., Rake W. N., Ramerfeld S. K.,

R. Michan I. W., Larsau L.F., Lacono M., Rake Y., Ramerfeld S.,

R. Michan I. W., Larsau L.F., Lacono M., Rake Y., Ramerfeld S.,

R. Michan I. W., Larsau L.F., Lacono M., Rake Y., Ramerfeld S.,

R. Michan I. W., Larsau L.F., Lacono M., Rake Y., Ramerfeld S.,

R. Michan I. W., Larsau L.F., Lacono M., Rake Y., Ramerfeld S.,

R. Misson M. W., Shindan S., Walke H., Mignone P., Miyake S., Morris K.,

R. Misson M. W., Shindan S., Walke H., Mignone P., Miyake S., Morris K.,

R. Misson M. W., Shindan S., Walke M., Sakaudi J., School M., School M.,

R. Misson M. W., Shindan S., Walke M., Shindan S., Mark F., Ghara S., Sessa L., Sheng Y.,

R. Misson M., Walk K., Respield R., Shindan S., Shira B., Shinda S.,

R. Misson M., Walk K., Mathik W., School W., School M., School M., School M., Shinda S., Shinda S., Shinda S., Sessa L., Sheng Y.,

R. Mahleredd C., Mattick J. S., Hueb D.A., Kai C., Sessa L., Sheng Y.,

R. Mahleredd C., Mattick J. S., Hueb D.A., Kai C., Sessa L., Sheng Y.,

R. Mahleredd C., Mattick J. Wattick M., Sach J., Andrew T.,

R. Manshing S., Katanori-K., Hue T., Birdi K., Shinda B., Makerda J., Markana T., Walka M., Kanda M., Makk K., Mathik M., Makk M., Makk M., Mathik M., Makh M., Mathik M., Makh M., Makh M., Mathik M., Mathik M., Mathik M., Mat
```

```
Matches
 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21085660; PubMed=11217851; DOT=10.1038/3505560;
NEDLINE-21085660; PubMed=11217851; DOT=10.1038/3505560;
NEDLINE-21085660; PubMed=11217851; DOT=10.1038/3505560;
NA Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Abbhurner M., Batalov S., Casavant T., Rachamann W., Gaasterland T., Gissi C., King B., Kochiwa H., Rubl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Itoh M., Aizawa K., Nagadaka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagadaka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumioto H., Sakaguchi S., Ikegami T., Rashiwagi K., Fujiwake S., Inoue K., Togawa M., Ohara E., Watshika M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawi J., Ckazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori M., Kanagawa S., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sanski D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Submitted (Apr-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI; MGI:98737; Thbs1.
GO: GO:0005615; C:extracellular space; IDA.
GO: 00:0005615; C:extracellular space; RCA.
GO: 00016525; P:negative regulation of angiogenesis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6J; TISSUE-Aorta and vein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK163092; BAE37190.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro, IPR006210; EGF.
InterPro, IPR001742; EGF 3.
Interpro, IPR001881; EGF 3.
InterPro, IPR001881; EGF Inke.
InterPro, IPR013032; EGF like.
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
```

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 55; DB 2; Length 1170; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley;
Iwabu A., Hirohata S., Kusachi S., Nakamura K., Murakami T.,
Ninomiya Y., Tsuji T.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1170 AA; 129619 MW; 55BF04A20D91B194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMR; Q71SA3; 834-1169.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005599; F:calcium ion binding; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY; PRT; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR013320; ConA like subgrp
InterPro; IPR006210; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000742; EGF 3.
InterPro; IPR01881; EGF Ca bd.
InterPro; IPR00509; EGF like.
InterPro; IPR013032; EGF like reg.
InterPro; IPR03129; Laminin_G_TSP_N.
InterPro; IPR000884; TSP1.
Laminin G TSP N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF309630; AAQ14549.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01186; EGF 2; UNKNOWN 1. PROSITE; PS50026; EGF 3; 2. PROSITE; PS50026; TSP1; 3. PROSITE; PS01208; VWFC 1; 1. PROSITE; PS50184; VWFC 2; 1. SEQUENCE 1170 AA; 129619 MW; 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 9. Thrombospondin 1.
                                              InterPro; IPR008085; TSP-1.
InterPro; IPR008367; tsp-3.
InterPro; IPR008599; TSP-C.
InterPro; IPR0080899; VWF-C.
Pfam; PP00008; EGF; 2.
Pfam; PP002412; TSP-1; 3.
Pfam; PP002412; TSP-7; IP-Pfam; PP005735; TSP-C; IP-Pfam; PP00093; VWC; I.
                                                                                                                                                                                                                                                                                7C; 1.
TSP1REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008085; TSP 1.
InterPro; IPR003367; tsp 3.
InterPro; IPR008859; TSP C.
                                                                                                                                                                                                                                                                                                 PRINTS; PRO1705; TSPIREPEA'
SMART; SM00181; EGF; 3.
SMART; SM00209; TSPI; 3.
SMART; SM00210; TSPI; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q71SA3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Tsp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q71SA3
```

```
Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
08/CGB2 MG
08/CGB2 MG
08/CGB2 MG
01-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DE Luli
DE Luli
CGN Name
CGN Name
CGN Name
(1]
RN (1]
RN (1]
RN (1]
RN STER
RA STER
RA KIAU
    ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RETRAIN=C57BL/6; TISSUE=Brain;

RETRAIN=C57BL/6; TISSUE=Brain;

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETRAIN=C57BL/6; TISSUE=Brain;

RETRAIN=C57BL/6; TISSUE=Brain;

RETRAIN=C57BL/6; TISSUE=Brain;

RA Strausberg R.L., Feringold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Maruaina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahatelo S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Sheven B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Gennerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                  100.0%; Score 55; DB 2; Length 1170; 100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                      1170 AA; 129671 MW; 6F38D3DCE733060F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CS7BL/6; TISSUB-Brain;
Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UUN-2003, integrated into UniProtKB/TrEMBL.
01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY; PRT; 1171 AA
                                                                                                                                                                                                                                                                                                 0; Mismatches
InterPro; IPR001007; VWF_C.
Pfam; PF00009; EGF; 2.
Pfam; PF00090; TSP_1; 3.
Pfam; PF001212; TSP_2; 1.
Pfam; PF00093; VWC; 1.
Pfam; PF00093; VWC; 1.
PRINTS; PR00105; TSPIC; 1.
PRINTS; SM00181; EGF; 3.
SWART; SM00210; TSP1; 3.
SWART; SM00210; TSP1; 3.
SWART; SM00210; TSP1; 3.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01086; EGF_3; 2.
PROSITE; PS50025; TSP1; 3.
PROSITE; PS50026; TSP1; 3.
PROSITE; PS50026; TSP1; 3.
PROSITE; PS50128; VWFC_1; UNKNOWN_1.
PROSITE; PS50128; VWFC_2; 1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                                                208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                              1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEOUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombospondin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 QBOYQ1_MOUSE
QBOYQ1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                          엄
```

```
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 2.
Thrombospondin 1 (Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library, clone:G930018021 product:thrombospondin 1, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATRAINS_CZECH II. TISSUB=Mammary tumor metastatized to lung. Tumor arose spontaneously,
MEDILNE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 2; Length 1171; 100.0%; Pred. No. 0.12; 1.ive 0; Mismatches 0; Indels (
                                        SMR; Q80YQ1; 835-1170.

Ensembl; ENSMG0000040152; Mus musculus.

MGI; MGI:98737; Thbs1.

GO; GO:0005615; C:extracellular space; RCA.

GO; GO:0005615; P:negative regulation of angiogenesis; IDA.

InterPro; IPR013320; ConA_like_subgrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1171 AA; 129690 MW; 12E077B50C64E2D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QECGB2_MOUSE PRELIMINARY; PRT; 1171 AA.
Q8CGB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PROCIJOS; TSPIREPEAT.
SMART; SMO0181; EGF; 3.
SMART; SM00210; TSP1; 3.
SMART; SM00210; TSP1; 3.
SMART; SM00214; VWC; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS501208; VWFC 1; UNKNOWN 1.
PROSITE; PS50141; VWFC 2; 1.
SEQUENCE 1171 AA; 129690 MW; 12E07;
                                                                                                                                                                                                                                                                                        InterPro; IPR000742; EGF 3.
InterPro; IPR001881; EGF Ca bd.
InterPro; IPR001809; EGF Tike.
InterPro; IPR013012; EGF Tike reg.
InterPro; IPR013129; Laminin G TSP N.
EMBL; BC050917; AAH50917.1; -; mRNA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000884; TSP1.
InterPro; IPR008085; TSP 1.
InterPro; IPR003657; tsp 3.
InterPro; IPR0018659; TSP C.
InterPro; IPR001007; VWF C.
Pfam; PF00008; BGF; 2.
Pfam; PF002412; TSP 3; 12.
Pfam; PF02412; TSP 3; 12.
Pfam; PF05735; TSP C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
```

```
Pubbed=16141072; DDC=10.1126/science.1112014;

Pubbed=16141072; DDC=10.1126/science.1112014;

Pubbed=16141072; DDC=10.1126/science.1112014;

Pubbed=16141072; DDC=10.1126/science.1112014;

Pajic V. B., Brenner S. B., Batelbov S., Forrest A. R., Zavolan M., A Bajic V. B., Brenner S. B., Aidhinis V., Allen J. E.,

Ambesi-Impiombato A., Apweiler R., Attrailya R.N., Bailey T.L., Banal M., Baxer L. Delsel K.W., Bersano T., Enon H., Chalk A.M., Achinis V., Allen J. E.,

Ambesi-Impiombato A., Apweiler R., Attrailya R.N., Bailey T.L., And G. Boro B., Della Gatta G., Adin B. B., Dalla E., Dallary B.P., Regiolini M., Faulkner G., Adin B. B., Dalla E., Dallary B.P., Regiolini M., Paulkner G., Fletcher C.F., Fukushima T., Furuno M., Putaki S., Gariboldi M., Georgil-Hemming P., Gingersa T.R., Golobort T. Green R.B.,

Adin D., Huminecki L., Iacono M., Ikeso J., Kitamura H., Kitano H., Kollias G., Krishna S.P., Kruger A., Kummerfeld S.K., Kitano H., Kollias G., Krishna S.P., Kruger A., Kummerfeld S.K., Auteudia S., Morkillam S., Madan Babu M., Madaera M., Marchiconni L., Mowilliam S., Madan Babu M., Madaera M., Marchiconni L., Mowilliam S., Madan Babu M., Nakano N., Nakaro N., Nakaroki M., Nakaroki
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Iu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schorts R.M., Schain J.E., Schmutz J., Myers R.M., Schain J.E., Ones S.J.M., Marra M.A., Schain J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 309:1559-1563(2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse
```

NUCLEOTIDE SEQUENCE

```
RA MEDILE-EZASPESSY, FURDINGER-LEGGESSING MEDILE-LASSY REAL TO.

RA ANGARIA E., FURDING M., KASUKAWA T., AGACHA J., BODO H., KONDO S.,

RA ANGAL S., FURDING M., KASUKAWA Y., NOGAMIA A., SCHORDACH C., GGJODORI T.,

RA ANGARIA Y., TARSEGWA Y., NOGAMIA A., SCHORDACH C., GGJODORI T.,

RA BALGARELLI R., HILL D.P., BULL C., HUME D.A., QUACKERDURD J.,

RA SCHRIMI L.M., KANADIN A., MATSUCH H., BATALOV S., BEISEL K.M.,

RA BASE J.A., Brach D., BRISIC V., Chothia C., Corbania L.E., Cousins S.,

RA GASTERLIANG T., GARIBOIGH M., GISSI C., GOGZIK A., GOUGH J.,

RA GASTERLIANG T., GARIBOIGH M., GISSI C., GOGZIK A., GOUGH J.,

RA GASTERLIANG T., GARIBOIGH M., GISSI C., GOGZIK A., GOUGH J.,

RA MAGIST H., KAWASHA Y., KEGZISETSKI R.M., KING B.L.,

KONAGAYA A., KUNCOKKIN I.V., Lee Y., Lenhard B.L., Mixi H.,

RA MAGASHIMA T., NUMATA K., ONIGO T., PAVAN M., J., PERTEAG G., PESOLE G.,

RA RAYSI T., Reed J.C., Reed D.J., Reid J., Ring B.L.,

RA SANTAIN R., SCHNEIGHE C., SEMPLE C.A., SECTOU M., Shimada K.,

SANTAIN G., WYNSHAW-BOTIS A., YARAGHA R.D., TOMITA M.,

SANTAIN G., WYNSHAW-BOTIS A., YARAGWA T., KAWAB I.,

RA SHIRRA T., WARIA K., TAYJOR M.S., TEAGGIA R.D., TOMITA M.,

RA SHIRRA T., WARK K., KAWAB J., AIZAWA K., SARAZWA T., FUKUGA S.,

RA SHIRRA T., WARK K., KAWAB J., AIZAWA K., ARARWA T., FUKUGA S.,

RA SHIRRA T., WARK K., KAWAB J., AIZAWA K., ARARWA T., FUKUGA S.,

RA HIROZANE-KISHIKAWA T., KONDO H., NAKAWAT M., SARAZWA T., FUKUGA S.,

RA ALATA A., HASHIZUME W., IMOTANI K., ISHINIA K., SARAI K.,

RA ANGARA A., HASHIZUME W., IMOTANI K., ISHINA K., SHINAGAWA A.,

RA BITNEY E., HAYSHIZAKI Y., SARAKI K., SARAWA I.,

RA BITNEY E., HAYSHIZAKI Y., SARAKI K., SARAWA T.,

RA BITNEY E., HAYSHIZAKI Y.,

RA BITNEY E., HAYSHIZAKI Y.,

RA BITNEY E., RANGERSTOROM EASED ON FUNCTIONAL AND S.,

RATANISHI A., YOSHINO M., WATETSTORME BASED ON FUNCTIONAL AND S.,

RATANISHIS A., YOSHINO M., WATETSTORME BASED ON FUNCTIONAL AND S.,

RATANISHIS A., YOSHINO W.,

RA BITNEY E., RANGERSTORME BASED ON FUNCTIONAL AND S.,

RA BANDAR S.,

RA BANDAR S.,

RA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Mammary gland;

RA Kawai J. Shinataw A., Yoshino M., Itch M., Ishii Y.,

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa H.A., Ashburner M., Batalov S., Casawant T.,

RA Aisto T., Okazaki Y., Golobri T., Bono H., Kasukawa T., Saito R.,

RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

ROCHON P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Havashizaki Y.,

RA Hayashizaki Y.,

RA Hayashizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Mammary gland;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Garninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muxamatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
TISSUE=Mammary gland;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001).
                                                                                                                                                                                                                                        IISSUE=Mammary gland;
                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional
```

```
Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                               esion;
Repeat; Signal.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heparin-binding;
SIGNAL 1
CHAIN 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       918
954
23
929
155
158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394
398
409
450
454
465
507
511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                    Gaps
          MEDINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Niahi K., Kiteunai T., Tashiro H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kwai J., Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                     NUCLEOTIDE SEQUENCE.

TISSUE-Mammary gland;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Submitted (MAR-2004) to the EMBI/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=thbāl; Synonyms=tspl;
Senopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Urry L.A., Ramos J., Duquette M., Desimone D.W., Lawler J., "Cloning, characterization and expression of thrombospondin-1 in
                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 2; Length 1171; 100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1173 AA
                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                 ЕМВL; BC042422; AAH42422.1; -; mRNA.
EMBL; AK145202; BAE26293.1; -; mRNA.
HSSP; P07996; 1LSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994, sequence version 1. 07-MAR-2006, entry version 54. Thrombospondin-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus; Xenopus.
NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               208 FÓGVLÓNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                         1 FOGVLONVRFV 11
   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSP1 XENLA
ID TSP1 XENLA
AC P35448;
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                   Matches
```

δ 셤

```
TSP type-1 1.
TSP type-1 2.
TSP type-1 2.
TSP type-1 3.
EGF-11ke 1.
EGF-11ke 2.
EGF-11ke 3.
TSP type-3 1.
TSP type-3 2.
TSP type-3 4.
TSP type-3 4.
TSP type-3 5.
TSP type-3 5.
TSP type-3 7.
TSP type
                           R HSSP; D04278; -; NOT ANNOTATED CDS; MENA.

R HSSP; P07996; 11SL.

SWR; P35448; 552-1172.

INTECPTO; IPRO10510; EGF.

INTECPTO; IPRO10510; EGF.

INTECPTO; IPRO106210; EGF.

INTECPTO; IPRO106209; EGF.

INTECPTO; IPRO106209; EGF.

INTECPTO; IPRO10884; TSP.1.

R INTECPTO; IPRO10884; TSP.1.

R INTECPTO; IPRO10885; TSP.2.

INTECPTO; IPRO10885; TSP.2.

R INTECPTO; IPRO10985; TSP.1.

R INTECPTO; IPRO10985; TSP.2.

R INTECPTO; IPRO1097; VWF.C.

R PÉAM; PF07042; TSP.2.

R PÉAM; PF0735; TSP.2.

R PÉAM; PF0735; TSP.2.

R R SMART; SM00209; TSPL; 3.

R SMART; SM00209; TSPL; 3.

R SMART; SM00214; VWC; 1.

R PROSITE; PS01086; EGF.2; 1.

R PROSITE; PS01086; EGF.2; 1.

R PROSITE; PS01086; EGF.2; 1.

R PROSITE; PS01086; WWC.2; 1.

R PROSITE; PS01086; WWC.2; 1.

R PROSITE; PS01086; WWC.2; 1.

R PROSITE; PS01086; WWFC.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombospondin-1.
/FTId=PRO_000035844.
TSP_N-terminal.
L04278; -; NOT_ANNOTATED_CDS; mRNA.
```

g

ઠે

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barker D.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
- cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
laminin and type V collagen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-DEC-2004, sequence version 1.
21-FBB-2006, entry version 12.
Novel protein similar to vertebrate thrombospondin 1.\n\ (Fragment).
OKFNames-DKEY-11B23.1-001;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxIb=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 2; Length 1225; 100.0%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                1225 AA; 134849 MW; 9888B16E57157B12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMR1, QSSPG3, 751-804, 754-1099.

SMR1, QSSPG3, 751-804, 754-1099.

Ensembl; ENSDARG0000107085; Danio rerio.

GO; GO:0005376; C:extracellular region; IEA.

GO; GO:0005201; F:calcium ion binding; IEA.

GO; GO:0005195; F:sprotein binding; IEA.

GO; GO:0005195; F:sprotein binding; IEA.

GO; GO:0005195; F:structural molecule activity; IEA.

GO; GO:0005195; F:structural molecule activity; IEA.

InterPro; IPR013220; ConA_like_subgrp.

InterPro; IPR006210; EGF_3.

InterPro; IPR006210; EGF_3.

InterPro; IPR006209; EGF_1Ke.

InterPro; IPR006209; EGF_1Ke.

InterPro; IPR013012; EGF_1Ke.

InterPro; IPR013012; EGF_1Ke.

InterPro; IPR013012; EGF_1Ke.

InterPro; IPR013012; EGF_1Ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1090 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL928866; CA120599.1; -; Genomic_DNA
SMR; QSSPG5; 751-804, 754-1089.
                                                                                                                                                                                                                                             PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50092; TSPI; 3.
PROSITE; PS501208; VWFC 1; 1.
PROSITE; PS50184; VWFC 2; 1.
Cell adhesion; EGF-like domain.
NON TER 1255 AA; 134849 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSSPGS_BRARE PRELIMINARY;
QSSPGS;
                                                                                                                C; 1.
TSP1REPEAT
                   Pfam; PF00008; EGF; 2. — Pfam; PF00009; TSP 1; 3. — Pfam; PF02412; TSP 1; 3. — Pfam; PF02412; TSP 2; 1. — Pfam; PF00093; VWC; 1. — PRINTS; PR01705; TSPL95; SMART; SM0181; EGF; 3. SMART; SM0209; TSPL; 3. — SMART; SM0209; TSPL; 3. — SMART; SM0219; TSPL; 3. — SMART; SM0214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR008085; TSP_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 FQGVLQNVRFV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FOGULONVRFV 11
  InterPro; IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
QSSPG5 BRA
  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DER NEUGLE DER NEUGLE DER NEUGLE DER PARTE DER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Aorta endothelial cell;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama Totoki Y., Toyoda A., Takeda T., Sikuno F.R.;
None Title:";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 1; Length 1173; 100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                MW; A9F036D6516C0F24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AB209912; BAD93149.1; -; mRNA.

SNR, Q59E99; 886-939, 889-1225.

Ensembl; ENSG00000137801; Homo sapiens.

G0; G0.0005576; C:extracellular region; IEA.

G0; G0.0005509; F:calcium ion binding; IEA.

G0; G0.000511; F:heparin binding; IEA.

G0; G0.0005115; F:protein binding; IEA.

G0; G0.0005115; F:sprotein binding; IEA.

G0; G0.0005115; P:sprotein binding; IEA.

G0; G0.0005115; P:sprotein binding; IEA.

InterPro; IPR013320; ConAlike_subgrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2005, integrated into UniProtKB/TrEMBL
                                                              similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                    similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY; PRT; 1225 AA
                                                                                                                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                              similarity
                                                                                                                                                                                                                                                                                                                            similarity
                                                                                                                                                                                                                                                                                                                                               similarity
                                                                                                                                                                                                                                                                                                                                                                         similarity
                                                                                                                                                                                                                                                                                                                                                                                             similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF 3.
EGF Ca bd.
EGF like.
EGF like reg.
Laminin G TSP N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-2005, sequence version 1.
21-FEB-2006, entry version 10.
Thrombospondin 1 variant (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٥;
  130020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008085; TSP 1.
InterPro; IPR003367; tsp 3.
InterPro; IPR008859; TSP C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100 es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 FOGVLONVRFV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FQGVLQNVRFV 11
                                                                                                                                                                                                    716
741
777
800
836
859
897
933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001881;
InterPro; IPR006209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR013032;
InterPro; IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000884;
                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  913
949
1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                      602
623
653
660
681
708
721
757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 HUMAN
Q59E99 HUMAN
Q59E99;
                   DISULFID
DISULFID
DISULFID
                                                                                   DISULFID
DISULFID
DISULFID
                                                                                                                                                       DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
Q59E99_HUN
```

ö

Gaps

DAR X TO DAR BENEFIT OF THE STATE OF THE STA

```
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Surserora (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang K., Mauco G., Hauet T.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133256 MW; 6E8781648FCEC7F2 CRC64;
                                                                                                                      GO; GO:0005576; C:extracellular region; IEA.
GO; GO:000576; C:extracellular region; IEA.
GO; GO:000509; F:calcium ion binding; IEA.
GO; GO:000519; F:peparin binding; IEA.
GO; GO:000519; F:protein binding; IEA.
GO; GO:0007155; P:protein binding; IEA.
GO; GO:0007155; P:protein binding; IEA.
INTERPRO; IPRO06210; EGF.
INTERPRO; IPRO01821; EGF.
INTERPRO; IPRO01821; EGF.
INTERPRO; IPRO01821; EGF.
INTERPRO; IPRO01831; EGF.
INTERPRO; IPRO01831; EGF.
INTERPRO; IPRO01841; EGF.
INTERPRO; IPRO01864; TSP1.
INTERPRO; IPRO018055; TSP 1.
INTERPRO; IPRO019075; VWF.C.
                                                                        EMBL; CAAE01014723; CAG03524.1; -; Genomic_DNA.
SMR; Q4S758; 811-1148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50; DB 2;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
07-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY773342; AAV38110.1; -; mRNA.
InterPro; IPR000884; TSP1.
InterPro; IPR0018085; TSP 1.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE, PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS50027; TSPI; 3.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSPIREPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombospondin 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PP00008; BGF; 2. Pfam; PP00009; TSP 1; 3. Pfam; PP00109; TSP 2; 12. Pfam; PP001093; VWC; 1. Pfam; PP001093; VWC; 1. SMART; SM00101; EGF; 2. SMART; SM00210; TSP1; 3. SMART; SM00210; TSP1; 1. SMART; SM00210; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 FMGVLONVRFV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGULQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Thbs1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q5U903_PIG
Q5U903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
Q5U903_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                When the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
19-JUL-2005, sequence version 1.
Chromosome 14 SCAF14723, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENG00022976001;
Terracodon nigroviridis (Green puffer).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
NCBL_TAXID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope, Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.9%; Score 50; DB 2; Length 1090; 90.9%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5A9320504A22D836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00018; EF HAND 1; UNKNOWN 1. PROSITE; PS01186; EGF 2; I. PROSITE; PS50026; EGF 3; 2. PROSITE; PS50002; TSP1; 2. PROSITE; PS01208; VWFC 1; 1. PROSITE; PS51208; VWFC 2; 1. Cell adhesion; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1090 AA; 120978 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                         PRINTS, PRO1705, TSPIREPEAT.
SMART; SM00181; EGF; 2.
SMART; SM00209; TSP1; 2.
SMART; SM00210; TSP1; 2.
                                                                              Pfam; PF00008; EGF; 1. Pfam; PF00009; TSP 1; 2. Pfam; PF02412; TSP 3; 12. Pfam; PF05735; TSP C; 1. Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.9
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 FMGVLQNVRFV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLONVRFV 11
                                                           IPR001007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q4S758 TETNG
Q4S758;
                                                           InterPro;
                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
```

ద

ઠે

ö

Gaps

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

PubMed=15496914; DOI=10.1038/nature03025;

Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Mancell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Anthouard V., Jubin C., Castelli V., Retinka M., Vacherie B.,

Riemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Riemont C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

Rellis M., Volff J.-N., Gügo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2005, sequence version 1.
21-FEB-2006, entry version 8.
Chromosome 10 SCAF15019, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENGG0032374001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Tetradontoidea; Tetradontoidea; Tetraodontiformes; NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                     89.1%; Score 49; DB 2; Length 249; 100.0%; Pred. No. 0.36; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   249 249
249 AA; 27560 MW; 465D664BE0329C32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L; CAAE01015019; CAG10667.1; -; Genomic_DNA.

; QARLRS; 834-887, 837-1171.

GO:0005576; Cestracellular region; IEA.

GO:0005209; F:calcium ion binding; IEA.

GO:0008201; F:heparin binding; IEA.

GO:000515; F:protein binding; IEA.

GO:0005198; F:structural molecule activity; IEA.

GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O4RLR5;
19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY; PRT; 1171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the early vertebrate proto-karyotype.";
                                                 PRINTS; PRO1705; TSPIREPEAT.
SWART; SM00209; TSP1; 1.
PROSITE; PSC0022; TSP1; 1.
PROSITE; PSC0022; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS0184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
Les 10; Conservative
Pfam; PF00090; TSP 1; 2.
Pfam; PF00093; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QGVLQNVRFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QARLRS_TETNG
                                                                                                                                                                                                                        NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q4RLR5
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DER DER REGEREN FOR DER PRESENTATION DE PRESENTATION D
```

```
DR INTERPROPOSATOR SER 3.

DR INTERPROPOSATOR SER 3.

DR INTERPROPOSATOR SER 3.

DR INTERPROPOSATOR SER 1.

DR PÉRMI, PRO000094, TSP 1.

DR PÉRMI, PRO000094, TSP 1.

DR PÉRMI, PRO000095, TSP 1.3.

DR PÉRMI, PRO000095, TSP 1.3.

DR PÉRMI, PRO000095, TSP 1.3.

DR PRANTI, SMOOLO SER 1.

DR SWART; SMOOLO SER 1.

DR SWART; SMOOLO SER 1.

DR SWART; SMOOLO SER 1.

DR PROSITE; PSOLOSO SER 2.

DR PROSITE
```

THIS PAGE BLANK (USPTO)

```
Sequence 97, Application US/09939853A

Sequence 97, Application US/09939853A

Patent No. 6989232

GENERAL INFORMATION:

APPLICANT: Burgess et al.

TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-099

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/228,191

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-08

PRIOR PLING DATE: 2001-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOGVLQNVRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-09-949-002-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 482
LENGTH: 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 482, App
Sequence 97, Appl
Sequence 20, Appl
Sequence 25, Appl
Sequence 4205, Appl
Sequence 11112, A
Sequence 19, Appl
Sequence 164, Appl
Sequence 164, Appl
Sequence 10, Appl
Sequence 27744, Appl
Sequence 27744, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4891, Ap
267, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16180,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                 5, 2006, 22:43:07; Search time 21.9052 Seconds (without alignments) 43.955 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued Patents AA:*
: / EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
:: / EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
:: / EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:*
:: / EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-002-482
US-09-939-853A-97
US-09-939-853A-97
US-09-657-472-2
US-09-949-002-350
US-09-949-016-3350
US-09-949-016-11112
US-09-949-016-6333
US-09-949-016-3311
US-09-134-000C-3511
US-09-134-000C-3511
US-08-484-593B-10
US-08-484-595A-10
US-08-484-595A-10
US-08-484-595A-10
US-08-484-595A-10
US-08-484-595A-10
US-08-484-595A-10
US-08-484-595A-10
US-08-484-596A-10
US-08-484-596A-10
US-08-484-596A-10
US-08-484-596A-10
US-08-484-596A-10
US-08-484-596A-10
US-08-484-596A-10
US-08-489-331-10
US-08-489-331-10
US-08-489-331-10
US-08-489-331-10
US-08-499-331-10
US-08-499-2334-10
US-08-149-233A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-328-352-4891
US-09-199-637A-267
US-09-248-796A-16180
                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                           650591 seqs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                          US-10-030-735-30
55
1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1170
1170
1170
731
1045
1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7115
7115
944
1133
1175
1175
446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465
169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
10000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1
                                                                                                                                        June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .......
                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
```

```
Sequence 482, Application US/09949002
Sequence 482, Application US/09949002
Patent NO. 6900016
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT PILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 10823
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: PRESENCE: 0000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                          AP
AP
APP
APP
                                                               533,
                                                                                                         9538,
9539,
9540,
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                    Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                               Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55; DB 2; Length 825; 100.0%; Pred. No. 0.023; ive 0; Mismatches 0; Indels
US-09-134-000C-4331

US-09-949-016-6004

US-09-949-016-6791

US-09-949-016-6792

US-09-949-016-6793

US-09-949-016-6793

US-09-949-016-9333

US-09-949-016-9335

US-09-949-016-9335

US-09-949-016-9336

US-09-949-016-9338

US-09-949-016-9943
                                                                                                                                                                                      ALIGNMENTS
   5538
743
750
750
751
751
751
751
751
751
751
751
```

```
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-002-350
; Sequence 350, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
                                                                                                                                                                                                                                       20:
                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.v.
..hes 11; Conservative
                                                                                                                                                                                              TELEFAX: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FQGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               US-08-313-288B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-657-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                               generic 98, Application US/09939853A

paquence 98, Application US/09939853A

patent No. 6989222

GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION: No. 6989232e1 Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-099

CURRENT PILING DATE: 2001-08-27

PRIOR PILING DATE: 2000-08-25

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-20

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 98

LENGTH 831
                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                        100.0%; Score 55; DB 2; Length 831; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 2; Length 831; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
APPLICANT: USBSELI, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCES:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 1036
COMPUTER: ROADELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILIN Release #1.0, Version #1.30
                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 11, Conservative
NUMBER OF SEQ ID NOS: 159
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 97
LENGTH: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 FOGVLÓNVRFV 218
                                                                                                                                                                                                                                         1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Mus musculus
US-09-939-853A-98
                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                 US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-313-288B-20
                                                                                                                       US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                g
```

```
Gaps
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o;
                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LARGARILON
APPLICANT: Cargill, Michele
APPLICANT: Cargill, Michele
APPLICANT: Leland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, Stacey
APPLICANT: Bolk, George Q.
APPLICANT: Daley, George Q.
APPLICANT: Moranette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT APPLICATION NUMBER: US 60/153,357
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR PELLING DATE: 1999-09-10
PRIOR FILING DATE: 2000-09-46
PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SEQ ID NOS: 2551
SEQ ID NOS: 2551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 2; Length 1170; 100.0%; Pred. No. 0.033; cive 0; Mismatches 0; Indels (
100.0%; Score 55; DB 1; Length 1170; 100.0%; Pred. No. 0.033; ive 0; Mismatches 0; Indels
```

```
Gaps
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                  67.3%; Score 37; DB 2; Length 1045; 63.6%; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.3%; Score 37; DB 1; Length 1172; 63.6%; Pred. No. 1.1e+02; tive 2; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUMPINITY OF THE COMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 1900 A 1000 A 1
                                                                                                                                                                                                                                                                                   2; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11112
LENGTH: 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %30-949-016-6333
; Sequence 6331, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 1172 amino acids
                                                                                                                                                                                           Query Match
Best Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.3
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    |:|:|||| |
281 FRGLLQNVHLV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|:|||| |
202 FRGLLQNVHLV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                              ORGANISM: Human
                                                                                                                                                           US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-313-288B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             쉽
                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11112, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPRENCE: CLOOM1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PLING DATE: 2000-09-08

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYEMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00790
CURRENT PAPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: u3/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42057
LENGTH: 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 2; Length 1170; 100.0%; Pred. No. 0.033; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.9%; Score 39; DB 2; Length 731; 80.0%; Pred. No. 27; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Xaa means any amino acid US-09-270-767-42057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42057, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 FÓGVLÓNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGULQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 QGVLQNVDFM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
US-09-949-002-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-270-767-42057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-016-11112
                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 350
LENGTH: 1170
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

```
76 FOGVLROIR 84
                                                                                                                                                                                                                                                                                                                                                                                              1 FOGVLQNVR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-583-110-3429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-484-993B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                ò
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO130
CURRENT PAPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR PELICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3511, Application US/09134000C
Sequence 3511, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%; Score 37; DB 2; Length 1172; 63.6%; Pred. No. 1.1e+02; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 2;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 164, Application US/09769787
Patent No. 6936252
GERERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Microbial Technics Limited
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proceins
CURRENT APPLICATION NUMBER: US/09/769, 787
CURRENT APPLICATION NUMBER: GB 9816337.1
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Streptococcus pneumoniae US-09-769-787-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.6%;
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.3
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|:||| |
202 FRGLLQNVHLV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | |:|::|
245 FNGTLENIKF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLONVRF 10
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-134-000C-3511
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-769-787-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

```
; NAME/KEY: MISC_FEATURE
; LOCATION: (29)...(70)
; OTHER INFORMATION: Amino acids 29, 30, 59 & 70 are Xaa wherein Xaa = any amino acid
US-09-134-000C-3511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3429.
Sequence Relating to Streptococcus TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus TITLE OF INVENTION: NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
NUMBER: OF SEQ ID NOS: 5322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08484993B

Sequence 10, Application US/08484993B

Patent No. 5837497

GENERAL INFORMATION:

APPLICANT: Harris Ph.D., Jeffrey D.

APPLICANT: Hau, Kuang T.

APPLICANT: Hau, Kuang T.

APPLICANT: How, Kuang T.

APPLICANT: APPLICANT: Application of Sequences: 59

CORRESPONDENCE ADDRESS: 59

CORRESPONDENCE ADDRESS: 0'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 459;
                                                                                                                                                                                                                                                                                                                              Score 34; DB 2; Length 169;
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 2; Length 459
Pred. No. 1.5e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3429
                                                                                                                                  TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%;
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3511
LENGTH: 169
                                                                                                                                                                                                                                                                                                                                    61.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                 Query Match 61.8
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 61.8
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 FKATLENVOFV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGULQNVRFV 11
```

```
Search completed: June
Job time: 21.9052 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-484-158B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.8%; Score 34; DB 1; Length 715; Best Local Similarity 70.0%; Pred. No. 2.5e+02; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Us-ue-que-loud Application US/08484158B

Patent No. 5976545

GENERAL INFORMATION:
Patent No. 5976545

GENERAL INFORMATION:
PAPPLICANT: Harris Ph.D., Jeffrey D. APPLICANT: Harris Pharmaceutical Compositions for TITLE OF INVENTION: Immunocontraception
TITLE OF INVENTION: Immunocontraception
TITLE OF INVENTION: Immunocontraception
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,158B
FILING DATE: 07-JUNE-95
CLASSIFICATION NUMBER: 08/149,223
FRIOR APPLICATION NUMBER: 08/149,223
FRIUNG DATE: 09-NOV-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-93
                       COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOSTAME: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,993B
FILING DATE: 09-NOV-1993
CLASSIFICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 31745
TELEPHONE: 312/474-6653
TELEFRAME/LOCKET NUMBER: 31745
TELEFRAME/LOCKET NUMBER: 31746
TELEFRAME 312/474-6653
TELEFRAME/LOCKET NUMBER: 31747-6653
TELEFRAME/LOCKET NUMBER: 317/474-6653
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 715 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 FPGKLQSVRF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FQGVLQNVRF 10
      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-08-484-158B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-484-993B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
```

```
## PRIOR APPLICATION DATA:

## APPLICATION NUMBER: 07/973,341

## PILING DATE: 09-NOV-92

## ATTORNEY AGENT INFORMATION:

## REGISTRATION NUMBER: 36,107

## REFERENCE/DOCKET NUMBER: 32794

## TELECOMMUNICATION INFORMATION:

## TELECOMMUNICATION:

## TELECOMMUNICATION INFORMATION:

## TELECOMMUNICATION:

## TELECCOMMUNICATION:

## TELECOMMUNICATION:

## TELECCOMMUNICATI
```

THIS PAGE BLANK (USPTO)

```
7, Appli
12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40, Appl
1020, Ap
1022, Ap
462, App
454, App
456, App
456, App
452, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97, Appl
98, Appl
461, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Appl
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Appl
Sequence 40, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appli
                                                                                                                                                                                                                                                                                               /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*/
                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    (without alignments)
70.701 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 452,
Sequence 453,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40,
Sequence 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 458,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 462
                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1
Sequence 4
Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3
Sequence 3
Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                          5, 2006, 23:46:43 ; Search time 72.069 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-419-462-40
US-10-741-600-1020
US-10-741-600-1020
US-11-043-806-462
US-11-043-806-454
US-11-043-806-454
US-11-043-806-454
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-455
US-11-043-806-451
US-11-043-806-451
US-11-043-806-451
US-10-029-733-1
US-10-029-733-1
US-10-021-818-7
US-10-021-818-7
US-10-021-818-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-295-027-1170
US-10-211-462-38
US-10-231-956A-482
                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        Published_Applications_AA_Main: *
                                                                                                                                                                       2097797 seqs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                   Listing first 45 summaries
                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                              Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                  US-10-030-735-30
55
1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              855
1000
1105
1150
1152
1169
                                                                                                                                          BLOSUM62
                                                          June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                        Database
                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š.
```

```
28 55 100.0 1170 4 US-10-419-462-38 Sequence 38, Appl 30 55 100.0 1170 5 US-10-741-600-1018 Sequence 1018, Ap 30 55 100.0 1170 5 US-10-741-600-1019 Sequence 1018, Ap 30 55 100.0 1170 5 US-10-741-600-1019 Sequence 1021, Ap 30 55 100.0 1170 5 US-10-748 Sequence 1021, Ap 30 55 100.0 1170 5 US-10-849-989-44 Sequence 348, Appl 34 55 100.0 1170 5 US-10-811-997-2 Sequence 548, Appl 35 55 100.0 1170 5 US-10-811-997-2 Sequence 548, Appl 36 55 100.0 1170 5 US-10-811-997-2 Sequence 596, Appl 37 55 100.0 1170 5 US-10-995-561-594 Sequence 596, Appl 38 55 100.0 1170 5 US-10-995-561-594 Sequence 596, Appl 40 55 100.0 1170 6 US-11-046-44-28 Sequence 596, Appl 41 55 100.0 1170 6 US-11-046-44-28 Sequence 21, Appl 42 51 100.0 1170 6 US-11-046-44-28 Sequence 21, Appl 44 39 70.9 226 5 US-10-46-359 Sequence 1133, Appl 44 39 70.9 226 5 US-10-46-359 Sequence 12287, Appl 45 39 70.9 721 6 US-11-097-143-13287 Sequence 13287, AUS-10-474-213-28
```

```
RESULT 6
US-11-043-806-462
US-11-043-806-462
Full-1043-806-462
Publication No. US20060051774A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                        Sequence 1022, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 1022
LEMETH: MINGOWS VERSION 4.0
SEQ ID NO 1022
LEMETH: MINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 55; DB 6; Length 459;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 5; Length 432; 100.0%; Pred. No. 0.048;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
COCATION: (1)...(432)
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1047, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                   208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOGVLQNVRFV 11
                                                                  1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-925-301-1047
                                                                                                                                                                              RESULT 5
US-10-741-600-1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-043-806-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                     ઠે
                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-10-782-968-40

Sequence 40, Application US/10782968

Publication No. US20050065324A1

GENERAL INFORMATION:
APPLICANT: Williams, Kevin J.

TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents;
FILE REPERENCE: Wil07-20005

CURRENT FILING DATE: 2004-02-20

FRIOR PELICATION NUMBER: US/10/782,968

CURRENT FILING DATE: 2003-04-21

NUMBER OF SEQ ID NOS: 53

SSOFTMARE: PatentIn version 3.2

LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4

US-10-741-600-1020

Sequence 1020, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001499

FURBRAY FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SEQ ID NO 1020

LENGTH A32
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                         ; OTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-419-462-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Thrombospondin Region plus N-terminal domain US-10-782-968-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 55; DB 5; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 432;
                                                                                                                                                       Score 55; DB 4; Length 240;
Pred. No. 0.025;
                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
LOCATION: (1)...(432)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative 0,
                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                             190 FOGVLONVRFV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 FOGVLONVRFV 200
                                                                                                                                                                                                                                                 1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-741-600-1020
      LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                    ઠે
```

```
Sequence 452, Application US/11043806

Publication No. US20060051774A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Method

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

FILE REFERENCE: 1847.1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Method
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION WINBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-043-806-455

Sequence 455, Application US/11043806

Sequence 455, Application No. US20060051774A1

Sequence 455, Application No. US20060051774A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer

FILE REFERENCE: 1847.1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT PILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 55; DB 6; Length 685; 100.0%; Pred. No. 0.079; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 6; Length 804; 100.0%; Pred. No. 0.093; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 453, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                     208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FÓGVLÓNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGULQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                  RESULT 10
US-11-043-806-452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-043-806-453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 453
LENGTH: 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                     g
                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 454, Application US/11043806
Publication No. US20060051774A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Infereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-11-043-806-456

Sequence 456, Application US/11043806

Sequence 456, Application US/11043806

Sequence 456, Application US/1104316

Fublication No. US20060051774A1

GENERAL INFORMATION:

TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer

TITLE OF INVENTION: Thereof for Diagnosis of Prostate Cancer

FILE REFERENCE: 1847-1003

CURRENT APPLICATION NUMBER: US/11/043,806

CURRENT FILING DATE: 2005-01-27

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 456

LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1047
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 6; Length 555; 100.0%; Pred. No. 0.063;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 55; DB 3; Length 466; Best Local Similarity 100.0%; Pred. No. 0.052; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 55; DB 6; Length 578; Best Local Similarity 100.0%; Pred. No. 0.065; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 FÓGVLÓNVRFV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 POGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-925-301-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT GAGANISM: Homo sapiens US-11-043-806-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-043-806-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

Gaps

ö

```
Publication No. US20060051774A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
TITLE OF INVENTION: US9200501774
TITLE OF INVENTION: UNABERIED OF US9300505
TITLE REPERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 461
LENGTH: 855
                                                     100.0%; Score 55; DB 3; Length 831; 100.0%; Pred. No. 0.097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 6; Length 855; 100.0%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6, 2006, 00:00:11
                                                        Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                  208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 FOGVLONVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FOGVLQNVRFV 11
                                                                                                                                                                            1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-11-043-806-461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: June
Job time: 72.069 secs
US-09-939-853A-98
                                                                                                                                                                                                                                                                                                                                                            US-11-043-806-461
                                                                                                                                                                                  ð
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13

US-09-939-853A-97

Squence 97, Application US/09939853A

Publication No. US20040039163A1

GENERAL INFORMATION:

APPLICANT BUGGES et al.

TILLE OF INVENTION: No. US2004003163A1el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099

CURRENT APPLICATION NUMBER: US/09/939,853A

CURRENT APPLICATION NUMBER: 60/228,191

PRIOR FILING DATE: 2001-08-25

PRIOR FILING DATE: 2001-08-26

PRIOR FILING DATE: 2001-02-20

PRIOR PRIOR APPLICATION NUMBER: 60/277,337

PRIOR FILING DATE: 2001-03-20

PRIOR APPLICATION NUMBER: 60/277,337

PRIOR PRIOR APPLICATION NUMBER: 60/277,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NESOUR 14

Sequence 98, Application US/09939853A

Sequence 98, Application US/09939853A

Sequence 98, Application US/09939853A

SEQUENCE 10 NO. US20040039163A1el Proteins and Nucleic Acids Encoding Same

FILE OF INVENTION: NO. US20040039163A1el Proteins and Nucleic Acids Encoding Same

FILE REPERENCE: 21402-099

CURRENT APPLICATION NUMBER: 06/228,191

PRIOR PILING DATE: 2001-08-25

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-03-06

PRIOR FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SEQ ID NOS: 159

SEQ ID NO 98

LENGTH: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 55; DB 3; Length 831; 100.0%; Pred. No. 0.097; ive 0; Mismatches 0; Indels
                                                                                                                                   Query Match
100.0%; Score 55; DB 6; Length 828;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                208 FQGVLQNVRFV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 FÓGVLÓNVRFV 218
                                                                                                                                                                                                                                                                          1 FOGULQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQGVLQNVRFV 11
; LENGTH: 828
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-806-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Homo sapiens
US-09-939-853A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

; 0

Gaps

°

4177, Ap 3000, Ap 15318, A 27518, A

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Run on:

Seguence:

₹.

```
Sequence 9347, Application US/10953349
Sequence 9347, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
THILE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34674, Application US/10953349
PUDLICATION NO. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDRO, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERRANCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: 204-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 34674
LENGTH: 331
TYPE: PRT
Sequence 28989, A Sequence 2388, Ap Sequence 2387, Ap Sequence 2898, A Sequence 2641, Ap Sequence 2641, Ap Sequence 31207, A Sequence 31207, A Sequence 31207, A Sequence 31207, A Sequence 36, Appl Sequence 36, Appli Sequence 37322, A Sequence 36, Appli Sequence 37322, A Sequence 36, Appli Sequence 37322, A Sequence 37322, A
                                                                                                                                                                                                                                                                                                               Sequence 3
Sequence 4
Sequence 3
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
US-10-953-349-28989
US-10-953-349-2888
US-10-953-349-2888
US-10-953-349-28988
US-10-953-349-28988
US-10-953-349-2644
US-10-953-349-2642
US-10-953-349-2642
US-11-293-697-4335
US-11-293-697-4335
US-11-247-366
US-11-247-376-5
US-11-247-376-5
US-110-953-349-31730
US-110-953-349-31730
US-110-953-349-31730
US-110-953-349-31730
US-110-953-349-31730
US-110-953-349-31730
US-110-953-349-31730
US-110-953-349-31730
US-110-953-349-31730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 6
Pred. No. 14;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Arabidopsis thaliana US-10-953-349-9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Zea mays subsp. mays US-10-953-349-34674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.0%;
Matches 4; Conservative !
    2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|::| |:|:
87 EGIIQGVKFI 96
    US-10-953-349-34674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 9347
LENGTH: 298
TYPE: PRT
      Query Match
      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9347, Ap Sequence 34674, A Sequence 34672, A Sequence 16526, A Sequence 16526, A Sequence 16526, A Sequence 2, Applisequence 2, Applisequence 2, Applisequence 39312, A Sequence 39134, A Sequence 39136, A Sequence 3586, Ap Sequence 24689, A Sequence 25200, A Sequence 25323, Ap Sequence 2323, Ap Sequence 2323,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3323, 1
Sequence 28990,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA New:*

1. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

4. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

6. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
                                                                                                                                              6, 2006, 00:00:38 ; Search time 3.41379 Seconds (without alignments) 37.266 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                            GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-953-349-9347

US-10-953-349-34673

US-10-953-349-34673

US-10-953-349-34673

US-10-511-937-2413

US-10-953-349-16526

US-10-953-349-16526

US-11-203-349-16526

US-11-203-349-16526

US-11-203-349-39312

US-10-953-349-39313

US-10-953-349-39136

US-10-953-349-39136

US-10-953-349-39136

US-10-953-349-39136

US-10-953-349-24689

US-10-953-349-26200

US-10-953-349-26200

US-10-953-349-26200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-511-937-2992
US-11-293-697-3323
US-10-953-349-28990
                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                58871 segs, 11565156 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                US-10-030-735-30
55
1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         June
```

ö

Gaps

ö

Score

Result Š.

```
Sequence 16527, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579P028
FULR REFERENCE: 2750-1579P028
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN Version 3.3
SEQ ID NO 16527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16526, Application US/10953349
Publication No. US20060107345A1
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                    APPLICANT: Freille, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104 [71]
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-0-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.2%; Score 32; DB 6; Length 843; 54.5%; Pred. No. 72; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.0%; Score 33; DB 6; Length 750; 40.0%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 54.8
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     780 FKGILDNYVFV 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: ::||::|
508 FENIIONLKF 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGVLQNVRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-10-953-349-16526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-953-349-16527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-953-349-16527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-511-937-2413
                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2413
LENGTH: 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICATION NO. U320060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
APPLICANT: ALEXANDROW, Nickolai et al.
APPLICANT: ALEXANDROW, Nickolai et al.
APPLICANT: BENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34672, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROY, Nickolai et al.
ATITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 60.0%; Score 33; DB 6; Length 358; Best Local Similarity 60.0%; Pred. No. 18; Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.0%; Score 33; DB 6; Length 382; 60.0%; Pred. No. 19; ive 3; Mismatches 1; Indels
                        Indels
                          1;
  Pred. No. 16;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-10-511-937-2413
Sequence 2413, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OKGANISM: Zea mays subsp. mays US-10-953-349-34672
    60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 6; Conservative
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 QGVLFNIQYV 285
                                                                                                225 QGVLFNIQYV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 QGVLFNIQYV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QGVLQNVRFV 11
                                                                      2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QGVLQNVRFV 11
                                                                                                                                                                                     RESULT 3
US-10-953-349-34673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-953-349-34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 34673
LENGTH: 358
                                                                      δ
                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
Sequence 39312, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROW, NICKOLAI EN APPLICANTON: ENCONDED THERRY
TITLE OF INVENTION: ENCONDED THERRY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                             APPLICANT: Genzyme Corporation
APPLICANT: Roberts, Bruce
TITLE OF INVENTION: METHODS TO DIAGNOSE AND TREAT LUNG CANCER
FILE REFERENCE: 5257C
CURRENT FILING DATE: 2005-10-11
PRIOR APPLICATION NUMBER: US/11/247,437
PRIOR PLILING DATE: 2005-10-11
PRIOR PLING DATE: 2004-04-12
PRIOR PLING DATE: 2003-04-10
PRIOR PLING DATE: 2003-04-10
PRIOR PLING DATE: 2003-04-10
SPRIOR PLING DATE: 2003-04-10
SPRIOR PLING DATE: 2003-04-10
SPRIOR PLING DATE: 2003-04-10
SPRIOR PLING DATE: 2003-04-10
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 7; Length 855;
Pred. No. 1.2e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 6; Length 132;
Pred. No. 23;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3713, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
SEQUENCY: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
FRIOR PPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
                                                            ; Sequence 2, Application US/11247437; Publication No. US20060110753A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays subsp. mays US-10-953-349-39312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|:| | |:
66 FEGILNNNVFI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||:||:|
445 RGVYENVKYV 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-247-437-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-953-349-39312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-293-697-3713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 39312
LENGTH: 132
                                              US-11-247-437-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                       Sequence 16525, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICATION NO. US20060107345A1
GENERAL INFORMATION:
APPLICATION NICKOLAI et al.
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARKE: PALENTIN VERSION 3.3
SOFTWARKE: PALENTIN VERSION 3.3
SEQ ID NO 16525
LENGTH: 1014
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/11203828
Publication No. US20060110390A1
GENERAL INFORMATION:
APPLICANT: LEINWAND, LESLIE
APPLICANT: SUCHAROV, CARMEN
TITLE OF INVENTION: INHIBITION OF KU AS A TREATMENT FOR CARDIOVASCULAR;
TITLE OF INVENTION: DISEASES
FILE REFERENCE: MYOG:58US
CURRENT APPLICATION NUMBER: US/11/203,828
CURRENT FILING DATE: 2005-08-15
PRIOR FILING DATE: 2004-08-24
PRIOR FILING DATE: 2004-08-24
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.2%; Score 32; DB 6; Length 1014; 54.5%; Pred. No. 89;
                                                                                                                                 DB 6; Length 962;
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 7; Length 608; Pred. No. 80; 3; Mismatches 1; Indels
                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                             Mismatches
                                                                                                                                 Score 32;
Pred. No. 8
                                                                                                                               Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.4%;
ilarity 55.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 608
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 54.8
Matches 6; Conservative
                                                                                                                                                                                                                                                   899 FKGILDNYVFV 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FOGVLONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : ::|||||
461 KAIVQNVRF 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus
US-11-203-828-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QGVLQNVRF 10
                                         TYPE: PRT
CORGANISM: Glycine max
US-10-953-349-16526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Glycine max
US-10-953-349-16525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                         US-10-953-349-16525
; SEQ ID NO 16526
; LENGTH: 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-11-203-828-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

ઠે

```
Sequence 39137, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROW, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2700-1579PUS2

CURRENT PELING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NO 39137
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 6; Length 265;
Pred. No. 50;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: June 6, 2006, 00:12:56 Job time : 3.51379 secs
                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Zea mays subsp. mays US-10-953-349-39137
                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 54.5
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 LRNVRFV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LQNVRFV 11
                        US-10-953-349-39137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3866, Application US/10953349
GENERAL INFORMATION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION UNMER: 0.5/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 3586
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39138, Application US/10953349
Sequence 39138, Application US/10953349
Sequence 39138, Application US/10953349
Sequence 39138, Application US/10953349
GENERAL INFORMATION: USCOUGO107345A1
GENERAL INFORMATION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579FUS2
CURRENT APPLICATION UNMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 39138
LENGTH: 227
TYPE: FRT
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 54.5%; Score 30; DB 6; Length 227; Best Local Similarity 85.7%; Pred. No. 42; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 6; Length 251;
Pred. No. 47;
4; Mismatches 2; Indels
                                                                                                                                                                            Score 30; DB 7; Length 178;
Pred. No. 32;
                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Zea mays subsp. mays US-10-953-349-39138
                                                                                                                                                                              54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.5%;
; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO 3713; LENGTH: 178; TYPE: PRT; TYPE: PRT; CAPANISM: Homo sapiens US-11-293-697-3713
                                                                                                                                                          Query Match
Best Local Similarity 45.57
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                  1 FOGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FQGVLQNVRFV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 FOCHIENLPFL 90
                                                                                                                                                                                                                                                                                                             4 FOAVVWNLNFI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|||||
183 LRNVRFV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LONVRFV 11
                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-10-953-349-39138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-953-349-3586
                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```